Title	Changes in Cell Wall Structure During Rhizoid Formation of Silvetia babingtonii (Fucales, Phaeophyceae) Zygotes
Author(s)	Yonamine, Rina; Ichihara, Kensuke; Tsuyuzaki, Shiro; Hervé, Cécile; Motomura, Taizo; Nagasato, Chikako
Citation	Journal of phycology, 57(4), 1356-1367 https://doi.org/10.1111/jpy.13178
Issue Date	2021-05-01
Doc URL	http://hdl.handle.net/2115/85093
Rights	This is the peer reviewed version of the following article: Yonamine, R., Ichihara, K., Tsuyuzaki, S., Hervé, C., Motomura, T. and Nagasato, C. (2021), Changes in Cell Wall Structure During Rhizoid Formation of Silvetia babingtonii (Fucales, Phaeophyceae) Zygotes. J. Phycol., which has been published in final form at https://doi.org/10.1111/jpy.13178. This article may be used for non-commercial purposes in accordance with Wiley Terms and Conditions for Use of Self-Archived Versions.
Type	article (author version)
Additional Information	There are other files related to this item in HUSCAP. Check the above URL.
File Information	Table S4-S9.pdf

Table S4. The list of longest ORF contigs in *S. babingtonii*

Contig name	description	e value	GO (GOID)	GO name
comp100001_c0_seq1.p1	sp|P0ADU5|YGIW_ECOLI_Protein_ygiW_OS=Escherichia_coli_(strain_K12)_GN=ygiW_PE=1_SV=1	2.00E-69	GO:0030288,GO:0030288,GO:0042597,GO:0042597,GO:0044011,GO:0070301,GO:0071276	outer membrane-bounded periplasmic space,outer membrane-bounded periplasmic space,periplasmic space,periplasmic space,single-species biofilm formation on inanimate substrate,cellular response to hydrogen peroxide,cellular response to cadmium ion
comp100008_c0_seq1.p1				
comp100032_c0_seq1.p1				
comp100068_c0_seq1.p1				
comp100098_c0_seq1.p1				
comp10012_c0_seq1.p1				
comp10013_c0_seq1.p3				
comp10013_c1_seq1.p1				
comp100145_c0_seq1.p1	sp|P75915|YCDY_ECOLI_Chaperone_protein_YcdY_OS=Escherichia_coli_(strain_K12)_GN=ycdY_PE=1_SV=1	4.00E-74	GO:0005515,GO:0005515,GO:0006974,GO:0071978	protein binding,protein binding,cellular response to DNA damage stimulus,bacterial-type flagellum-dependent swarming motility
comp100158_c0_seq1.p2	sp|P0AGI0|PSTC_SHIFL_Phosphate_transport_system_permease_protein_pstC_OS=Shigella_flexneri_GN=pstC_PE=3_SV=1	5.00E-62	GO:0005315,GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006810,GO:0006817,GO:0006817,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0055085	inorganic phosphate transmembrane transporter activity,plasma membrane,plasma membrane,plasma membrane,transport,transport,phosphate ion transport,phosphate ion transport,membrane,membrane,integral component of membrane,integral component of membrane,transmembrane transport
comp10025_c0_seq1.p1				
comp100258_c0_seq1.p2				
comp10036_c0_seq1.p1	sp|Q86FP7|RS23_DERVA_40S_ribosomal_protein_S23_OS=Dermacentor_variabilis_GN=RpS23_PE=2_SV=1	1.00E-79	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0015935,GO:0030529	structural constituent of ribosome,intracellular,ribosome,ribosome,translation,small ribosomal subunit,ribonucleoprotein complex
comp100369_c0_seq1.p1	sp|P00957|SYA_ECOLI_Alanine--tRNA_ligase_OS=Escherichia_coli_(strain_K12)_GN=alaS_PE=1_SV=2	1.00E-101	GO:0000049,GO:0000166,GO:0000166,GO:0001141,GO:0002161,GO:0002161,GO:0003676,GO:0003723,GO:0004812,GO:0004813,GO:0004813,GO:0004813,GO:0004813,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0006412,GO:0006419,GO:0006419,GO:0006419,GO:0006450,GO:0006450,GO:0008270,GO:0008270,GO:0016020,GO:0016874,GO:0016876,GO:0042802,GO:0043039,GO:0045892,GO:0046872	tRNA binding,nucleotide binding,nucleotide binding,bacterial-type RNA polymerase core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription,aminoacyl-tRNA editing activity,aminoacyl-tRNA editing activity,nucleic acid binding,RNA binding,aminoacyl-tRNA ligase activity,alanine-tRNA ligase activity,alanine-tRNA ligase activity,alanine-tRNA ligase activity,alanine-tRNA ligase activity,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytosol,translation,alanyl-tRNA aminoacylation,alanyl-tRNA aminoacylation,alanyl-tRNA aminoacylation,regulation of translational fidelity,regulation of translational fidelity,zinc ion binding,zinc ion binding,membrane,ligase activity,ligase activity, forming aminoacyl-tRNA and related compounds,identical protein binding,tRNA aminoacylation,negative regulation of transcription, DNA-templated,metal ion binding
comp10038_c0_seq1.p1				
comp10039_c0_seq1.p1				
comp10039_c0_seq1.p2				
comp100428_c0_seq1.p1	sp|P43644|DNJH_ATRNU_DnaJ_protein_homolog_ANJ1_OS=Atriplex_nummularia_PE=2_SV=1	2.00E-22	GO:0005524,GO:0006457,GO:0009408,GO:0016020,GO:0016020,GO:0031072,GO:0046872,GO:0051082	ATP binding,protein folding,response to heat,membrane,membrane,heat shock protein binding,metal ion binding,unfolded protein binding
comp10045_c0_seq2.p1				
comp100467_c0_seq1.p1	sp|P36683|ACON2_ECOLI_Aconitate_hydratase_2_OS=Escherichia_coli_(strain_K12)_GN=acnB_PE=1_SV=3	6.00E-17	GO:0003729,GO:0003729,GO:0003730,GO:0003994,GO:0003994,GO:0003994,GO:0003994,GO:0005515,GO:0005829,GO:0006097,GO:0006099,GO:0006099,GO:0006099,GO:0006099,GO:0006417,GO:0008152,GO:0016829,GO:0019629,GO:0046872,GO:0047456,GO:0047456,GO:0051536,GO:0051539,GO:0051539,GO:0051539	mRNA binding,mRNA binding,mRNA 3'-UTR binding,aconitate hydratase activity,aconitate hydratase activity,aconitate hydratase activity,aconitate hydratase activity,protein binding,cytosol,glyoxylate cycle,tricarboxylic acid cycle,tricarboxylic acid cycle,tricarboxylic acid cycle,tricarboxylic acid cycle,regulation of translation,metabolic process,lyase activity,propionate catabolic process, 2-methylcitrate cycle,metal ion binding,2-methylisocitrate dehydratase activity,2-methylisocitrate dehydratase activity,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp10050_c0_seq1.p1	sp|P53007|TXTP_HUMAN_Tricarboxylate_transport_protein,_mitochondrial_OS=Homo_sapiens_GN=SLC25A1_PE=1_SV=2	1.00E-31	GO:0005634,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0005743,GO:0005743,GO:0005975,GO:0006006,GO:0006094,GO:0006810,GO:0015137,GO:0015746,GO:0016020,GO:0016021,GO:0019432,GO:0035338,GO:0044255,GO:0044281,GO:0055085,GO:0070062,GO:0070062	nucleus,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,carbohydrate metabolic process,glucose metabolic process,gluconeogenesis,transport,citrate transmembrane transporter activity,citrate transport,membrane,integral component of membrane,triglyceride biosynthetic process,long-chain fatty-acyl-CoA biosynthetic process,cellular lipid metabolic process,small molecule metabolic process,transmembrane transport,extracellular vesicular exosome,extracellular vesicular exosome
comp100520_c0_seq1.p1	sp|P23930|LNT_ECOLI_Apolipoprotein_N-acyltransferase_OS=Escherichia_coli_(strain_K12)_GN=lnt_PE=1_SV=1	5.00E-91	GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005887,GO:0006807,GO:0016020,GO:0016021,GO:0016021,GO:0016410,GO:0016410,GO:0016410,GO:0016740,GO:0016746,GO:0016787,GO:0016810,GO:0042158,GO:0042158,GO:0042158	plasma membrane,plasma membrane,plasma membrane,plasma membrane,integral component of plasma membrane,nitrogen compound metabolic process,membrane,integral component of membrane,integral component of membrane,N-acyltransferase activity,N-acyltransferase activity,N-acyltransferase activity,transferase activity,transferase activity, transferring acyl groups,hydrolase activity,hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds,lipoprotein biosynthetic process,lipoprotein biosynthetic process,lipoprotein biosynthetic process
comp100546_c0_seq1.p1	sp|P43329|HRPA_ECOLI_ATP-dependent_RNA_helicase_hrpA_OS=Escherichia_coli_(strain_K12)_GN=hrpA_PE=3_SV=3	8.00E-94	GO:0000166,GO:0003676,GO:0004004,GO:0004004,GO:0004386,GO:0004386,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0006200,GO:0006200,GO:0006200,GO:0006397,GO:0008026,GO:0009451,GO:0016787,GO:0044822	nucleotide binding,nucleic acid binding,ATP-dependent RNA helicase activity,ATP-dependent RNA helicase activity,helicase activity,helicase activity,helicase activity,ATP binding,ATP binding,nucleus,ATP catabolic process,ATP catabolic process,ATP catabolic process,mRNA processing,ATP-dependent helicase activity,RNA modification,hydrolase activity,poly(A) RNA binding
comp10066_c0_seq1.p1				
comp100685_c0_seq1.p1				
comp100697_c0_seq1.p1				
comp10070_c0_seq1.p1				
comp100734_c0_seq1.p1	sp|Q9MBF8|DYH1B_CHLRE_Dynein-1-beta_heavy_chain,_flagellar_inner_arm_I1_complex_OS=Chlamydomonas_reinhardtii_GN=DHC10_PE=1_SV=1	4.00E-28	GO:0000166,GO:0003774,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005874,GO:0005929,GO:0005930,GO:0006200,GO:0007018,GO:0008152,GO:0008152,GO:0016887,GO:0030030,GO:0030286,GO:0030286,GO:0031514,GO:0042995	nucleotide binding,motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,microtubule,cilium,axoneme,ATP catabolic process,microtubule-based movement,metabolic process,metabolic process,ATPase activity,cell projection organization,dynein complex,dynein complex,motile cilium,cell projection
comp100770_c0_seq1.p1	sp|Q3Z3I9|PNCB_SHISS_Nicotinate_phosphoribosyltransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=pncB_PE=3_SV=1	9.00E-98	GO:0004514,GO:0004516,GO:0004516,GO:0009435,GO:0009435,GO:0009435,GO:0016740,GO:0016874,GO:0019357,GO:0019363	nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate phosphoribosyltransferase activity,nicotinate phosphoribosyltransferase activity,NAD biosynthetic process,NAD biosynthetic process,NAD biosynthetic process,transferase activity,ligase activity,nicotinate nucleotide biosynthetic process,pyridine nucleotide biosynthetic process
comp10078_c0_seq1.p1	sp|Q5RC56|NDKA_PONAB_Nucleoside_diphosphate_kinase_A_OS=Pongo_abelii_GN=NME1_PE=2_SV=1	3.00E-64	GO:0000166,GO:0004550,GO:0004550,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006165,GO:0006183,GO:0006228,GO:0006241,GO:0006897,GO:0007399,GO:0009117,GO:0016301,GO:0016310,GO:0016740,GO:0030154,GO:0046872	nucleotide binding,nucleoside diphosphate kinase activity,nucleoside diphosphate kinase activity,ATP binding,ATP binding,nucleus,nucleus,cytoplasm,cytoplasm,nucleoside diphosphate phosphorylation,GTP biosynthetic process,UTP biosynthetic process,CTP biosynthetic process,endocytosis,nervous system development,nucleotide metabolic process,kinase activity,phosphorylation,transferase activity,cell differentiation,metal ion binding
comp100783_c0_seq1.p1				
comp10079_c0_seq1.p1				
comp10080_c0_seq1.p2	sp|Q2EN81|ATPO_PIG_ATP_synthase_subunit_O,_mitochondrial_OS=Sus_scrofa_GN=ATP5O_PE=1_SV=1	2.00E-22	GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005753,GO:0006754,GO:0006810,GO:0006811,GO:0015986,GO:0015992,GO:0016020,GO:0016020,GO:0046933	mitochondrion,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial proton-transporting ATP synthase complex,ATP biosynthetic process,transport,ion transport,ATP synthesis coupled proton transport,proton transport,membrane,membrane,proton-transporting ATP synthase activity, rotational mechanism
comp100812_c0_seq1.p2	sp|P10346|GLNQ_ECOLI_Glutamine_transport_ATP-binding_protein_GlnQ_OS=Escherichia_coli_(strain_K12)_GN=glnQ_PE=1_SV=1	7.00E-65	GO:0000166,GO:0005524,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006200,GO:0006810,GO:0006865,GO:0016020,GO:0016887	nucleotide binding,ATP binding,ATP binding,plasma membrane,plasma membrane,plasma membrane,plasma membrane,ATP catabolic process,transport,amino acid transport,membrane,ATPase activity
comp10084_c0_seq1.p1				
comp10085_c0_seq1.p1				
comp100886_c0_seq1.p1	sp|P0AFG6|ODO2_ECOLI_Dihydrolipoyllysine-residue_succinyltransferase_component_of_2-oxoglutarate_dehydrogenase_complex_OS=Escherichia_coli_(strain_K12)_GN=sucB_PE=1_SV=2	9.00E-98	GO:0004149,GO:0004149,GO:0004149,GO:0004149,GO:0005515,GO:0005515,GO:0006099,GO:0006099,GO:0006099,GO:0008152,GO:0016740,GO:0016746,GO:0016746,GO:0031405,GO:0033512,GO:0045252,GO:0045252	dihydrolipoyllysine-residue succinyltransferase activity,dihydrolipoyllysine-residue succinyltransferase activity,dihydrolipoyllysine-residue succinyltransferase activity,dihydrolipoyllysine-residue succinyltransferase activity,protein binding,protein binding,tricarboxylic acid cycle,tricarboxylic acid cycle,tricarboxylic acid cycle,metabolic process,transferase activity,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups,lipoic acid binding,L-lysine catabolic process to acetyl-CoA via saccharopine,oxoglutarate dehydrogenase complex,oxoglutarate dehydrogenase complex
comp10089_c0_seq1.p2				
comp10094_c0_seq1.p1	sp|Q9NZJ4|SACS_HUMAN_Sacsin_OS=Homo_sapiens_GN=SACS_PE=1_SV=2	3.00E-43	GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0006457,GO:0030424,GO:0030425,GO:0030544,GO:0051087,GO:0070628,GO:0070852,GO:0090084	nucleus,cytoplasm,cytoplasm,cytoplasm,mitochondrion,protein folding,axon,dendrite,Hsp70 protein binding,chaperone binding,proteasome binding,cell body fiber,negative regulation of inclusion body assembly
comp100953_c0_seq1.p1	sp|Q3YYG6|SYA_SHISS_Alanine--tRNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=alaS_PE=3_SV=1	3.00E-67	GO:0000049,GO:0000166,GO:0000166,GO:0003676,GO:0003723,GO:0004812,GO:0004813,GO:0004813,GO:0004813,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006419,GO:0006419,GO:0008270,GO:0016874,GO:0016876,GO:0043039,GO:0046872	tRNA binding,nucleotide binding,nucleotide binding,nucleic acid binding,RNA binding,aminoacyl-tRNA ligase activity,alanine-tRNA ligase activity,alanine-tRNA ligase activity,alanine-tRNA ligase activity,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,translation,alanyl-tRNA aminoacylation,alanyl-tRNA aminoacylation,zinc ion binding,ligase activity,ligase activity, forming aminoacyl-tRNA and related compounds,tRNA aminoacylation,metal ion binding
comp10096_c0_seq1.p1	sp|Q6CC79|NHP6_YARLI_Non-histone_chromosomal_protein_6_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=NHP6_PE=3_SV=1	4.00E-12	GO:0003677,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0006281,GO:0006351,GO:0006355,GO:0006974	DNA binding,nucleus,nucleus,chromosome,chromosome,DNA repair,transcription, DNA-templated,regulation of transcription, DNA-templated,cellular response to DNA damage stimulus
comp100969_c0_seq1.p1	sp|Q1R8X7|YFEO_ECOUT_Putative_ion-transport_protein_yfeO_OS=Escherichia_coli_(strain_UTI89_/_UPEC)_GN=yfeO_PE=3_SV=1	5.00E-32	GO:0005216,GO:0005216,GO:0005247,GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006811,GO:0006821,GO:0006821,GO:0016020,GO:0016020,GO:0016021,GO:0034220,GO:0034220,GO:0044070,GO:0055085	ion channel activity,ion channel activity,voltage-gated chloride channel activity,plasma membrane,plasma membrane,plasma membrane,transport,ion transport,chloride transport,chloride transport,membrane,membrane,integral component of membrane,ion transmembrane transport,ion transmembrane transport,regulation of anion transport,transmembrane transport
comp10106_c0_seq1.p1	sp|Q9CU62|SMC1A_MOUSE_Structural_maintenance_of_chromosomes_protein_1A_OS=Mus_musculus_GN=Smc1a_PE=1_SV=4	8.00E-18	GO:0000166,GO:0000775,GO:0000775,GO:0000776,GO:0000776,GO:0003682,GO:0003682,GO:0003682,GO:0003682,GO:0003682,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005654,GO:0005654,GO:0005654,GO:0005654,GO:0005654,GO:0005694,GO:0005694,GO:0005694,GO:0005737,GO:0006281,GO:0006281,GO:0006974,GO:0007049,GO:0007062,GO:0007064,GO:0007067,GO:0007093,GO:0007093,GO:0007126,GO:0007126,GO:0008280,GO:0009314,GO:0009314,GO:0019827,GO:0030893,GO:0030893,GO:0030893,GO:0032876,GO:0036033,GO:0042770,GO:0042770,GO:0044822,GO:0046982,GO:0051276,GO:0051301,GO:0051321	nucleotide binding,chromosome, centromeric region,chromosome, centromeric region,kinetochore,kinetochore,chromatin binding,chromatin binding,chromatin binding,chromatin binding,chromatin binding,protein binding,protein binding,ATP binding,ATP binding,nucleus,nucleus,nucleus,nucleus,nucleoplasm,nucleoplasm,nucleoplasm,nucleoplasm,nucleoplasm,nucleoplasm,chromosome,chromosome,chromosome,cytoplasm,DNA repair,DNA repair,cellular response to DNA damage stimulus,cell cycle,sister chromatid cohesion,mitotic sister chromatid cohesion,mitotic nuclear division,mitotic cell cycle checkpoint,mitotic cell cycle checkpoint,meiotic nuclear division,meiotic nuclear division,cohesin core heterodimer,response to radiation,response to radiation,stem cell maintenance,meiotic cohesin complex,meiotic cohesin complex,meiotic cohesin complex,negative regulation of DNA endoreduplication,mediator complex binding,signal transduction in response to DNA damage,signal transduction in response to DNA damage,poly(A) RNA binding,protein heterodimerization activity,chromosome organization,cell division,meiotic cell cycle
comp101072_c0_seq1.p2	sp|P0AAE0|CYCA_ECOLI_D-serine/D-alanine/glycine_transporter_OS=Escherichia_coli_(strain_K12)_GN=cycA_PE=1_SV=1	4.00E-66	GO:0001761,GO:0001762,GO:0003333,GO:0005886,GO:0005886,GO:0005886,GO:0005887,GO:0006810,GO:0006810,GO:0006865,GO:0006865,GO:0015171,GO:0015180,GO:0015187,GO:0015808,GO:0015816,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0042891,GO:0042895,GO:0042941,GO:0042942,GO:0042944,GO:0042945,GO:0055085	beta-alanine transmembrane transporter activity,beta-alanine transport,amino acid transmembrane transport,plasma membrane,plasma membrane,plasma membrane,integral component of plasma membrane,transport,transport,amino acid transport,amino acid transport,amino acid transmembrane transporter activity,L-alanine transmembrane transporter activity,glycine transmembrane transporter activity,L-alanine transport,glycine transport,membrane,membrane,integral component of membrane,integral component of membrane,antibiotic transport,antibiotic transporter activity,D-alanine transport,D-serine transport,D-alanine transmembrane transporter activity,D-serine transmembrane transporter activity,transmembrane transport
comp101091_c0_seq1.p1				
comp101131_c0_seq1.p1	sp|P12758|UDP_ECOLI_Uridine_phosphorylase_OS=Escherichia_coli_(strain_K12)_GN=udp_PE=1_SV=3	3.00E-61	GO:0003824,GO:0004850,GO:0004850,GO:0004850,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0006974,GO:0009116,GO:0009166,GO:0016020,GO:0016740,GO:0016757,GO:0016763,GO:0042802,GO:0044206	catalytic activity,uridine phosphorylase activity,uridine phosphorylase activity,uridine phosphorylase activity,cytoplasm,cytoplasm,cytoplasm,cytosol,cellular response to DNA damage stimulus,nucleoside metabolic process,nucleotide catabolic process,membrane,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring pentosyl groups,identical protein binding,UMP salvage
comp10116_c0_seq1.p1	sp|Q9ATN0|PIP16_MAIZE_Aquaporin_PIP1-6_OS=Zea_mays_GN=PIP1-6_PE=2_SV=1	2.00E-20	GO:0005215,GO:0005886,GO:0005886,GO:0006810,GO:0006810,GO:0016020,GO:0016020,GO:0016021	transporter activity,plasma membrane,plasma membrane,transport,transport,membrane,membrane,integral component of membrane
comp10125_c0_seq1.p1				
comp101253_c0_seq1.p1	sp|P32137|YIHP_ECOLI_Inner_membrane_symporter_yihP_OS=Escherichia_coli_(strain_K12)_GN=yihP_PE=1_SV=3	9.00E-76	GO:0005215,GO:0005215,GO:0005886,GO:0005886,GO:0005886,GO:0005887,GO:0006810,GO:0006814,GO:0015293,GO:0016020,GO:0016020,GO:0016021,GO:0055085	transporter activity,transporter activity,plasma membrane,plasma membrane,plasma membrane,integral component of plasma membrane,transport,sodium ion transport,symporter activity,membrane,membrane,integral component of membrane,transmembrane transport
comp10140_c0_seq2.p1	sp|Q8WXX0|DYH7_HUMAN_Dynein_heavy_chain_7,_axonemal_OS=Homo_sapiens_GN=DNAH7_PE=1_SV=2	9.00E-84	GO:0000166,GO:0001539,GO:0003341,GO:0003774,GO:0003777,GO:0003777,GO:0005509,GO:0005524,GO:0005737,GO:0005856,GO:0005858,GO:0005858,GO:0005874,GO:0005929,GO:0005929,GO:0006200,GO:0007018,GO:0008152,GO:0008152,GO:0008152,GO:0016887,GO:0030286,GO:0030286,GO:0042995	nucleotide binding,cilium or flagellum-dependent cell motility,cilium movement,motor activity,microtubule motor activity,microtubule motor activity,calcium ion binding,ATP binding,cytoplasm,cytoskeleton,axonemal dynein complex,axonemal dynein complex,microtubule,cilium,cilium,ATP catabolic process,microtubule-based movement,metabolic process,metabolic process,metabolic process,ATPase activity,dynein complex,dynein complex,cell projection
comp101442_c0_seq1.p1				
comp101502_c0_seq1.p1	sp|P37645|YHJG_ECOLI_Uncharacterized_protein_yhjG_OS=Escherichia_coli_(strain_K12)_GN=yhjG_PE=4_SV=3	4.00E-114	GO:0005886,GO:0005886,GO:0016020,GO:0016021	plasma membrane,plasma membrane,membrane,integral component of membrane
comp10151_c0_seq1.p1				
comp101569_c0_seq1.p1				
comp101588_c0_seq1.p2	sp|B1LI92|GLGX_ECOSM_Glycogen_debranching_enzyme_OS=Escherichia_coli_(strain_SMS-3-5_/_SECEC)_GN=glgX_PE=3_SV=1	5.00E-77	GO:0003824,GO:0004133,GO:0004133,GO:0004553,GO:0005975,GO:0005975,GO:0005977,GO:0005977,GO:0005980,GO:0005980,GO:0005980,GO:0008152,GO:0016787,GO:0016798,GO:0043169	catalytic activity,glycogen debranching enzyme activity,glycogen debranching enzyme activity,hydrolase activity, hydrolyzing O-glycosyl compounds,carbohydrate metabolic process,carbohydrate metabolic process,glycogen metabolic process,glycogen metabolic process,glycogen catabolic process,glycogen catabolic process,glycogen catabolic process,metabolic process,hydrolase activity,hydrolase activity, acting on glycosyl bonds,cation binding
comp10159_c0_seq1.p1				
comp10163_c0_seq1.p1	sp|Q9UA41|PPID_DICDI_Peptidyl-prolyl_cis-trans_isomerase_D,_mitochondrial_OS=Dictyostelium_discoideum_GN=cypD_PE=1_SV=1	5.00E-66	GO:0000413,GO:0000413,GO:0003755,GO:0003755,GO:0003755,GO:0003755,GO:0005739,GO:0005739,GO:0006457,GO:0016853,GO:0042277,GO:0044351	protein peptidyl-prolyl isomerization,protein peptidyl-prolyl isomerization,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,mitochondrion,mitochondrion,protein folding,isomerase activity,peptide binding,macropinocytosis
comp101662_c0_seq1.p1	sp|Q3Z4Y6|THII_SHISS_tRNA_sulfurtransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=thiI_PE=3_SV=1	5.00E-56	GO:0000049,GO:0000049,GO:0000166,GO:0003723,GO:0003723,GO:0003723,GO:0004810,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0009228,GO:0009228,GO:0009229,GO:0016740,GO:0016783,GO:0016783,GO:0034227,GO:0034227,GO:0052837	tRNA binding,tRNA binding,nucleotide binding,RNA binding,RNA binding,RNA binding,tRNA adenylyltransferase activity,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,thiamine biosynthetic process,thiamine biosynthetic process,thiamine diphosphate biosynthetic process,transferase activity,sulfurtransferase activity,sulfurtransferase activity,tRNA thio-modification,tRNA thio-modification,thiazole biosynthetic process
comp101696_c0_seq1.p1				
comp10176_c0_seq1.p1				
comp101768_c0_seq1.p1	sp|P13518|CSRD_ECOLI_RNase_E_specificity_factor_CsrD_OS=Escherichia_coli_(strain_K12)_GN=csrD_PE=1_SV=2	4.00E-76	GO:0005886,GO:0005886,GO:0016020,GO:0016021,GO:0034661,GO:0051252	plasma membrane,plasma membrane,membrane,integral component of membrane,ncRNA catabolic process,regulation of RNA metabolic process
comp10179_c0_seq2.p1				
comp101846_c0_seq1.p1	sp|Q55FK2|RAB6_DICDI_Ras-related_protein_Rab-6_OS=Dictyostelium_discoideum_GN=rab6_PE=3_SV=1	4.00E-31	GO:0000166,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0005794,GO:0006184,GO:0006810,GO:0006886,GO:0006890,GO:0006891,GO:0007264,GO:0015031,GO:0015031,GO:0019003,GO:0032482,GO:0042147,GO:0044351	nucleotide binding,GTPase activity,GTP binding,GTP binding,GTP binding,Golgi apparatus,GTP catabolic process,transport,intracellular protein transport,retrograde vesicle-mediated transport, Golgi to ER,intra-Golgi vesicle-mediated transport,small GTPase mediated signal transduction,protein transport,protein transport,GDP binding,Rab protein signal transduction,retrograde transport, endosome to Golgi,macropinocytosis
comp101852_c0_seq1.p1	sp|P33934|NAPH_ECOLI_Ferredoxin-type_protein_napH_OS=Escherichia_coli_(strain_K12)_GN=napH_PE=4_SV=1	6.00E-61	GO:0005506,GO:0005886,GO:0005886,GO:0005886,GO:0016020,GO:0016020,GO:0016021,GO:0046872,GO:0051536,GO:0051536,GO:0051539,GO:0055114	iron ion binding,plasma membrane,plasma membrane,plasma membrane,membrane,membrane,integral component of membrane,metal ion binding,iron-sulfur cluster binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,oxidation-reduction process
comp101870_c0_seq1.p2	sp|P09152|NARG_ECOLI_Respiratory_nitrate_reductase_1_alpha_chain_OS=Escherichia_coli_(strain_K12)_GN=narG_PE=1_SV=4	2.00E-83	GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005886,GO:0005886,GO:0008940,GO:0008940,GO:0009055,GO:0009061,GO:0009325,GO:0016020,GO:0016020,GO:0016491,GO:0016491,GO:0016651,GO:0017004,GO:0030151,GO:0030151,GO:0031224,GO:0042126,GO:0042128,GO:0046872,GO:0051536,GO:0051539,GO:0051539,GO:0051539,GO:0055114,GO:0055114,GO:0055114	protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,plasma membrane,plasma membrane,nitrate reductase activity,nitrate reductase activity,electron carrier activity,anaerobic respiration,nitrate reductase complex,membrane,membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on NAD(P)H,cytochrome complex assembly,molybdenum ion binding,molybdenum ion binding,intrinsic component of membrane,nitrate metabolic process,nitrate assimilation,metal ion binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp10188_c0_seq1.p1				
comp101913_c0_seq1.p2	sp|P41579|6PGD_SHIDY_6-phosphogluconate_dehydrogenase,_decarboxylating_(Fragment)_OS=Shigella_dysenteriae_GN=gnd_PE=3_SV=1	7.00E-95	GO:0004616,GO:0004616,GO:0004616,GO:0006098,GO:0006098,GO:0006098,GO:0006098,GO:0016491,GO:0016491,GO:0016616,GO:0019521,GO:0050661,GO:0050662,GO:0055114,GO:0055114	phosphogluconate dehydrogenase (decarboxylating) activity,phosphogluconate dehydrogenase (decarboxylating) activity,phosphogluconate dehydrogenase (decarboxylating) activity,pentose-phosphate shunt,pentose-phosphate shunt,pentose-phosphate shunt,pentose-phosphate shunt,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,D-gluconate metabolic process,NADP binding,coenzyme binding,oxidation-reduction process,oxidation-reduction process
comp10200_c0_seq2.p2	sp|O65050|RL15A_PICMA_60S_ribosomal_protein_L15-1_OS=Picea_mariana_GN=SB61_PE=2_SV=1	3.00E-84	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0030529	structural constituent of ribosome,intracellular,ribosome,ribosome,translation,ribonucleoprotein complex
comp10201_c0_seq1.p1				
comp102036_c0_seq1.p1	sp|P25772|LIGB_ECOLI_DNA_ligase_B_OS=Escherichia_coli_(strain_K12)_GN=ligB_PE=1_SV=2	5.00E-97	GO:0003911,GO:0003911,GO:0003911,GO:0003911,GO:0005829,GO:0006259,GO:0006259,GO:0006260,GO:0006260,GO:0006266,GO:0006281,GO:0006281,GO:0006288,GO:0006974,GO:0016874	DNA ligase (NAD+) activity,DNA ligase (NAD+) activity,DNA ligase (NAD+) activity,DNA ligase (NAD+) activity,DNA ligase (NAD+) activity,cytosol,DNA metabolic process,DNA metabolic process,DNA replication,DNA replication,DNA ligation,DNA repair,DNA repair,base-excision repair, DNA ligation,cellular response to DNA damage stimulus,ligase activity
comp102117_c0_seq1.p2				
comp102136_c0_seq1.p1				
comp102142_c0_seq1.p1	sp|P0ADS1|YGDH_SHIFL_LOG_family_protein_ygdH_OS=Shigella_flexneri_GN=ygdH_PE=3_SV=1	3.00E-105		
comp102156_c0_seq1.p1	sp|P76559|YPFG_ECOLI_Uncharacterized_protein_ypfG_OS=Escherichia_coli_(strain_K12)_GN=ypfG_PE=4_SV=1	5.00E-88		
comp102214_c0_seq1.p1				
comp10222_c0_seq1.p1	sp|P76004|YCGM_ECOLI_Uncharacterized_protein_ycgM_OS=Escherichia_coli_(strain_K12)_GN=ycgM_PE=1_SV=1	1.00E-72	GO:0003824,GO:0008152,GO:0046872	catalytic activity,metabolic process,metal ion binding
comp102223_c0_seq1.p1				
comp102251_c0_seq1.p1				
comp10227_c0_seq1.p1				
comp10230_c0_seq1.p1				
comp10234_c0_seq1.p1				
comp102397_c0_seq1.p1				
comp102401_c0_seq1.p1	sp|P21189|DPO2_ECOLI_DNA_polymerase_II_OS=Escherichia_coli_(strain_K12)_GN=polB_PE=1_SV=2	2.00E-75	GO:0000166,GO:0000738,GO:0003676,GO:0003677,GO:0003677,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0005694,GO:0006139,GO:0006260,GO:0006261,GO:0006281,GO:0006297,GO:0006974,GO:0008296,GO:0008408,GO:0009432,GO:0009432,GO:0016740,GO:0016779,GO:0019985,GO:0045004,GO:0090305	nucleotide binding,DNA catabolic process, exonucleolytic,nucleic acid binding,DNA binding,DNA binding,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,chromosome,nucleobase-containing compound metabolic process,DNA replication,DNA-dependent DNA replication,DNA repair,nucleotide-excision repair, DNA gap filling,cellular response to DNA damage stimulus,3'-5'-exodeoxyribonuclease activity,3'-5' exonuclease activity,SOS response,SOS response,transferase activity,nucleotidyltransferase activity,translesion synthesis,DNA replication proofreading,nucleic acid phosphodiester bond hydrolysis
comp10241_c0_seq1.p1				
comp10243_c0_seq1.p1				
comp102446_c0_seq1.p1				
comp10256_c0_seq1.p1				
comp10260_c0_seq1.p1	sp|P27484|GRP2_NICSY_Glycine-rich_protein_2_OS=Nicotiana_sylvestris_GN=GRP-2_PE=2_SV=1	2.00E-24	GO:0003676,GO:0003677,GO:0003723,GO:0006355,GO:0008270,GO:0046872	nucleic acid binding,DNA binding,RNA binding,regulation of transcription, DNA-templated,zinc ion binding,metal ion binding
comp10261_c0_seq1.p1	sp|P71229|HYFR_ECOLI_Hydrogenase-4_transcriptional_activator_OS=Escherichia_coli_(strain_K12)_GN=hyfR_PE=4_SV=1	3.00E-151	GO:0000156,GO:0000160,GO:0000160,GO:0000166,GO:0000785,GO:0003677,GO:0003677,GO:0003677,GO:0003700,GO:0005524,GO:0005524,GO:0006351,GO:0006352,GO:0006355,GO:0006355,GO:0008134,GO:0043565,GO:0043565,GO:0044212,GO:2000142	phosphorelay response regulator activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,chromatin,DNA binding,DNA binding,DNA binding,sequence-specific DNA binding transcription factor activity,ATP binding,ATP binding,transcription, DNA-templated,DNA-templated transcription, initiation,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,transcription factor binding,sequence-specific DNA binding,sequence-specific DNA binding,transcription regulatory region DNA binding,regulation of DNA-templated transcription, initiation
comp102686_c0_seq1.p1				
comp102755_c0_seq1.p2	sp|P06660|HSP85_TRYCR_Heat_shock-like_85_kDa_protein_OS=Trypanosoma_cruzi_PE=3_SV=1	4.00E-19	GO:0000166,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0006457,GO:0006950,GO:0051082	nucleotide binding,ATP binding,ATP binding,cytoplasm,cytoplasm,protein folding,response to stress,unfolded protein binding
comp102807_c0_seq1.p1				
comp102817_c0_seq1.p1	sp|P37127|AEGA_ECOLI_Protein_AegA_OS=Escherichia_coli_(strain_K12)_GN=aegA_PE=3_SV=2	1.00E-80	GO:0005737,GO:0006537,GO:0006537,GO:0016491,GO:0016491,GO:0016491,GO:0016639,GO:0046872,GO:0051536,GO:0051536,GO:0051539,GO:0055114,GO:0055114	cytoplasm,glutamate biosynthetic process,glutamate biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,metal ion binding,iron-sulfur cluster binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,oxidation-reduction process,oxidation-reduction process
comp102834_c0_seq1.p3				
comp102879_c0_seq1.p1				
comp102887_c0_seq1.p1	sp|Q9LR78|BSU1_ARATH_Serine/threonine-protein_phosphatase_BSU1_OS=Arabidopsis_thaliana_GN=BSU1_PE=2_SV=2	2.00E-13	GO:0004721,GO:0004721,GO:0004721,GO:0004722,GO:0005506,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0006869,GO:0008152,GO:0008152,GO:0009742,GO:0016311,GO:0016311,GO:0016311,GO:0016311,GO:0016787,GO:0016787,GO:0030145,GO:0032880,GO:0046872	phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,protein serine/threonine phosphatase activity,iron ion binding,protein binding,nucleus,nucleus,nucleus,lipid transport,metabolic process,metabolic process,brassinosteroid mediated signaling pathway,dephosphorylation,dephosphorylation,dephosphorylation,dephosphorylation,hydrolase activity,hydrolase activity,manganese ion binding,regulation of protein localization,metal ion binding
comp10293_c0_seq1.p1				
comp10294_c0_seq1.p1	sp|P52808|RL30A_SCHPO_60S_ribosomal_protein_L30-1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpl30a_PE=2_SV=2	1.00E-42	GO:0002181,GO:0003735,GO:0003735,GO:0005622,GO:0005829,GO:0005840,GO:0005840,GO:0006364,GO:0006412,GO:0022625,GO:0030529	cytoplasmic translation,structural constituent of ribosome,structural constituent of ribosome,intracellular,cytosol,ribosome,ribosome,rRNA processing,translation,cytosolic large ribosomal subunit,ribonucleoprotein complex
comp10312_c0_seq1.p1	sp|Q39575|DYHG_CHLRE_Dynein_gamma_chain,_flagellar_outer_arm_OS=Chlamydomonas_reinhardtii_GN=ODA2_PE=1_SV=1	1.00E-35	GO:0000166,GO:0003774,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005874,GO:0005929,GO:0006200,GO:0007018,GO:0008152,GO:0008152,GO:0016887,GO:0030030,GO:0030286,GO:0030286,GO:0031514,GO:0042995	nucleotide binding,motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,microtubule,cilium,ATP catabolic process,microtubule-based movement,metabolic process,metabolic process,ATPase activity,cell projection organization,dynein complex,dynein complex,motile cilium,cell projection
comp103168_c0_seq1.p2				
comp10324_c0_seq1.p1	sp|P09099|XYLB_ECOLI_Xylulose_kinase_OS=Escherichia_coli_(strain_K12)_GN=xylB_PE=1_SV=1	1.00E-90	GO:0000166,GO:0004856,GO:0004856,GO:0004856,GO:0005524,GO:0005975,GO:0005975,GO:0005997,GO:0005998,GO:0016301,GO:0016310,GO:0016740,GO:0016773,GO:0042732,GO:0042843,GO:0046835,GO:0046835,GO:0046835	nucleotide binding,xylulokinase activity,xylulokinase activity,xylulokinase activity,ATP binding,carbohydrate metabolic process,carbohydrate metabolic process,xylulose metabolic process,xylulose catabolic process,kinase activity,phosphorylation,transferase activity,phosphotransferase activity, alcohol group as acceptor,D-xylose metabolic process,D-xylose catabolic process,carbohydrate phosphorylation,carbohydrate phosphorylation,carbohydrate phosphorylation
comp103269_c0_seq1.p1	sp|P77319|HSCC_ECOLI_Chaperone_protein_hscC_OS=Escherichia_coli_(strain_K12)_GN=hscC_PE=1_SV=1	1.00E-108	GO:0000166,GO:0005515,GO:0005524,GO:0006200,GO:0016887	nucleotide binding,protein binding,ATP binding,ATP catabolic process,ATPase activity
comp10328_c0_seq1.p1				
comp103305_c0_seq1.p1	sp|P05704|MCP3_ECOLI_Methyl-accepting_chemotaxis_protein_III_OS=Escherichia_coli_(strain_K12)_GN=trg_PE=1_SV=3	2.00E-56	GO:0004871,GO:0004871,GO:0004888,GO:0004888,GO:0004888,GO:0005515,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005887,GO:0006935,GO:0006935,GO:0006935,GO:0007165,GO:0007165,GO:0007165,GO:0007165,GO:0016020,GO:0016020,GO:0016021,GO:0016021	signal transducer activity,signal transducer activity,transmembrane signaling receptor activity,transmembrane signaling receptor activity,transmembrane signaling receptor activity,protein binding,plasma membrane,plasma membrane,plasma membrane,plasma membrane,integral component of plasma membrane,chemotaxis,chemotaxis,chemotaxis,signal transduction,signal transduction,signal transduction,signal transduction,membrane,membrane,integral component of membrane,integral component of membrane
comp10331_c0_seq1.p1	sp|Q54EW1|GLYC2_DICDI_Serine_hydroxymethyltransferase_2_OS=Dictyostelium_discoideum_GN=shmt2_PE=3_SV=1	2.00E-102	GO:0003824,GO:0004372,GO:0004372,GO:0004372,GO:0005759,GO:0006544,GO:0006563,GO:0006730,GO:0006730,GO:0016740,GO:0030170,GO:0035999,GO:0044351	catalytic activity,glycine hydroxymethyltransferase activity,glycine hydroxymethyltransferase activity,glycine hydroxymethyltransferase activity,mitochondrial matrix,glycine metabolic process,L-serine metabolic process,one-carbon metabolic process,one-carbon metabolic process,transferase activity,pyridoxal phosphate binding,tetrahydrofolate interconversion,macropinocytosis
comp103338_c0_seq1.p1	sp|P69451|LCFA_ECOLI_Long-chain-fatty-acid--CoA_ligase_OS=Escherichia_coli_(strain_K12)_GN=fadD_PE=1_SV=1	6.00E-16	GO:0000166,GO:0001676,GO:0001676,GO:0001676,GO:0001676,GO:0003824,GO:0004467,GO:0004467,GO:0004467,GO:0004467,GO:0005504,GO:0005524,GO:0005737,GO:0005829,GO:0006629,GO:0006629,GO:0006631,GO:0006631,GO:0006635,GO:0006637,GO:0008152,GO:0008654,GO:0009898,GO:0016020,GO:0016020,GO:0016874,GO:0070538	nucleotide binding,long-chain fatty acid metabolic process,long-chain fatty acid metabolic process,long-chain fatty acid metabolic process,long-chain fatty acid metabolic process,catalytic activity,long-chain fatty acid-CoA ligase activity,long-chain fatty acid-CoA ligase activity,long-chain fatty acid-CoA ligase activity,long-chain fatty acid-CoA ligase activity,fatty acid binding,ATP binding,cytoplasm,cytosol,lipid metabolic process,lipid metabolic process,fatty acid metabolic process,fatty acid metabolic process,fatty acid beta-oxidation,acyl-CoA metabolic process,metabolic process,phospholipid biosynthetic process,cytoplasmic side of plasma membrane,membrane,membrane,ligase activity,oleic acid binding
comp103397_c0_seq1.p1	sp|Q92PX0|SYM_RHIME_Methionine--tRNA_ligase_OS=Rhizobium_meliloti_(strain_1021)_GN=metG_PE=3_SV=1	7.00E-41	GO:0000166,GO:0000166,GO:0004812,GO:0004812,GO:0004825,GO:0004825,GO:0004825,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006418,GO:0006431,GO:0006431,GO:0016874	nucleotide binding,nucleotide binding,aminoacyl-tRNA ligase activity,aminoacyl-tRNA ligase activity,methionine-tRNA ligase activity,methionine-tRNA ligase activity,methionine-tRNA ligase activity,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,translation,tRNA aminoacylation for protein translation,methionyl-tRNA aminoacylation,methionyl-tRNA aminoacylation,ligase activity
comp103402_c0_seq1.p1				
comp103415_c0_seq1.p1	sp|P25438|YI61_XANEU_Insertion_element_IS476_uncharacterized_39.2_kDa_protein_OS=Xanthomonas_euvesicatoria_PE=4_SV=1	2.00E-24	GO:0003676,GO:0015074	nucleic acid binding,DNA integration
comp10343_c0_seq1.p1				
comp103457_c0_seq1.p1	sp|P25747|YEIB_ECOLI_Uncharacterized_protein_yeiB_OS=Escherichia_coli_(strain_K12)_GN=yeiB_PE=4_SV=2	1.00E-38	GO:0005886,GO:0005886,GO:0006810,GO:0016020,GO:0016021	plasma membrane,plasma membrane,transport,membrane,integral component of membrane
comp10351_c0_seq1.p2				
comp10357_c0_seq3.p1				
comp10360_c0_seq1.p2	sp|P48589|RS12_YEAST_40S_ribosomal_protein_S12_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=RPS12_PE=1_SV=1	1.00E-11	GO:0002181,GO:0003735,GO:0003735,GO:0005622,GO:0005737,GO:0005737,GO:0005840,GO:0005840,GO:0006412,GO:0022627,GO:0030529	cytoplasmic translation,structural constituent of ribosome,structural constituent of ribosome,intracellular,cytoplasm,cytoplasm,ribosome,ribosome,translation,cytosolic small ribosomal subunit,ribonucleoprotein complex
comp10365_c0_seq1.p1	sp|P00781|SUBD_BACLI_Subtilisin_DY_OS=Bacillus_licheniformis_GN=apr_PE=1_SV=1	1.00E-35	GO:0004252,GO:0005576,GO:0005576,GO:0006508,GO:0006508,GO:0008233,GO:0008236,GO:0016787,GO:0030435,GO:0046872	serine-type endopeptidase activity,extracellular region,extracellular region,proteolysis,proteolysis,peptidase activity,serine-type peptidase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,metal ion binding
comp10370_c0_seq1.p1				
comp10374_c0_seq1.p1				
comp103758_c0_seq1.p1				
comp103764_c0_seq1.p1				
comp10381_c0_seq1.p3				
comp103813_c0_seq1.p1				
comp10385_c0_seq1.p1	sp|Q3YYG4|RECA_SHISS_Protein_RecA_OS=Shigella_sonnei_(strain_Ss046)_GN=recA_PE=3_SV=1	0	GO:0000166,GO:0003677,GO:0003677,GO:0003684,GO:0003697,GO:0003697,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0006200,GO:0006200,GO:0006259,GO:0006281,GO:0006281,GO:0006310,GO:0006310,GO:0006974,GO:0006974,GO:0008094,GO:0008094,GO:0009432,GO:0009432,GO:0009432	nucleotide binding,DNA binding,DNA binding,damaged DNA binding,single-stranded DNA binding,single-stranded DNA binding,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,ATP catabolic process,ATP catabolic process,DNA metabolic process,DNA repair,DNA repair,DNA recombination,DNA recombination,cellular response to DNA damage stimulus,cellular response to DNA damage stimulus,DNA-dependent ATPase activity,DNA-dependent ATPase activity,SOS response,SOS response,SOS response
comp103857_c0_seq1.p1				
comp103858_c0_seq1.p1				
comp10389_c0_seq2.p1				
comp10390_c0_seq1.p1				
comp10391_c0_seq1.p1				
comp10395_c1_seq1.p1	sp|P06134|ADA_ECOLI_Bifunctional_transcriptional_activator/DNA_repair_enzyme_Ada_OS=Escherichia_coli_(strain_K12)_GN=ada_PE=1_SV=2	2.00E-78	GO:0003677,GO:0003677,GO:0003684,GO:0003700,GO:0003824,GO:0003824,GO:0003908,GO:0003908,GO:0003908,GO:0005515,GO:0006281,GO:0006281,GO:0006307,GO:0006351,GO:0006355,GO:0006355,GO:0006974,GO:0008152,GO:0008168,GO:0008168,GO:0008168,GO:0008270,GO:0008270,GO:0016740,GO:0032259,GO:0043565,GO:0046872,GO:0080111	DNA binding,DNA binding,damaged DNA binding,sequence-specific DNA binding transcription factor activity,catalytic activity,catalytic activity,methylated-DNA-[protein]-cysteine S-methyltransferase activity,methylated-DNA-[protein]-cysteine S-methyltransferase activity,methylated-DNA-[protein]-cysteine S-methyltransferase activity,protein binding,DNA repair,DNA repair,DNA dealkylation involved in DNA repair,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,cellular response to DNA damage stimulus,metabolic process,methyltransferase activity,methyltransferase activity,methyltransferase activity,zinc ion binding,zinc ion binding,transferase activity,methylation,sequence-specific DNA binding,metal ion binding,DNA demethylation
comp104024_c0_seq1.p1				
comp10403_c0_seq1.p1				
comp10408_c0_seq1.p1				
comp10416_c0_seq1.p1				
comp10420_c0_seq1.p1	sp|Q31YL1|RLML_SHIBS_Ribosomal_RNA_large_subunit_methyltransferase_L_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=rlmL_PE=3_SV=1	2.00E-145	GO:0003676,GO:0003723,GO:0003723,GO:0003723,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006364,GO:0008168,GO:0008168,GO:0008990,GO:0016740,GO:0031167,GO:0031167,GO:0032259,GO:0032259,GO:0052915,GO:0052915,GO:0070043,GO:0070476	nucleic acid binding,RNA binding,RNA binding,RNA binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,rRNA processing,methyltransferase activity,methyltransferase activity,rRNA (guanine-N2-)-methyltransferase activity,transferase activity,rRNA methylation,rRNA methylation,methylation,methylation,23S rRNA (guanine(2445)-N(2))-methyltransferase activity,23S rRNA (guanine(2445)-N(2))-methyltransferase activity,rRNA (guanine-N7)-methyltransferase activity,rRNA (guanine-N7)-methylation
comp104216_c0_seq1.p1	sp|P23538|PPSA_ECOLI_Phosphoenolpyruvate_synthase_OS=Escherichia_coli_(strain_K12)_GN=ppsA_PE=1_SV=5	6.00E-68	GO:0000166,GO:0000287,GO:0003824,GO:0005524,GO:0005524,GO:0006090,GO:0006094,GO:0006094,GO:0008986,GO:0008986,GO:0008986,GO:0016301,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0046872	nucleotide binding,magnesium ion binding,catalytic activity,ATP binding,ATP binding,pyruvate metabolic process,gluconeogenesis,gluconeogenesis,pyruvate, water dikinase activity,pyruvate, water dikinase activity,pyruvate, water dikinase activity,kinase activity,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,metal ion binding
comp10427_c0_seq1.p1				
comp10437_c0_seq1.p1				
comp10449_c0_seq1.p1	sp|P42657|RAD25_SCHPO_DNA_damage_checkpoint_protein_rad25_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rad25_PE=1_SV=1	5.00E-26	GO:0004860,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005829,GO:0006469,GO:0006974,GO:0007049,GO:0007095,GO:0019904,GO:0032153,GO:0034613,GO:0044773,GO:0051286	protein kinase inhibitor activity,protein binding,protein binding,protein binding,protein binding,protein binding,nucleus,cytosol,negative regulation of protein kinase activity,cellular response to DNA damage stimulus,cell cycle,mitotic G2 DNA damage checkpoint,protein domain specific binding,cell division site,cellular protein localization,mitotic DNA damage checkpoint,cell tip
comp10451_c0_seq2.p1	sp|P0AB97|ARSC_SHIFL_Arsenate_reductase_OS=Shigella_flexneri_GN=arsC_PE=3_SV=1	5.00E-89	GO:0008794,GO:0008794,GO:0016491,GO:0046685,GO:0055114,GO:0055114	arsenate reductase (glutaredoxin) activity,arsenate reductase (glutaredoxin) activity,oxidoreductase activity,response to arsenic-containing substance,oxidation-reduction process,oxidation-reduction process
comp10452_c0_seq1.p1	sp|P76097|YDCJ_ECOLI_Uncharacterized_protein_ydcJ_OS=Escherichia_coli_(strain_K12)_GN=ydcJ_PE=4_SV=1	3.00E-111		
comp10456_c0_seq1.p1				
comp104718_c0_seq1.p1				
comp104769_c0_seq1.p1				
comp10477_c0_seq1.p1	sp|Q9VC45|ASP_DROME_Protein_abnormal_spindle_OS=Drosophila_melanogaster_GN=asp_PE=1_SV=3	2.00E-12	GO:0000132,GO:0000226,GO:0000922,GO:0000922,GO:0005516,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005813,GO:0005815,GO:0005819,GO:0005856,GO:0005874,GO:0005875,GO:0005875,GO:0007017,GO:0007049,GO:0007051,GO:0007052,GO:0007067,GO:0007097,GO:0007275,GO:0007282,GO:0008017,GO:0008017,GO:0008017,GO:0030037,GO:0030154,GO:0030706,GO:0030723,GO:0030954,GO:0032027,GO:0032027,GO:0048132,GO:0048477,GO:0048477,GO:0048854,GO:0051295,GO:0051297,GO:0051301,GO:0051383,GO:0051642	establishment of mitotic spindle orientation,microtubule cytoskeleton organization,spindle pole,spindle pole,calmodulin binding,nucleus,nucleus,cytoplasm,cytoplasm,centrosome,microtubule organizing center,spindle,cytoskeleton,microtubule,microtubule associated complex,microtubule associated complex,microtubule-based process,cell cycle,spindle organization,mitotic spindle organization,mitotic nuclear division,nuclear migration,multicellular organismal development,cystoblast division,microtubule binding,microtubule binding,microtubule binding,actin filament reorganization involved in cell cycle,cell differentiation,germarium-derived oocyte differentiation,ovarian fusome organization,astral microtubule nucleation,myosin light chain binding,myosin light chain binding,female germ-line stem cell asymmetric division,oogenesis,oogenesis,brain morphogenesis,establishment of meiotic spindle localization,centrosome organization,cell division,kinetochore organization,centrosome localization
comp104831_c0_seq1.p1	sp|P58578|GSHB_ECO57_Glutathione_synthetase_OS=Escherichia_coli_O157:H7_GN=gshB_PE=3_SV=1	2.00E-65	GO:0000166,GO:0000166,GO:0000287,GO:0003824,GO:0004363,GO:0004363,GO:0004363,GO:0005524,GO:0005524,GO:0005524,GO:0005829,GO:0006750,GO:0006750,GO:0006750,GO:0016874,GO:0030145,GO:0046872,GO:0046872	nucleotide binding,nucleotide binding,magnesium ion binding,catalytic activity,glutathione synthase activity,glutathione synthase activity,glutathione synthase activity,ATP binding,ATP binding,ATP binding,cytosol,glutathione biosynthetic process,glutathione biosynthetic process,glutathione biosynthetic process,ligase activity,manganese ion binding,metal ion binding,metal ion binding
comp10486_c0_seq1.p1	sp|P29691|EF2_CAEEL_Elongation_factor_2_OS=Caenorhabditis_elegans_GN=eef-2_PE=1_SV=4	9.00E-97	GO:0000166,GO:0003746,GO:0003924,GO:0005525,GO:0005525,GO:0005737,GO:0005737,GO:0006184,GO:0006412,GO:0006414	nucleotide binding,translation elongation factor activity,GTPase activity,GTP binding,GTP binding,cytoplasm,cytoplasm,GTP catabolic process,translation,translational elongation
comp104878_c0_seq1.p1				
comp10506_c0_seq1.p1				
comp105093_c0_seq1.p2	sp|Q8I8U2|AP1G_DICDI_AP-1_complex_subunit_gamma_OS=Dictyostelium_discoideum_GN=ap1g1_PE=1_SV=1	4.00E-14	GO:0005515,GO:0005794,GO:0005794,GO:0005794,GO:0006810,GO:0006886,GO:0006895,GO:0008565,GO:0015031,GO:0015031,GO:0016020,GO:0016192,GO:0030117,GO:0030121,GO:0030130,GO:0030131,GO:0030276,GO:0030665,GO:0031410,GO:0044351	protein binding,Golgi apparatus,Golgi apparatus,Golgi apparatus,transport,intracellular protein transport,Golgi to endosome transport,protein transporter activity,protein transport,protein transport,membrane,vesicle-mediated transport,membrane coat,AP-1 adaptor complex,clathrin coat of trans-Golgi network vesicle,clathrin adaptor complex,clathrin binding,clathrin-coated vesicle membrane,cytoplasmic vesicle,macropinocytosis
comp10512_c0_seq1.p1				
comp10515_c0_seq1.p1	sp|Q9P2D7|DYH1_HUMAN_Dynein_heavy_chain_1,_axonemal_OS=Homo_sapiens_GN=DNAH1_PE=1_SV=4	2.00E-27	GO:0000166,GO:0001539,GO:0003341,GO:0003774,GO:0003777,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005858,GO:0005858,GO:0005874,GO:0005929,GO:0006200,GO:0007018,GO:0007018,GO:0008152,GO:0008152,GO:0008152,GO:0009612,GO:0016887,GO:0030286,GO:0030286,GO:0030286,GO:0042995	nucleotide binding,cilium or flagellum-dependent cell motility,cilium movement,motor activity,microtubule motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,axonemal dynein complex,axonemal dynein complex,microtubule,cilium,ATP catabolic process,microtubule-based movement,microtubule-based movement,metabolic process,metabolic process,metabolic process,response to mechanical stimulus,ATPase activity,dynein complex,dynein complex,dynein complex,cell projection
comp10519_c0_seq1.p1	sp|Q83SQ7|FIXC_SHIFL_Protein_fixC_OS=Shigella_flexneri_GN=fixC_PE=3_SV=1	1.00E-67	GO:0008152,GO:0016491,GO:0016491,GO:0055114,GO:0055114,GO:0055114	metabolic process,oxidoreductase activity,oxidoreductase activity,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp105193_c0_seq1.p1				
comp10520_c0_seq1.p1				
comp10524_c0_seq1.p1	sp|O21272|NDUS7_RECAM_NADH-ubiquinone_oxidoreductase_20_kDa_subunit_OS=Reclinomonas_americana_GN=NAD10_PE=3_SV=1	4.00E-96	GO:0005739,GO:0005739,GO:0008137,GO:0008137,GO:0016491,GO:0046872,GO:0048038,GO:0051536,GO:0051539,GO:0051539,GO:0055114,GO:0055114,GO:0055114,GO:0070469	mitochondrion,mitochondrion,NADH dehydrogenase (ubiquinone) activity,NADH dehydrogenase (ubiquinone) activity,oxidoreductase activity,metal ion binding,quinone binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,respiratory chain
comp10526_c0_seq1.p1	sp|P77187|YAHF_ECOLI_Uncharacterized_protein_yahF_OS=Escherichia_coli_(strain_K12)_GN=yahF_PE=4_SV=1	2.00E-23	GO:0003824,GO:0008152,GO:0048037	catalytic activity,metabolic process,cofactor binding
comp105266_c0_seq1.p1	sp|A1L0Z6|RSH6A_XENTR_Radial_spoke_head_protein_6_homolog_A_OS=Xenopus_tropicalis_GN=rsph6a_PE=2_SV=1	7.00E-28		
comp10527_c0_seq1.p1	sp|Q9P720|RL16_NEUCR_60S_ribosomal_protein_L16_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=rpl-16_PE=3_SV=1	8.00E-56	GO:0003735,GO:0005840,GO:0005840,GO:0006412,GO:0015934,GO:0030529	structural constituent of ribosome,ribosome,ribosome,translation,large ribosomal subunit,ribonucleoprotein complex
comp10528_c0_seq1.p2	sp|Q3YXW7|GCSP_SHISS_Glycine_dehydrogenase_[decarboxylating]_OS=Shigella_sonnei_(strain_Ss046)_GN=gcvP_PE=3_SV=1	1.00E-145	GO:0003824,GO:0004375,GO:0004375,GO:0006544,GO:0006546,GO:0016491,GO:0019464,GO:0030170,GO:0055114,GO:0055114	catalytic activity,glycine dehydrogenase (decarboxylating) activity,glycine dehydrogenase (decarboxylating) activity,glycine metabolic process,glycine catabolic process,oxidoreductase activity,glycine decarboxylation via glycine cleavage system,pyridoxal phosphate binding,oxidation-reduction process,oxidation-reduction process
comp10533_c0_seq1.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	5.00E-20	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp105349_c0_seq1.p1				
comp10536_c0_seq1.p1				
comp10540_c0_seq1.p3				
comp10541_c0_seq1.p1	sp|Q83LU7|DING_SHIFL_Probable_ATP-dependent_helicase_dinG_OS=Shigella_flexneri_GN=dinG_PE=3_SV=4	2.00E-69	GO:0000166,GO:0003676,GO:0003677,GO:0003677,GO:0004003,GO:0004386,GO:0005524,GO:0005524,GO:0006139,GO:0006200,GO:0006281,GO:0006310,GO:0006974,GO:0008026,GO:0016787,GO:0016818,GO:0032508,GO:0046872,GO:0051536,GO:0051539	nucleotide binding,nucleic acid binding,DNA binding,DNA binding,ATP-dependent DNA helicase activity,helicase activity,ATP binding,ATP binding,nucleobase-containing compound metabolic process,ATP catabolic process,DNA repair,DNA recombination,cellular response to DNA damage stimulus,ATP-dependent helicase activity,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,DNA duplex unwinding,metal ion binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp10541_c1_seq1.p1	sp|P27296|DING_ECOLI_Probable_ATP-dependent_helicase_dinG_OS=Escherichia_coli_(strain_K12)_GN=dinG_PE=3_SV=3	2.00E-78	GO:0000166,GO:0003676,GO:0003677,GO:0003677,GO:0003678,GO:0004003,GO:0004003,GO:0004386,GO:0005515,GO:0005524,GO:0005524,GO:0006139,GO:0006200,GO:0006281,GO:0006281,GO:0006310,GO:0006974,GO:0008026,GO:0009432,GO:0016787,GO:0016818,GO:0016887,GO:0032508,GO:0033680,GO:0046872,GO:0051536,GO:0051539,GO:0051539,GO:0051539	nucleotide binding,nucleic acid binding,DNA binding,DNA binding,DNA helicase activity,ATP-dependent DNA helicase activity,ATP-dependent DNA helicase activity,helicase activity,protein binding,ATP binding,ATP binding,nucleobase-containing compound metabolic process,ATP catabolic process,DNA repair,DNA repair,DNA recombination,cellular response to DNA damage stimulus,ATP-dependent helicase activity,SOS response,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,ATPase activity,DNA duplex unwinding,ATP-dependent DNA/RNA helicase activity,metal ion binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp105429_c0_seq1.p1				
comp105506_c0_seq1.p1				
comp10551_c0_seq1.p1				
comp105525_c0_seq1.p1	sp|P64432|YPJD_ECOLI_Inner_membrane_protein_ypjD_OS=Escherichia_coli_(strain_K12)_GN=ypjD_PE=1_SV=1	5.00E-66	GO:0005886,GO:0005886,GO:0005886,GO:0016020,GO:0016021,GO:0017004,GO:0020037	plasma membrane,plasma membrane,plasma membrane,membrane,integral component of membrane,cytochrome complex assembly,heme binding
comp10555_c0_seq1.p1				
comp105602_c0_seq1.p1	sp|P15977|MALQ_ECOLI_4-alpha-glucanotransferase_OS=Escherichia_coli_(strain_K12)_GN=malQ_PE=3_SV=2	2.00E-66	GO:0000025,GO:0000025,GO:0000025,GO:0004134,GO:0004134,GO:0004134,GO:0005737,GO:0005737,GO:0005829,GO:0005975,GO:0005975,GO:0005977,GO:0005977,GO:0005977,GO:0016740,GO:0016757	maltose catabolic process,maltose catabolic process,maltose catabolic process,4-alpha-glucanotransferase activity,4-alpha-glucanotransferase activity,4-alpha-glucanotransferase activity,cytoplasm,cytoplasm,cytosol,carbohydrate metabolic process,carbohydrate metabolic process,glycogen metabolic process,glycogen metabolic process,glycogen metabolic process,transferase activity,transferase activity, transferring glycosyl groups
comp105634_c0_seq1.p1				
comp105637_c0_seq1.p1	sp|Q5T655|CC147_HUMAN_Coiled-coil_domain-containing_protein_147_OS=Homo_sapiens_GN=CCDC147_PE=2_SV=1	2.00E-12	GO:0005615	extracellular space
comp10568_c0_seq1.p1				
comp10571_c0_seq1.p1	sp|Q07171|GELS_DROME_Gelsolin_OS=Drosophila_melanogaster_GN=Gel_PE=1_SV=2	1.00E-20	GO:0003779,GO:0003779,GO:0003779,GO:0005576,GO:0005576,GO:0005576,GO:0005576,GO:0005576,GO:0005737,GO:0005829,GO:0005829,GO:0005856,GO:0005856,GO:0005884,GO:0006909,GO:0030041,GO:0046872	actin binding,actin binding,actin binding,extracellular region,extracellular region,extracellular region,extracellular region,cytoplasm,cytosol,cytosol,cytoskeleton,cytoskeleton,actin filament,phagocytosis,actin filament polymerization,metal ion binding
comp10573_c0_seq1.p1	sp|A4IIB8|TTC26_XENTR_Tetratricopeptide_repeat_protein_26_OS=Xenopus_tropicalis_GN=ttc26_PE=2_SV=1	4.00E-174	GO:0005929,GO:0005929,GO:0007224,GO:0030030,GO:0030992,GO:0042073,GO:0042995,GO:0072372	cilium,cilium,smoothened signaling pathway,cell projection organization,intraciliary transport particle B,intraciliary transport,cell projection,primary cilium
comp10580_c0_seq1.p1				
comp10584_c0_seq1.p1	sp|P08368|CREB_ECOLI_Transcriptional_regulatory_protein_CreB_OS=Escherichia_coli_(strain_K12)_GN=creB_PE=1_SV=1	7.00E-126	GO:0000160,GO:0000160,GO:0003677,GO:0003677,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0006355,GO:0042802,GO:0042802	phosphorelay signal transduction system,phosphorelay signal transduction system,DNA binding,DNA binding,cytoplasm,cytoplasm,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,identical protein binding,identical protein binding
comp105847_c0_seq1.p1	sp|P15078|CSTA_ECOLI_Carbon_starvation_protein_A_OS=Escherichia_coli_(strain_K12)_GN=cstA_PE=1_SV=3	9.00E-99	GO:0005886,GO:0005886,GO:0005886,GO:0009267,GO:0009267,GO:0016020,GO:0016020,GO:0016021	plasma membrane,plasma membrane,plasma membrane,cellular response to starvation,cellular response to starvation,membrane,membrane,integral component of membrane
comp105851_c0_seq1.p1				
comp10591_c0_seq1.p1	sp|P0ABF1|PCNB_ECOLI_Poly(A)_polymerase_OS=Escherichia_coli_(strain_K12)_GN=pcnB_PE=1_SV=2	2.00E-127	GO:0000166,GO:0003723,GO:0003723,GO:0003723,GO:0003723,GO:0004652,GO:0004652,GO:0004652,GO:0004652,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005886,GO:0005886,GO:0005886,GO:0006276,GO:0006276,GO:0006351,GO:0006378,GO:0006378,GO:0006396,GO:0006397,GO:0006397,GO:0009451,GO:0009451,GO:0009451,GO:0016020,GO:0016740,GO:0016779,GO:0043631	nucleotide binding,RNA binding,RNA binding,RNA binding,RNA binding,polynucleotide adenylyltransferase activity,polynucleotide adenylyltransferase activity,polynucleotide adenylyltransferase activity,polynucleotide adenylyltransferase activity,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,plasma membrane,plasma membrane,plasma membrane,plasmid maintenance,plasmid maintenance,transcription, DNA-templated,mRNA polyadenylation,mRNA polyadenylation,RNA processing,mRNA processing,mRNA processing,RNA modification,RNA modification,RNA modification,membrane,transferase activity,nucleotidyltransferase activity,RNA polyadenylation
comp105924_c0_seq1.p1	sp|Q83P81|MALF_SHIFL_Maltose_transport_system_permease_protein_malF_OS=Shigella_flexneri_GN=malF_PE=3_SV=2	3.00E-79	GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006810,GO:0008643,GO:0016020,GO:0016020,GO:0016021	plasma membrane,plasma membrane,plasma membrane,transport,transport,carbohydrate transport,membrane,membrane,integral component of membrane
comp10594_c0_seq2.p1				
comp10605_c0_seq1.p1	sp|P27830|RMLB2_ECOLI_dTDP-glucose_4,6-dehydratase_2_OS=Escherichia_coli_(strain_K12)_GN=rffG_PE=1_SV=3	1.00E-118	GO:0003824,GO:0008460,GO:0008460,GO:0008460,GO:0008460,GO:0009103,GO:0009103,GO:0009225,GO:0009243,GO:0016829,GO:0019305,GO:0045226,GO:0050662	catalytic activity,dTDP-glucose 4,6-dehydratase activity,dTDP-glucose 4,6-dehydratase activity,dTDP-glucose 4,6-dehydratase activity,dTDP-glucose 4,6-dehydratase activity,lipopolysaccharide biosynthetic process,lipopolysaccharide biosynthetic process,nucleotide-sugar metabolic process,O antigen biosynthetic process,lyase activity,dTDP-rhamnose biosynthetic process,extracellular polysaccharide biosynthetic process,coenzyme binding
comp106123_c0_seq1.p1				
comp10615_c0_seq1.p1				
comp106201_c0_seq1.p1				
comp106229_c0_seq1.p1	sp|Q3Z2Y7|HFLD_SHISS_High_frequency_lysogenization_protein_HflD_homolog_OS=Shigella_sonnei_(strain_Ss046)_GN=hflD_PE=3_SV=1	2.00E-64	GO:0005737,GO:0005737,GO:0005737,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0016020	cytoplasm,cytoplasm,cytoplasm,plasma membrane,plasma membrane,plasma membrane,plasma membrane,membrane
comp10627_c0_seq1.p1	sp|P21577|6PGD_SYNE7_6-phosphogluconate_dehydrogenase,_decarboxylating_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=gnd_PE=1_SV=4	8.00E-59	GO:0004616,GO:0004616,GO:0006098,GO:0006098,GO:0006098,GO:0016491,GO:0016491,GO:0016616,GO:0019521,GO:0050661,GO:0050662,GO:0055114,GO:0055114	phosphogluconate dehydrogenase (decarboxylating) activity,phosphogluconate dehydrogenase (decarboxylating) activity,pentose-phosphate shunt,pentose-phosphate shunt,pentose-phosphate shunt,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,D-gluconate metabolic process,NADP binding,coenzyme binding,oxidation-reduction process,oxidation-reduction process
comp106375_c0_seq1.p1				
comp10638_c0_seq1.p1				
comp106420_c0_seq1.p2	sp|Q47622|SAPA_ECOLI_Peptide_transport_periplasmic_protein_sapA_OS=Escherichia_coli_(strain_K12)_GN=sapA_PE=3_SV=1	2.00E-89	GO:0005215,GO:0006810,GO:0006810,GO:0015031,GO:0015833,GO:0030288,GO:0042597,GO:0042597,GO:0055052	transporter activity,transport,transport,protein transport,peptide transport,outer membrane-bounded periplasmic space,periplasmic space,periplasmic space,ATP-binding cassette (ABC) transporter complex, substrate-binding subunit-containing
comp106546_c0_seq1.p1	sp|Q3YVI4|RHLB_SHISS_ATP-dependent_RNA_helicase_rhlB_OS=Shigella_sonnei_(strain_Ss046)_GN=rhlB_PE=3_SV=1	4.00E-94	GO:0000166,GO:0000166,GO:0003676,GO:0003723,GO:0003723,GO:0004004,GO:0004004,GO:0004386,GO:0004386,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0006200,GO:0006200,GO:0006200,GO:0006401,GO:0008026,GO:0016787,GO:0016787	nucleotide binding,nucleotide binding,nucleic acid binding,RNA binding,RNA binding,ATP-dependent RNA helicase activity,ATP-dependent RNA helicase activity,helicase activity,helicase activity,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,ATP catabolic process,ATP catabolic process,ATP catabolic process,RNA catabolic process,ATP-dependent helicase activity,hydrolase activity,hydrolase activity
comp10657_c0_seq1.p1				
comp10660_c0_seq1.p2				
comp10670_c0_seq1.p1				
comp106706_c0_seq1.p2				
comp106713_c0_seq1.p1	sp|P09831|GLTB_ECOLI_Glutamate_synthase_[NADPH]_large_chain_OS=Escherichia_coli_(strain_K12)_GN=gltB_PE=1_SV=3	4.00E-99	GO:0003824,GO:0004355,GO:0004355,GO:0005515,GO:0005515,GO:0005737,GO:0006537,GO:0006537,GO:0006537,GO:0006541,GO:0006807,GO:0006807,GO:0008152,GO:0008152,GO:0008652,GO:0015930,GO:0016491,GO:0016491,GO:0016638,GO:0019676,GO:0046872,GO:0051536,GO:0051538,GO:0055114,GO:0055114,GO:0097054	catalytic activity,glutamate synthase (NADPH) activity,glutamate synthase (NADPH) activity,protein binding,protein binding,cytoplasm,glutamate biosynthetic process,glutamate biosynthetic process,glutamate biosynthetic process,glutamine metabolic process,nitrogen compound metabolic process,nitrogen compound metabolic process,metabolic process,metabolic process,cellular amino acid biosynthetic process,glutamate synthase activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors,ammonia assimilation cycle,metal ion binding,iron-sulfur cluster binding,3 iron, 4 sulfur cluster binding,oxidation-reduction process,oxidation-reduction process,L-glutamate biosynthetic process
comp10675_c0_seq1.p1				
comp10678_c0_seq1.p3				
comp10681_c0_seq1.p2				
comp10681_c0_seq2.p1				
comp10684_c0_seq1.p1				
comp10689_c0_seq1.p1	sp|Q07078|HSP83_ORYSJ_Heat_shock_protein_81-3_OS=Oryza_sativa_subsp._japonica_GN=HSP81-3_PE=2_SV=2	3.00E-63	GO:0000166,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0006457,GO:0006950,GO:0051082	nucleotide binding,ATP binding,ATP binding,cytoplasm,cytoplasm,protein folding,response to stress,unfolded protein binding
comp106909_c0_seq1.p1	sp|P0AGM4|YICG_SHIFL_UPF0126_inner_membrane_protein_yicG_OS=Shigella_flexneri_GN=yicG_PE=3_SV=1	1.00E-66	GO:0005886,GO:0005886,GO:0005886,GO:0016020,GO:0016021	plasma membrane,plasma membrane,plasma membrane,membrane,integral component of membrane
comp10693_c0_seq1.p1				
comp10693_c1_seq1.p1				
comp10698_c0_seq1.p1				
comp10703_c0_seq1.p1	sp|P0AEE7|DGAL_SHIFL_D-galactose-binding_periplasmic_protein_OS=Shigella_flexneri_GN=mglB_PE=3_SV=1	9.00E-99	GO:0006810,GO:0006935,GO:0008643,GO:0042597,GO:0042597,GO:0046872	transport,chemotaxis,carbohydrate transport,periplasmic space,periplasmic space,metal ion binding
comp107079_c0_seq1.p1				
comp10713_c0_seq1.p1	sp|P06710|DPO3X_ECOLI_DNA_polymerase_III_subunit_tau_OS=Escherichia_coli_(strain_K12)_GN=dnaX_PE=1_SV=1	2.00E-81	GO:0000166,GO:0003677,GO:0003887,GO:0003887,GO:0003887,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005663,GO:0006200,GO:0006200,GO:0006260,GO:0006260,GO:0006260,GO:0006261,GO:0009360,GO:0016740,GO:0016779,GO:0016887,GO:0017111,GO:0030337,GO:0030337,GO:0042802,GO:0042802,GO:0043846,GO:0071897,GO:0071897,GO:0071897,GO:0003689	nucleotide binding,DNA binding,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,protein binding,ATP binding,ATP binding,nucleus,DNA replication factor C complex,ATP catabolic process,ATP catabolic process,DNA replication,DNA replication,DNA replication,DNA-dependent DNA replication,DNA polymerase III complex,transferase activity,nucleotidyltransferase activity,ATPase activity,nucleoside-triphosphatase activity,DNA polymerase processivity factor activity,DNA polymerase processivity factor activity,identical protein binding,identical protein binding,DNA polymerase III, clamp loader complex,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process,DNA clamp loader activity
comp107145_c0_seq1.p1				
comp10715_c0_seq1.p1	sp|P39057|DYHC_ANTCR_Dynein_beta_chain,_ciliary_OS=Anthocidaris_crassispina_PE=1_SV=1	1.00E-14	GO:0000166,GO:0003774,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005874,GO:0005929,GO:0006200,GO:0007018,GO:0008152,GO:0008152,GO:0016887,GO:0030030,GO:0030286,GO:0030286,GO:0031514,GO:0042995	nucleotide binding,motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,microtubule,cilium,ATP catabolic process,microtubule-based movement,metabolic process,metabolic process,ATPase activity,cell projection organization,dynein complex,dynein complex,motile cilium,cell projection
comp107181_c0_seq1.p2				
comp10727_c0_seq1.p1				
comp10737_c0_seq1.p1				
comp107401_c0_seq1.p1	sp|Q3YVE9|CORA_SHISS_Magnesium_transport_protein_CorA_OS=Shigella_sonnei_(strain_Ss046)_GN=corA_PE=3_SV=1	3.00E-71	GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006811,GO:0006824,GO:0015087,GO:0015095,GO:0015693,GO:0016020,GO:0016020,GO:0016021,GO:0030001,GO:0046873,GO:0055085	plasma membrane,plasma membrane,plasma membrane,transport,ion transport,cobalt ion transport,cobalt ion transmembrane transporter activity,magnesium ion transmembrane transporter activity,magnesium ion transport,membrane,membrane,integral component of membrane,metal ion transport,metal ion transmembrane transporter activity,transmembrane transport
comp10741_c0_seq1.p1				
comp107420_c0_seq1.p1	sp|B2TXT9|SYH_SHIB3_Histidine--tRNA_ligase_OS=Shigella_boydii_serotype_18_(strain_CDC_3083-94_/_BS512)_GN=hisS_PE=3_SV=1	1.00E-82	GO:0000166,GO:0004812,GO:0004812,GO:0004821,GO:0004821,GO:0004821,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006418,GO:0006427,GO:0006427,GO:0016874	nucleotide binding,aminoacyl-tRNA ligase activity,aminoacyl-tRNA ligase activity,histidine-tRNA ligase activity,histidine-tRNA ligase activity,histidine-tRNA ligase activity,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,translation,tRNA aminoacylation for protein translation,histidyl-tRNA aminoacylation,histidyl-tRNA aminoacylation,ligase activity
comp10744_c0_seq1.p1	sp|O74439|YJE9_SCHPO_Uncharacterized_mitochondrial_carrier_C1682.09c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC1682.09c_PE=2_SV=1	3.00E-73	GO:0000002,GO:0001408,GO:0001409,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0006810,GO:0006879,GO:0016020,GO:0016021	mitochondrial genome maintenance,guanine nucleotide transport,guanine nucleotide transmembrane transporter activity,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,transport,cellular iron ion homeostasis,membrane,integral component of membrane
comp10753_c0_seq1.p2				
comp10759_c0_seq1.p1				
comp10759_c0_seq2.p1				
comp107660_c0_seq1.p1	sp|Q9SX03|MCM33_MAIZE_DNA_replication_licensing_factor_MCM3_homolog_3_OS=Zea_mays_GN=ROA3_PE=2_SV=1	1.00E-22	GO:0000166,GO:0003677,GO:0003677,GO:0003678,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006260,GO:0006260,GO:0006270,GO:0007049,GO:0016787,GO:0032508,GO:0042555	nucleotide binding,DNA binding,DNA binding,DNA helicase activity,helicase activity,ATP binding,ATP binding,nucleus,nucleus,nucleus,DNA replication,DNA replication,DNA replication initiation,cell cycle,hydrolase activity,DNA duplex unwinding,MCM complex
comp107695_c0_seq1.p1	sp|Q51649|T408_BURM1_Putative_transposase_for_insertion_sequence_IS408_OS=Burkholderia_multivorans_(strain_ATCC_17616_/_249)_GN=Bmul_4730_PE=3_SV=1	1.00E-16	GO:0003676,GO:0003677,GO:0006310,GO:0015074,GO:0032196	nucleic acid binding,DNA binding,DNA recombination,DNA integration,transposition
comp107696_c0_seq1.p1	sp|P22314|UBA1_HUMAN_Ubiquitin-like_modifier-activating_enzyme_1_OS=Homo_sapiens_GN=UBA1_PE=1_SV=3	2.00E-18	GO:0000166,GO:0003824,GO:0004839,GO:0004839,GO:0004839,GO:0004842,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0005739,GO:0005739,GO:0005829,GO:0006464,GO:0006974,GO:0008641,GO:0016567,GO:0016567,GO:0016874,GO:0019941,GO:0044822,GO:0044822,GO:0070062,GO:0070062,GO:0070062,GO:0070062,GO:0070062,GO:0000792,GO:0005765,GO:0010008,GO:0030057,GO:0030867	nucleotide binding,catalytic activity,ubiquitin activating enzyme activity,ubiquitin activating enzyme activity,ubiquitin activating enzyme activity,ubiquitin-protein transferase activity,protein binding,protein binding,protein binding,ATP binding,ATP binding,nucleus,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,mitochondrion,mitochondrion,mitochondrion,cytosol,cellular protein modification process,cellular response to DNA damage stimulus,small protein activating enzyme activity,protein ubiquitination,protein ubiquitination,ligase activity,modification-dependent protein catabolic process,poly(A) RNA binding,poly(A) RNA binding,extracellular vesicular exosome,extracellular vesicular exosome,extracellular vesicular exosome,extracellular vesicular exosome,extracellular vesicular exosome,heterochromatin,lysosomal membrane,endosome membrane,desmosome,rough endoplasmic reticulum membrane
comp10774_c0_seq1.p1				
comp107779_c0_seq1.p2				
comp10783_c0_seq1.p2				
comp107843_c0_seq1.p2	sp|P77495|PRPE_ECOLI_Propionate--CoA_ligase_OS=Escherichia_coli_(strain_K12)_GN=prpE_PE=3_SV=1	2.00E-63	GO:0000166,GO:0003824,GO:0005524,GO:0008152,GO:0016874,GO:0019629,GO:0050218,GO:0050218,GO:0050218	nucleotide binding,catalytic activity,ATP binding,metabolic process,ligase activity,propionate catabolic process, 2-methylcitrate cycle,propionate-CoA ligase activity,propionate-CoA ligase activity,propionate-CoA ligase activity
comp107850_c0_seq1.p2	sp|Q6QNL9|KC1_EIMTE_Casein_kinase_I_OS=Eimeria_tenella_PE=2_SV=1	2.00E-51	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp107911_c0_seq1.p1	sp|P71229|HYFR_ECOLI_Hydrogenase-4_transcriptional_activator_OS=Escherichia_coli_(strain_K12)_GN=hyfR_PE=4_SV=1	6.00E-61	GO:0000156,GO:0000160,GO:0000160,GO:0000166,GO:0000785,GO:0003677,GO:0003677,GO:0003677,GO:0003700,GO:0005524,GO:0005524,GO:0006351,GO:0006352,GO:0006355,GO:0006355,GO:0008134,GO:0043565,GO:0043565,GO:0044212,GO:2000142	phosphorelay response regulator activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,chromatin,DNA binding,DNA binding,DNA binding,sequence-specific DNA binding transcription factor activity,ATP binding,ATP binding,transcription, DNA-templated,DNA-templated transcription, initiation,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,transcription factor binding,sequence-specific DNA binding,sequence-specific DNA binding,transcription regulatory region DNA binding,regulation of DNA-templated transcription, initiation
comp10795_c0_seq1.p1				
comp107958_c0_seq1.p1				
comp108071_c0_seq1.p2				
comp108098_c0_seq1.p1	sp|Q03498|VATA_PLAFA_V-type_proton_ATPase_catalytic_subunit_A_OS=Plasmodium_falciparum_GN=vapA_PE=3_SV=1	9.00E-35	GO:0000166,GO:0005524,GO:0005524,GO:0006810,GO:0006811,GO:0015991,GO:0015992,GO:0015992,GO:0016787,GO:0016820,GO:0033178,GO:0033180,GO:0046034,GO:0046961	nucleotide binding,ATP binding,ATP binding,transport,ion transport,ATP hydrolysis coupled proton transport,proton transport,proton transport,hydrolase activity,hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances,proton-transporting two-sector ATPase complex, catalytic [illegible]
comp10812_c0_seq1.p1				
comp10813_c0_seq1.p1				
comp10814_c0_seq1.p1				
comp10816_c0_seq2.p2				
comp10822_c0_seq2.p2				
comp10823_c0_seq1.p1				
comp108281_c0_seq1.p1				
comp10840_c0_seq1.p1				
comp10843_c0_seq1.p2				
comp108557_c0_seq1.p1	sp|P09549|DEDD_ECOLI_Protein_dedD_OS=Escherichia_coli_(strain_K12)_GN=dedD_PE=4_SV=2	7.00E-47	GO:0030428,GO:0032153,GO:0032506,GO:0042834	[illegible]
comp108622_c0_seq1.p1	sp|P05042|FUMC_ECOLI_Fumarate_hydratase_class_II_OS=Escherichia_coli_(strain_K12)_GN=fumC_PE=1_SV=1	1.00E-108	GO:0003824,GO:0003824,GO:0004333,GO:0004333,GO:0004333,GO:0004333,GO:0005737,GO:0005737,GO:0005737,GO:0006099,GO:0006099,GO:0006099,GO:0006099,GO:0006106,GO:0006979,GO:0008152,GO:0016829,GO:0016829,GO:0045239	[illegible]
comp108709_c0_seq1.p2				
comp108719_c0_seq1.p1	sp|P77366|PGMB_ECOLI_Putative_beta-phosphoglucomutase_OS=Escherichia_coli_(strain_K12)_GN=ycjU_PE=3_SV=1	8.00E-146	GO:0000287,GO:0000287,GO:0005737,GO:0005737,GO:0005975,GO:0005975,GO:0005975,GO:0006974,GO:0008152,GO:0008801,GO:0008801,GO:0008801,GO:0009294,GO:0016787,GO:0016853,GO:0046677,GO:0046872	[illegible]
comp10876_c0_seq1.p1				
comp10877_c0_seq1.p1				
comp108870_c0_seq1.p1	sp|Q3Z5G3|SYP_SHISS_Proline--tRNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=proS_PE=3_SV=1	1.00E-89	GO:0000166,GO:0000166,GO:0002161,GO:0004812,GO:0004812,GO:0004827,GO:0004827,GO:0004827,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006418,GO:0006433,GO:0006433,GO:0006450,GO:0016874	[illegible]
comp10893_c0_seq1.p1	sp|Q23381|MUTA_CAEEL_Probable_methylmalonyl-CoA_mutase,_mitochondrial_OS=Caenorhabditis_elegans_GN=mmcm-1_PE=2_SV=2	0	GO:0003824,GO:0004494,GO:0004494,GO:0004494,GO:0005739,GO:0005739,GO:0005759,GO:0008152,GO:0016853,GO:0016853,GO:0016866,GO:0031419,GO:0031419,GO:0046872,GO:0046872	[illegible]
comp10897_c0_seq1.p1	sp|P31320|KAPR_BLAEM_cAMP-dependent_protein_kinase_regulatory_subunit_OS=Blastocladiella_emersonii_GN=PKAR_PE=2_SV=1	1.00E-65	GO:0000166,GO:0001932,GO:0005952,GO:0008603,GO:0030552,GO:0045859	[illegible]
comp10905_c0_seq1.p1				
comp109141_c0_seq1.p1	sp|P76524|YPDF_ECOLI_Aminopeptidase_ypdF_OS=Escherichia_coli_(strain_K12)_GN=ypdF_PE=3_SV=1	5.00E-65	GO:0004177,GO:0004177,GO:0004177,GO:0004177,GO:0005515,GO:0005515,GO:0006508,GO:0006508,GO:0006508,GO:0008233,GO:0008235,GO:0016787,GO:0016787	[illegible]
comp109160_c0_seq1.p1	sp|Q3Z0G0|HIS6_SHISS_Imidazole_glycerol_phosphate_synthase_subunit_HisF_OS=Shigella_sonnei_(strain_Ss046)_GN=hisF_PE=3_SV=1	2.00E-63	GO:0000105,GO:0000105,GO:0000105,GO:0000105,GO:0000107,GO:0000107,GO:0003824,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0008152,GO:0008652,GO:0016829	[illegible]

comp11207_c0_seq1.p1				
comp11214_c0_seq1.p1				
comp112141_c0_seq1.p1	sp|P0AAQ9|YBAA_SHIFL_Uncharacterized_protein_ybaA_OS=Shigella_flexneri_GN=ybaA_PE=1_SV=1	8.00E-65		
comp11226_c0_seq1.p1				
comp11228_c0_seq2.p1				
comp11238_c0_seq1.p1				
comp11240_c0_seq1.p1				
comp11241_c0_seq2.p1	sp|P0CP86|PPIL3_CRYNJ_Peptidyl-prolyl_cis-trans_isomerase-like_3_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=CYP10_PE=3_SV=1	8.00E-76	GO:0000413,GO:0003755,GO:0003755,GO:0003755,GO:0006457,GO:0016853	protein peptidyl-prolyl isomerization,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,protein folding,isomerase activity
comp11248_c0_seq2.p1				
comp112484_c0_seq1.p1	sp|Q688J2|LAX2_ORYSJ_Auxin_transporter-like_protein_2_OS=Oryza_sativa_subsp._japonica_GN=Os05g0447200_PE=2_SV=1	8.00E-17	GO:0005886,GO:0005886,GO:0006810,GO:0006865,GO:0009734,GO:0015293,GO:0016020,GO:0016021,GO:0055085	plasma membrane,plasma membrane,transport,amino acid transport,auxin-activated signaling pathway,symporter activity,membrane,integral component of membrane,transmembrane transport
comp112601_c0_seq1.p1				
comp112645_c0_seq1.p2				
comp11269_c0_seq1.p1	sp|Q8SPQ7|FMO3_MACMU_Dimethylaniline_monooxygenase_[N-oxide-forming]_3_OS=Macaca_mulatta_GN=FMO3_PE=2_SV=3	8.00E-15	GO:0004497,GO:0004499,GO:0004499,GO:0005783,GO:0005789,GO:0016020,GO:0016021,GO:0016491,GO:0031090,GO:0034899,GO:0043231,GO:0050660,GO:0050661,GO:0055114,GO:0055114	monooxygenase activity,N,N-dimethylaniline monooxygenase activity,N,N-dimethylaniline monooxygenase activity,endoplasmic reticulum,endoplasmic reticulum membrane,membrane,integral component of membrane,oxidoreductase activity,organelle membrane,trimethylamine monooxygenase activity,intracellular membrane-bounded organelle,flavin adenine dinucleotide binding,NADP binding,oxidation-reduction process,oxidation-reduction process
comp112695_c0_seq1.p1				
comp11276_c0_seq1.p1				
comp11277_c0_seq1.p2				
comp11277_c0_seq2.p1				
comp112780_c0_seq1.p1	sp|P16690|PHNN_ECOLI_Ribose_1,5-bisphosphate_phosphokinase_PhnN_OS=Escherichia_coli_(strain_K12)_GN=phnN_PE=1_SV=1	8.00E-86	GO:0000166,GO:0005524,GO:0006015,GO:0006015,GO:0006015,GO:0006015,GO:0009435,GO:0016740,GO:0019634,GO:0019634,GO:0033863,GO:0033863,GO:0033863,GO:0033863,GO:0033863,GO:0046835,GO:0046835,GO:0046835,GO:0046835	nucleotide binding,ATP binding,5-phosphoribose 1-diphosphate biosynthetic process,5-phosphoribose 1-diphosphate biosynthetic process,5-phosphoribose 1-diphosphate biosynthetic process,5-phosphoribose 1-diphosphate biosynthetic process,NAD biosynthetic process,transferase activity,organic phosphonate metabolic process,organic phosphonate metabolic process,ribose 1,5-bisphosphate phosphokinase activity,ribose 1,5-bisphosphate phosphokinase activity,ribose 1,5-bisphosphate phosphokinase activity,ribose 1,5-bisphosphate phosphokinase activity,ribose 1,5-bisphosphate phosphokinase activity,carbohydrate phosphorylation,carbohydrate phosphorylation,carbohydrate phosphorylation,carbohydrate phosphorylation
comp11280_c0_seq1.p1	sp|Q566V0|ARCH_DANRE_Protein_archease_OS=Danio_rerio_GN=zbtb8os_PE=2_SV=2	2.00E-24	GO:0003674,GO:0006388,GO:0008033,GO:0046872,GO:0072669	molecular_function,tRNA splicing, via endonucleolytic cleavage and ligation,tRNA processing,metal ion binding,tRNA-splicing ligase complex
comp11282_c0_seq1.p1				
comp11284_c0_seq1.p1	sp|P08793|XDH_CALVI_Xanthine_dehydrogenase_OS=Calliphora_vicina_GN=XDH_PE=2_SV=1	3.00E-24	GO:0003824,GO:0004854,GO:0004854,GO:0004854,GO:0004855,GO:0005506,GO:0005777,GO:0005777,GO:0008762,GO:0009055,GO:0009115,GO:0016491,GO:0016491,GO:0016614,GO:0043546,GO:0043546,GO:0043546,GO:0046872,GO:0046872,GO:0050660,GO:0050660,GO:0050660,GO:0051536,GO:0051536,GO:0051537,GO:0051537,GO:0051537,GO:0051537,GO:0055114,GO:0055114	catalytic activity,xanthine dehydrogenase activity,xanthine dehydrogenase activity,xanthine dehydrogenase activity,xanthine oxidase activity,iron ion binding,peroxisome,peroxisome,UDP-N-acetylmuramate dehydrogenase activity,electron carrier activity,xanthine catabolic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on CH-OH group of donors,molybdopterin cofactor binding,molybdopterin cofactor binding,molybdopterin cofactor binding,metal ion binding,metal ion binding,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,iron-sulfur cluster binding,iron-sulfur cluster binding,2 iron, 2 sulfur cluster binding,2 iron, 2 sulfur cluster binding,2 iron, 2 sulfur cluster binding,2 iron, 2 sulfur cluster binding,oxidation-reduction process,oxidation-reduction process
comp112878_c0_seq1.p1				
comp11291_c0_seq1.p1				
comp113027_c0_seq1.p1	sp|P40032|TPA1_YEAST_PKHD-type_hydroxylase_TPA1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TPA1_PE=1_SV=1	2.00E-23	GO:0000288,GO:0005506,GO:0005634,GO:0005634,GO:0006415,GO:0006415,GO:0006449,GO:0008143,GO:0016491,GO:0016491,GO:0016705,GO:0016706,GO:0018188,GO:0031418,GO:0031418,GO:0031543,GO:0046872,GO:0051213,GO:0055114,GO:0055114	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay,iron ion binding,nucleus,nucleus,translational termination,translational termination,regulation of translational termination,poly(A) binding,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,peptidyl-proline di-hydroxylation,L-ascorbic acid binding,L-ascorbic acid binding,peptidyl-proline dioxygenase activity,metal ion binding,dioxygenase activity,oxidation-reduction process,oxidation-reduction process
comp11309_c0_seq1.p1				
comp113107_c0_seq1.p1				
comp11313_c0_seq1.p1				
comp11314_c0_seq1.p1	sp|Q54NQ9|SFXN_DICDI_Sideroflexin_OS=Dictyostelium_discoideum_GN=sfxn_PE=3_SV=1	4.00E-19	GO:0005739,GO:0006810,GO:0006812,GO:0008324,GO:0016020,GO:0016020,GO:0016021,GO:0031966,GO:0055085,GO:0098655	mitochondrion,transport,cation transport,cation transmembrane transporter activity,membrane,membrane,integral component of membrane,mitochondrial membrane,transmembrane transport,cation transmembrane transport
comp11314_c0_seq2.p1	sp|Q54NQ9|SFXN_DICDI_Sideroflexin_OS=Dictyostelium_discoideum_GN=sfxn_PE=3_SV=1	3.00E-32	GO:0005739,GO:0006810,GO:0006812,GO:0008324,GO:0016020,GO:0016020,GO:0016021,GO:0031966,GO:0055085,GO:0098655	mitochondrion,transport,cation transport,cation transmembrane transporter activity,membrane,membrane,integral component of membrane,mitochondrial membrane,transmembrane transport,cation transmembrane transport
comp11315_c0_seq1.p1				
comp11316_c0_seq1.p2				
comp11317_c0_seq2.p1				
comp113178_c0_seq1.p1				
comp11319_c0_seq1.p1				
comp113197_c0_seq1.p1	sp|Q29RM3|REEP5_BOVIN_Receptor_expression-enhancing_protein_5_OS=Bos_taurus_GN=REEP5_PE=2_SV=1	1.00E-25	GO:0016020,GO:0016020,GO:0016021	membrane,membrane,integral component of membrane
comp11327_c0_seq2.p1				
comp113305_c0_seq1.p1	sp|P54211|PMA1_DUNBI_Plasma_membrane_ATPase_OS=Dunaliella_bioculata_GN=PMA1_PE=2_SV=1	7.00E-18	GO:0000166,GO:0000166,GO:0005524,GO:0005886,GO:0005886,GO:0006200,GO:0006754,GO:0006810,GO:0006811,GO:0006812,GO:0008553,GO:0015992,GO:0016020,GO:0016021,GO:0016021,GO:0016787,GO:0016887,GO:0019829,GO:0046872,GO:0046872,GO:0098655,GO:1902600	nucleotide binding,nucleotide binding,ATP binding,plasma membrane,plasma membrane,ATP catabolic process,ATP biosynthetic process,transport,ion transport,cation transport,hydrogen-exporting ATPase activity, phosphorylative mechanism,proton transport,membrane,integral component of membrane,integral component of membrane,hydrolase activity,ATPase activity,cation-transporting ATPase activity,metal ion binding,metal ion binding,cation transmembrane transport,hydrogen ion transmembrane transport
comp11336_c0_seq2.p1	sp|Q7NFN6|RIMP_GLOVI_Ribosome_maturation_factor_RimP_OS=Gloeobacter_violaceus_(strain_PCC_7421)_GN=rimP_PE=3_SV=2	1.00E-16	GO:0005737,GO:0005737,GO:0005737,GO:0042254,GO:0042274	cytoplasm,cytoplasm,cytoplasm,ribosome biogenesis,ribosomal small subunit biogenesis
comp11340_c0_seq1.p1				
comp11344_c0_seq1.p1				
comp113455_c0_seq1.p2	sp|P43344|RPOD_SERMA_RNA_polymerase_sigma_factor_rpoD_(Fragment)_OS=Serratia_marcescens_GN=rpoD_PE=3_SV=1	9.00E-96	GO:0003677,GO:0003677,GO:0003700,GO:0005737,GO:0005737,GO:0006351,GO:0006352,GO:0006355,GO:0006355,GO:0006355,GO:0016987,GO:0016987	DNA binding,DNA binding,sequence-specific DNA binding transcription factor activity,cytoplasm,cytoplasm,transcription, DNA-templated,DNA-templated transcription, initiation,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,sigma factor activity,sigma factor activity
comp113458_c0_seq1.p1				
comp11346_c0_seq1.p1				
comp11351_c0_seq1.p2				
comp113529_c0_seq1.p1	sp|Q3Z5I8|EFTS_SHISS_Elongation_factor_Ts_OS=Shigella_sonnei_(strain_Ss046)_GN=tsf_PE=3_SV=1	6.00E-68	GO:0003746,GO:0003746,GO:0003746,GO:0005622,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006414,GO:0006414,GO:0006414	translation elongation factor activity,translation elongation factor activity,translation elongation factor activity,intracellular,cytoplasm,cytoplasm,cytoplasm,translation,translational elongation,translational elongation,translational elongation
comp11354_c0_seq1.p1	sp|D3ZVF4|TPPC2_RAT_Trafficking_protein_particle_complex_subunit_2_OS=Rattus_norvegicus_GN=Trappc2_PE=3_SV=1	3.00E-33	GO:0005622,GO:0005634,GO:0005634,GO:0005737,GO:0005783,GO:0005783,GO:0005794,GO:0005794,GO:0006351,GO:0006810,GO:0006810,GO:0006888,GO:0016192,GO:0048471	intracellular,nucleus,nucleus,cytoplasm,endoplasmic reticulum,endoplasmic reticulum,Golgi apparatus,Golgi apparatus,transcription, DNA-templated,transport,transport,ER to Golgi vesicle-mediated transport,vesicle-mediated transport,perinuclear region of cytoplasm
comp113561_c0_seq1.p1				
comp11358_c0_seq1.p3	sp|Q5I0K7|ALG13_RAT_UDP-N-acetylglucosamine_transferase_subunit_ALG13_homolog_OS=Rattus_norvegicus_GN=Alg13_PE=1_SV=1	3.00E-16	GO:0004577,GO:0005783,GO:0005783,GO:0005975,GO:0016740,GO:0016757,GO:0016758,GO:0030246,GO:0030259	N-acetylglucosaminyldiphosphodolichol N-acetylglucosaminyltransferase activity,endoplasmic reticulum,endoplasmic reticulum,carbohydrate metabolic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups,carbohydrate binding,lipid glycosylation
comp11358_c0_seq2.p1	sp|Q5I0K7|ALG13_RAT_UDP-N-acetylglucosamine_transferase_subunit_ALG13_homolog_OS=Rattus_norvegicus_GN=Alg13_PE=1_SV=1	1.00E-31	GO:0004577,GO:0005783,GO:0005783,GO:0005975,GO:0016740,GO:0016757,GO:0016758,GO:0030246,GO:0030259	N-acetylglucosaminyldiphosphodolichol N-acetylglucosaminyltransferase activity,endoplasmic reticulum,endoplasmic reticulum,carbohydrate metabolic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups,carbohydrate binding,lipid glycosylation
comp11360_c0_seq1.p1	sp|A5FJ42|RSMG_FLAJ1_Ribosomal_RNA_small_subunit_methyltransferase_G_OS=Flavobacterium_johnsoniae_(strain_ATCC_17061_/_DSM_2064_/_UW101)_GN=rsmG_PE=3_SV=1	9.00E-40	GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006364,GO:0006364,GO:0006364,GO:0008168,GO:0008649,GO:0016740,GO:0031167,GO:0032259,GO:0070043,GO:0070476	cytoplasm,cytoplasm,cytoplasm,cytoplasm,rRNA processing,rRNA processing,rRNA processing,methyltransferase activity,rRNA methyltransferase activity,transferase activity,rRNA methylation,methylation,rRNA (guanine-N7-)-methyltransferase activity,rRNA (guanine-N7)-methylation
comp11361_c0_seq1.p1				
comp11363_c0_seq1.p1	sp|Q11GT5|DNLJ_MESSB_DNA_ligase_OS=Mesorhizobium_sp._(strain_BNC1)_GN=ligA_PE=3_SV=1	6.00E-22	GO:0003911,GO:0003911,GO:0003911,GO:0006259,GO:0006260,GO:0006260,GO:0006266,GO:0006266,GO:0006266,GO:0006281,GO:0006281,GO:0006974,GO:0016874,GO:0046872	DNA ligase (NAD+) activity,DNA ligase (NAD+) activity,DNA ligase (NAD+) activity,DNA metabolic process,DNA replication,DNA replication,DNA ligation,DNA ligation,DNA ligation,DNA repair,DNA repair,cellular response to DNA damage stimulus,ligase activity,metal ion binding
comp11364_c0_seq1.p1				
comp11365_c0_seq1.p1				

comp11877_c0_seq1.p1	sp|Q54G78|SSRP1_DICDI_FACT_complex_subunit_SSRP1_OS=Dictyostelium_discoideum_GN=ssrp1_PE=3_SV=1	9.00E-76
comp11878_c0_seq1.p1	sp|P51281|YCF45_PORPU_Uncharacterized_protein_ycf45_OS=Porphyra_purpurea_GN=ycf45_PE=3_SV=1	6.00E-31
comp11879_c0_seq2.p1		
comp11880_c0_seq1.p1		
comp11881_c0_seq2.p1		
comp11882_c0_seq1.p1	sp|P04786|TOP1_YEAST_DNA_topoisomerase_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TOP1_PE=1_SV=2	9.00E-145
comp11885_c0_seq2.p1		
comp11888_c0_seq1.p1	sp|Q9JJZ4|UB2J1_MOUSE_Ubiquitin-conjugating_enzyme_E2_J1_OS=Mus_musculus_GN=Ube2j1_PE=1_SV=2	5.00E-33
comp11890_c0_seq1.p1	sp|Q9DBB4|NAA16_MOUSE_N-alpha-acetyltransferase_16,_NatA_auxiliary_subunit_OS=Mus_musculus_GN=Naa16_PE=2_SV=1	1.00E-138
comp11891_c0_seq1.p1		
comp11892_c0_seq1.p1	sp|Q8BS95|GPHR_MOUSE_Golgi_pH_regulator_OS=Mus_musculus_GN=Gpr89a_PE=2_SV=2	2.00E-54
comp11894_c0_seq1.p1	sp|Q9JLR1|S61A2_MOUSE_Protein_transport_protein_Sec61_subunit_alpha_isoform_2_OS=Mus_musculus_GN=Sec61a2_PE=2_SV=3	0
comp11895_c0_seq1.p1	sp|Q7Z8P9|NDK_ASPFU_Nucleoside_diphosphate_kinase_OS=Neosartorya_fumigata_(strain_ATCC_MYA-4609_/_Af293_/_CBS_101355_/_FGSC_A1100)_GN=ndk1_PE=3_SV=1	3.00E-67
comp11895_c0_seq1.p3		
comp11896_c0_seq2.p1	sp|B8HTK3|AMPA_CYAP4_Probable_cytosol_aminopeptidase_OS=Cyanothece_sp._(strain_PCC_7425_/_ATCC_29141)_GN=pepA_PE=3_SV=1	1.00E-147
comp11897_c0_seq1.p1		
comp11898_c0_seq1.p1		
comp11899_c0_seq1.p1	sp|O75845|SC5D_HUMAN_Lathosterol_oxidase_OS=Homo_sapiens_GN=SC5DL_PE=1_SV=2	3.00E-12
comp11901_c0_seq1.p1	sp|E0IWI3|DCDA_ECOLW_Diaminopimelate_decarboxylase_OS=Escherichia_coli_(strain_ATCC_9637_/_CCM_2024_/_DSM_1116_/_NCIMB_8666_/_NRRL_B-766_/_W)_GN=lysA_PE=1_SV=1	5.00E-68
comp11902_c0_seq1.p1	sp|Q6DF30|DHDH_XENTR_Trans-1,2-dihydrobenzene-1,2-diol_dehydrogenase_OS=Xenopus_tropicalis_GN=dhdh_PE=2_SV=1	2.00E-19
comp11902_c0_seq1.p2	sp|Q9R0M5|TPK1_MOUSE_Thiamin_pyrophosphokinase_1_OS=Mus_musculus_GN=Tpk1_PE=1_SV=1	7.00E-39
comp11904_c0_seq1.p1	sp|Q8KEM4|Y663_CHLTE_UPF0301_protein_CT0663_OS=Chlorobium_tepidum_(strain_ATCC_49652_/_DSM_12025_/_TLS)_GN=CT0663_PE=3_SV=1	2.00E-23
comp11905_c0_seq1.p1		
comp11906_c0_seq1.p1		
comp11907_c0_seq1.p1	sp|Q9UDX5|MTFP1_HUMAN_Mitochondrial_fission_process_protein_1_OS=Homo_sapiens_GN=MTFP1_PE=1_SV=1	5.00E-24
comp11908_c0_seq1.p1		
comp11909_c0_seq1.p1		
comp11912_c0_seq2.p1		
comp11913_c0_seq1.p1		
comp11916_c0_seq1.p1	sp|Q9P3U1|YKX5_SCHPO_Uncharacterized_RNA-binding_protein_C328.05_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC328.05_PE=2_SV=2	2.00E-32
comp11917_c0_seq1.p1	sp|O35790|PIGL_RAT_N-acetylglucosaminyl-phosphatidylinositol_de-N-acetylase_OS=Rattus_norvegicus_GN=Pigl_PE=2_SV=1	1.00E-49
comp11919_c0_seq1.p1		
comp11920_c0_seq1.p1		
comp11924_c0_seq1.p1	sp|Q54LN2|VP13D_DICDI_Putative_vacuolar_protein_sorting-associated_protein_13D_OS=Dictyostelium_discoideum_GN=vps13D_PE=3_SV=1	6.00E-33
comp11925_c0_seq1.p1		
comp11926_c0_seq1.p1	sp|Q05B83|RFC2_BOVIN_Replication_factor_C_subunit_2_OS=Bos_taurus_GN=RFC2_PE=2_SV=1	3.00E-134
comp11927_c0_seq1.p1	sp|P56558|OGT1_RAT_UDP-N-acetylglucosamine--peptide_N-acetylglucosaminyltransferase_110_kDa_subunit_OS=Rattus_norvegicus_GN=Ogt_PE=1_SV=1	4.00E-15
comp11928_c0_seq3.p1		
comp11930_c0_seq1.p1	sp|P62457|HISX_DESVH_Histidinol_dehydrogenase_OS=Desulfovibrio_vulgaris_(strain_Hildenborough_/_ATCC_29579_/_NCIMB_8303)_GN=hisD_PE=3_SV=1	3.00E-71
comp11931_c0_seq1.p1		
comp11932_c0_seq1.p1		
comp11933_c0_seq1.p1		
comp11933_c0_seq2.p1		
comp11934_c0_seq1.p1	sp|Q8DRY7|ZUPT_STRMU_Zinc_transporter_ZupT_OS=Streptococcus_mutans_GN=zupT_PE=3_SV=1	4.00E-41
comp11935_c0_seq1.p1	sp|P06281|RENI1_MOUSE_Renin-1_OS=Mus_musculus_GN=Ren1_PE=1_SV=1	3.00E-39
comp11938_c0_seq1.p1	sp|Q54XX9|PX24B_DICDI_PXMP2/4_family_protein_2_OS=Dictyostelium_discoideum_GN=DDB_G0278529_PE=3_SV=1	7.00E-21
comp11939_c0_seq1.p1		
comp11942_c0_seq1.p1	sp|O65607|MSH3_ARATH_DNA_mismatch_repair_protein_Msh3_OS=Arabidopsis_thaliana_GN=MSH3_PE=2_SV=2	9.00E-31
comp11944_c0_seq1.p1	sp|Q9RRT0|UBIE_DEIRA_Demethylmenaquinone_methyltransferase_OS=Deinococcus_radiodurans_(strain_ATCC_13939_/_DSM_20539_/_JCM_16871_/_LMG_4051_/_NBRC_15346_/_NCIMB_9279_/_R1_/_VKM_B-1422)_GN=ubiE_PE=3_SV=1	7.00E-13
comp11948_c0_seq1.p1	sp|P49165|RL4_URECA_60S_ribosomal_protein_L4_OS=Urechis_caupo_GN=RPL4_PE=2_SV=1	4.00E-114
comp11950_c0_seq1.p1	sp|Q9R9N3|ODP2_RHIME_Dihydrolipoyllysine-residue_acetyltransferase_component_of_pyruvate_dehydrogenase_complex_OS=Rhizobium_meliloti_(strain_1021)_GN=pdhC_PE=3_SV=1	7.00E-41
comp11951_c0_seq1.p1		
comp119539_c0_seq1.p1	sp|P77338|KEFA_ECOLI_Potassium_efflux_system_KefA_OS=Escherichia_coli_(strain_K12)_GN=kefA_PE=1_SV=1	5.00E-59
comp11954_c0_seq1.p1		
comp11955_c0_seq1.p1	sp|Q2RV59|RS16_RHORT_30S_ribosomal_protein_S16_OS=Rhodospirillum_rubrum_(strain_ATCC_11170_/_NCIB_8255)_GN=rpsP_PE=3_SV=1	9.00E-28
comp11958_c0_seq1.p1	sp|Q6Q4H1|JMJD6_HYDVU_Bifunctional_arginine_demethylase_and_lysyl-hydroxylase_PSR_OS=Hydra_vulgaris_GN=PSR_PE=1_SV=1	4.00E-58
comp11959_c0_seq1.p1	sp|Q9UJZ1|STML2_HUMAN_Stomatin-like_protein_2_OS=Homo_sapiens_GN=STOML2_PE=1_SV=1	4.00E-61
comp11960_c0_seq1.p1		
comp119603_c0_seq1.p1		
comp11961_c0_seq1.p1	sp|P30574|CBPY_CANAX_Carboxypeptidase_Y_OS=Candida_albicans_GN=CPY1_PE=2_SV=2	7.00E-100
comp11962_c0_seq1.p1		
comp11963_c0_seq1.p1		
comp11965_c0_seq1.p1		
comp11966_c0_seq1.p1	sp|Q8BHJ5|TBL1R_MOUSE_F-box-like/WD_repeat-containing_protein_TBL1XR1_OS=Mus_musculus_GN=Tbl1xr1_PE=2_SV=1	3.00E-141
comp11967_c0_seq1.p1		
comp11967_c0_seq2.p1		
comp11968_c0_seq1.p1		
comp11969_c0_seq2.p1	sp|Q01667|CAB6_ARATH_Chlorophyll_a-b_binding_protein_6,_chloroplastic_OS=Arabidopsis_thaliana_GN=LHCA1_PE=1_SV=1	3.00E-14
comp11971_c0_seq1.p1		
comp11972_c0_seq1.p2		
comp11974_c0_seq1.p1		
comp11975_c0_seq1.p1	sp|P15288|PEPD_ECOLI_Cytosol_non-specific_dipeptidase_OS=Escherichia_coli_(strain_K12)_GN=pepD_PE=1_SV=3	1.00E-101
comp11976_c0_seq1.p1		
comp11977_c0_seq1.p1	sp|Q9LDU6|ST7R_ARATH_7-dehydrocholesterol_reductase_OS=Arabidopsis_thaliana_GN=DWF5_PE=1_SV=1	1.00E-158
comp11978_c0_seq1.p1	sp|Q1RJD8|TRXB_RICBR_Thioredoxin_reductase_OS=Rickettsia_bellii_(strain_RML369-C)_GN=trxB_PE=3_SV=1	2.00E-82
comp11979_c0_seq1.p1	sp|Q9LHJ9|P2C38_ARATH_Probable_protein_phosphatase_2C_38_OS=Arabidopsis_thaliana_GN=At3g12620_PE=2_SV=1	2.00E-29
comp11981_c0_seq1.p1	sp|Q9FS87|IVD2_SOLTU_Isovaleryl-CoA_dehydrogenase_2,_mitochondrial_(Fragment)_OS=Solanum_tuberosum_GN=IVD2_PE=1_SV=1	5.00E-75
comp11981_c0_seq2.p1	sp|Q9FS87|IVD2_SOLTU_Isovaleryl-CoA_dehydrogenase_2,_mitochondrial_(Fragment)_OS=Solanum_tuberosum_GN=IVD2_PE=1_SV=1	1.00E-75
comp11983_c0_seq1.p1	sp|Q54NZ1|MEMO1_DICDI_Protein_MEMO1_homolog_OS=Dictyostelium_discoideum_GN=memo1_PE=3_SV=1	1.00E-88
comp11984_c0_seq1.p1	sp|Q27974|AUXI_BOVIN_Putative_tyrosine-protein_phosphatase_auxilin_OS=Bos_taurus_GN=DNAJC6_PE=1_SV=1	3.00E-16
comp11989_c0_seq1.p1		
comp11990_c0_seq1.p1		
comp11990_c0_seq2.p1		
comp11993_c0_seq1.p4		
comp11995_c0_seq1.p1	sp|Q5R7Z5|MARE1_PONAB_Microtubule-associated_protein_RP/EB_family_member_1_OS=Pongo_abelii_GN=MAPRE1_PE=2_SV=3	1.00E-29
comp11996_c0_seq1.p1		
comp11997_c0_seq1.p1	sp|Q8TCT9|HM13_HUMAN_Minor_histocompatibility_antigen_H13_OS=Homo_sapiens_GN=HM13_PE=1_SV=1	2.00E-56
comp11998_c0_seq1.p1		
comp12000_c0_seq1.p1		
comp12001_c0_seq1.p1	sp|Q9CVB6|ARPC2_MOUSE_Actin-related_protein_2/3_complex_subunit_2_OS=Mus_musculus_GN=Arpc2_PE=1_SV=3	4.00E-51
comp12002_c0_seq1.p1	sp|Q55DL2|MET18_DICDI_Histidine_protein_methyltransferase_1_homolog_OS=Dictyostelium_discoideum_GN=DDB_G0270580_PE=3_SV=1	1.00E-37
comp12003_c0_seq1.p1		
comp12005_c0_seq1.p1	sp|P54927|IMP2_SOLLC_Inositol_monophosphatase_2_OS=Solanum_lycopersicum_GN=IMP2_PE=2_SV=1	1.00E-19
comp12006_c0_seq1.p1	sp|Q9JJI6|PIGO_MOUSE_GPI_ethanolamine_phosphate_transferase_3_OS=Mus_musculus_GN=Pigo_PE=1_SV=2	4.00E-60
comp12007_c0_seq2.p1	sp|Q9LSD0|RIR2C_ARATH_Ribonucleoside-diphosphate_reductase_small_chain_C_OS=Arabidopsis_thaliana_GN=TSO2_PE=2_SV=1	4.00E-153
comp12008_c0_seq1.p1	sp|Q9LDH3|PT112_ARATH_Probable_sugar_phosphate/phosphate_translocator_At1g12500_OS=Arabidopsis_thaliana_GN=At1g12500_PE=2_SV=1	4.00E-13
comp12008_c0_seq1.p2	sp|O95336|6PGL_HUMAN_6-phosphogluconolactonase_OS=Homo_sapiens_GN=PGLS_PE=1_SV=2	2.00E-49
comp12009_c0_seq1.p1		
comp12010_c0_seq1.p1	sp|O52733|XYLT_LACBR_D-xylose-proton_symporter_OS=Lactobacillus_brevis_GN=xylT_PE=3_SV=1	4.00E-68
comp12011_c0_seq1.p1	sp|Q9H7Z6|KAT8_HUMAN_Histone_acetyltransferase_KAT8_OS=Homo_sapiens_GN=KAT8_PE=1_SV=2	2.00E-139
comp12011_c0_seq1.p2	sp|Q8GT74|NIP2_ARATH_NEP1-interacting_protein_2_OS=Arabidopsis_thaliana_GN=NIP2_PE=1_SV=1	8.00E-12
comp12012_c0_seq2.p1	sp|Q9VHY5|TAF7_DROME_Transcription_initiation_factor_TFIID_subunit_7_OS=Drosophila_melanogaster_GN=Taf7_PE=1_SV=1	5.00E-14
comp12016_c0_seq1.p1	sp|Q06908|ATPG_ODOSI_ATP_synthase_gamma_chain,_chloroplastic_OS=Odontella_sinensis_GN=ATPC_PE=1_SV=1	3.00E-129
comp12017_c0_seq1.p1		
comp12018_c0_seq1.p1		
comp12019_c0_seq1.p1	sp|Q9SZ30|HIS5_ARATH_Imidazole_glycerol_phosphate_synthase_hisHF,_chloroplastic_OS=Arabidopsis_thaliana_GN=At4g26900_PE=1_SV=1	4.00E-128
comp12019_c0_seq1.p2	sp|Q9SZ30|HIS5_ARATH_Imidazole_glycerol_phosphate_synthase_hisHF,_chloroplastic_OS=Arabidopsis_thaliana_GN=At4g26900_PE=1_SV=1	4.00E-54
comp12020_c0_seq1.p1		
comp12021_c0_seq1.p1		
comp120218_c0_seq1.p1		
comp12022_c0_seq1.p1		
comp12023_c0_seq1.p1		
comp12024_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	2.00E-16
comp12024_c0_seq2.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	7.00E-17
comp12025_c0_seq1.p1	sp|Q9LD55|EIF3A_ARATH_Eukaryotic_translation_initiation_factor_3_subunit_A_OS=Arabidopsis_thaliana_GN=TIF3A1_PE=1_SV=1	2.00E-107
comp12026_c0_seq1.p1	sp|Q8JGR4|RL24_DANRE_60S_ribosomal_protein_L24_OS=Danio_rerio_GN=rpl24_PE=2_SV=1	2.00E-29
comp12027_c0_seq1.p1		
comp12028_c0_seq1.p1	sp|Q9M069|E137_ARATH_Glucan_endo-1,3-beta-glucosidase_7_OS=Arabidopsis_thaliana_GN=At4g34480_PE=1_SV=2	4.00E-31
comp12029_c0_seq1.p1		
comp12031_c0_seq1.p1	sp|P0C8Z0|Y8359_ORYSI_Uncharacterized_protein_OsI_027940_OS=Oryza_sativa_subsp._indica_GN=OsI_027940_PE=1_SV=2	3.00E-13
comp12032_c0_seq1.p1		
comp12033_c0_seq1.p1		
comp12035_c0_seq1.p1	sp|P12955|PEPD_HUMAN_Xaa-Pro_dipeptidase_OS=Homo_sapiens_GN=PEPD_PE=1_SV=3	1.00E-160
comp12036_c0_seq2.p1	sp|Q9UHB4|NDOR1_HUMAN_NADPH-dependent_diflavin_oxidoreductase_1_OS=Homo_sapiens_GN=NDOR1_PE=1_SV=1	5.00E-121
comp12037_c0_seq1.p1		
comp12038_c0_seq1.p1		
comp12039_c0_seq1.p1		
comp12040_c0_seq1.p1	sp|Q40412|ABA2_NICPL_Zeaxanthin_epoxidase,_chloroplastic_OS=Nicotiana_plumbaginifolia_GN=ABA2_PE=1_SV=1	2.00E-73
comp12042_c0_seq1.p1		
comp12043_c0_seq1.p1	sp|Q39575|DYHG_CHLRE_Dynein_gamma_chain,_flagellar_outer_arm_OS=Chlamydomonas_reinhardtii_GN=ODA2_PE=1_SV=1	1.00E-18
comp12044_c0_seq1.p1		
comp12044_c0_seq2.p1		
comp12045_c0_seq2.p1		
comp12049_c0_seq1.p1		
comp12052_c0_seq1.p1		
comp12054_c0_seq1.p1		
comp12055_c0_seq1.p1	sp|Q9NZN3|EHD3_HUMAN_EH_domain-containing_protein_3_OS=Homo_sapiens_GN=EHD3_PE=1_SV=2	2.00E-129
comp12056_c0_seq1.p1		
comp12058_c0_seq1.p2		
comp12059_c0_seq1.p1		
comp12062_c0_seq1.p1	sp|Q96MX6|WDR92_HUMAN_WD_repeat-containing_protein_92_OS=Homo_sapiens_GN=WDR92_PE=1_SV=1	1.00E-149
comp12063_c0_seq1.p1		
comp12064_c0_seq1.p1		
comp12065_c0_seq1.p1	sp|Q80YE7|DAPK1_MOUSE_Death-associated_protein_kinase_1_OS=Mus_musculus_GN=Dapk1_PE=1_SV=3	1.00E-31
comp12066_c0_seq1.p1		
comp12067_c0_seq1.p1	sp|Q9UT88|ERG8_SCHPO_Probable_phosphomevalonate_kinase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=erg8_PE=2_SV=1	5.00E-38
comp12069_c0_seq1.p1		
comp120695_c0_seq1.p2		
comp12070_c0_seq1.p1		
comp12073_c0_seq1.p1		
comp12074_c0_seq1.p1		
comp12075_c0_seq1.p1		
comp12075_c0_seq2.p1		
comp12076_c0_seq1.p1		
comp12077_c0_seq1.p1		
comp12079_c0_seq1.p1		
comp12084_c0_seq3.p1		
comp12085_c0_seq1.p1	sp|Q552W5|CCHL_DICDI_Probable_cytochrome_c-type_heme_lyase_OS=Dictyostelium_discoideum_GN=cchl_PE=3_SV=1	2.00E-37
comp12086_c0_seq1.p1	sp|A7F8T1|MKAR_SCLS1_3-ketoacyl-CoA_reductase_OS=Sclerotinia_sclerotiorum_(strain_ATCC_18683_/_1980_/_Ss-1)_GN=SS1G_14012_PE=3_SV=1	3.00E-60
comp12088_c0_seq1.p1	sp|Q9Y2Y1|RPC10_HUMAN_DNA-directed_RNA_polymerase_III_subunit_RPC10_OS=Homo_sapiens_GN=POLR3K_PE=1_SV=2	1.00E-32
comp12089_c0_seq1.p1		
comp12090_c0_seq2.p1	sp|Q95Q18|LACB2_CAEEL_Beta-lactamase-like_protein_2_homolog_OS=Caenorhabditis_elegans_GN=Y53F4B.39_PE=3_SV=1	9.00E-66
comp12091_c0_seq1.p1	sp|P40393|RIC2_ORYSJ_Ras-related_protein_RIC2_OS=Oryza_sativa_subsp._japonica_GN=RIC2_PE=2_SV=2	5.00E-53
comp12092_c0_seq1.p1	sp|O82059|G6PI_SPIOL_Glucose-6-phosphate_isomerase,_cytosolic_OS=Spinacia_oleracea_GN=PGIC_PE=2_SV=2	0
comp12092_c0_seq2.p1	sp|O82059|G6PI_SPIOL_Glucose-6-phosphate_isomerase,_cytosolic_OS=Spinacia_oleracea_GN=PGIC_PE=2_SV=2	0
comp12093_c0_seq1.p1	sp|Q03441|RMD1_YEAST_Sporulation_protein_RMD1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=RMD1_PE=1_SV=1	1.00E-10
comp12094_c0_seq1.p1	sp|Q3EAQ5|PTR36_ARATH_Probable_peptide/nitrate_transporter_At3g43790_OS=Arabidopsis_thaliana_GN=ZIFL2_PE=2_SV=2	4.00E-40
comp12096_c0_seq1.p1	sp|Q9SS94|CD48C_ARATH_Cell_division_control_protein_48_homolog_C_OS=Arabidopsis_thaliana_GN=CDC48C_PE=2_SV=2	3.00E-34
comp12097_c0_seq1.p1		
comp12098_c0_seq1.p1		
comp12099_c0_seq1.p1	sp|Q03168|ASPP_AEDAE_Lysosomal_aspartic_protease_OS=Aedes_aegypti_GN=AAEL006169_PE=1_SV=2	7.00E-82
comp12099_c0_seq1.p2		
comp12103_c0_seq1.p1	sp|Q7ZXB5|RBM22_XENLA_Pre-mRNA-splicing_factor_RBM22_OS=Xenopus_laevis_GN=rbm22_PE=2_SV=1	1.00E-105
comp12105_c0_seq1.p1		
comp12105_c0_seq1.p3	sp|Q54JC0|CMBB_DICDI_Calmodulin-binding_protein_CmbB_OS=Dictyostelium_discoideum_GN=cmbB_PE=1_SV=1	5.00E-14
comp12106_c0_seq1.p1	sp|Q92769|HDAC2_HUMAN_Histone_deacetylase_2_OS=Homo_sapiens_GN=HDAC2_PE=1_SV=2	0
comp12107_c0_seq1.p2	sp|Q6GVM3|IF1AY_PANTR_Eukaryotic_translation_initiation_factor_1A,_Y-chromosomal_OS=Pan_troglodytes_GN=EIF1AY_PE=2_SV=3	1.00E-44
comp12108_c0_seq1.p2	sp|P91924|ARF_DUGJA_ADP-ribosylation_factor_OS=Dugesia_japonica_PE=2_SV=3	5.00E-64
comp12109_c0_seq1.p1		
comp12111_c0_seq1.p1	sp|Q80TV8|CLAP1_MOUSE_CLIP-associating_protein_1_OS=Mus_musculus_GN=Clasp1_PE=1_SV=2	8.00E-12
comp12112_c0_seq1.p1		
comp12114_c0_seq1.p1		
comp12114_c0_seq2.p1		
comp12116_c0_seq1.p1		
comp12117_c0_seq1.p1		
comp12118_c0_seq1.p1	sp|Q9CY45|N6MT2_MOUSE_N(6)-adenine-specific_DNA_methyltransferase_2_OS=Mus_musculus_GN=N6amt2_PE=2_SV=1	3.00E-25
comp12119_c0_seq1.p1	sp|Q8EPF5|IF3_OCEIH_Translation_initiation_factor_IF-3_OS=Oceanobacillus_iheyensis_(strain_DSM_14371_/_JCM_11309_/_KCTC_3954_/_HTE831)_GN=infC_PE=3_SV=2	2.00E-12
comp12123_c0_seq1.p1		
comp12124_c0_seq1.p1	sp|P49642|PRI1_HUMAN_DNA_primase_small_subunit_OS=Homo_sapiens_GN=PRIM1_PE=1_SV=1	1.00E-115
comp12125_c0_seq1.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	2.00E-51
comp12126_c0_seq1.p2		
comp12128_c0_seq1.p1	sp|Q1DCU1|RLMN1_MYXXD_Ribosomal_RNA_large_subunit_methyltransferase_N_1_OS=Myxococcus_xanthus_(strain_DK_1622)_GN=rlmN1_PE=3_SV=1	2.00E-94
comp12130_c0_seq1.p1	sp|P82861|ADRO_SALFO_NADPH:adrenodoxin_oxidoreductase,_mitochondrial_OS=Salvelinus_fontinalis_GN=fdxr_PE=2_SV=1	4.00E-102
comp12131_c0_seq1.p1		
comp12134_c0_seq1.p2		
comp12136_c0_seq2.p1	sp|Q9SHU7|TIC21_ARATH_Protein_TIC_21,_chloroplastic_OS=Arabidopsis_thaliana_GN=TIC21_PE=1_SV=1	4.00E-19
comp12138_c0_seq1.p1	sp|Q5TTG1|VATA_ANOGA_V-type_proton_ATPase_catalytic_subunit_A_OS=Anopheles_gambiae_GN=Vha68-2_PE=3_SV=1	0
comp12139_c0_seq1.p1		
comp12140_c0_seq1.p1	sp|Q6GQA6|CSN8_XENLA_COP9_signalosome_complex_subunit_8_OS=Xenopus_laevis_GN=csn8_PE=2_SV=2	1.00E-19
comp12141_c0_seq1.p1	sp|Q6AYM4|DPCD_RAT_Protein_DPCD_OS=Rattus_norvegicus_GN=Dpcd_PE=2_SV=2	3.00E-41
comp12145_c0_seq1.p1	sp|O65282|CH10C_ARATH_20_kDa_chaperonin,_chloroplastic_OS=Arabidopsis_thaliana_GN=CPN21_PE=1_SV=2	2.00E-25
comp12146_c0_seq1.p1		
comp12149_c0_seq1.p1		
comp12151_c0_seq1.p1		
comp12152_c0_seq1.p1		
comp12153_c0_seq1.p1	sp|O95714|HERC2_HUMAN_E3_ubiquitin-protein_ligase_HERC2_OS=Homo_sapiens_GN=HERC2_PE=1_SV=2	2.00E-28
comp12154_c0_seq1.p1	sp|Q9VCR7|CTNS_DROME_Cystinosin_homolog_OS=Drosophila_melanogaster_GN=CG17119_PE=1_SV=2	3.00E-49
comp12155_c0_seq2.p1		
comp12156_c0_seq1.p1	sp|P46285|S17P_WHEAT_Sedoheptulose-1,7-bisphosphatase,_chloroplastic_OS=Triticum_aestivum_PE=2_SV=1	7.00E-110
comp12157_c0_seq1.p1	sp|Q6DRC3|CU059_DANRE_Uncharacterized_protein_C21orf59_homolog_OS=Danio_rerio_PE=2_SV=1	3.00E-73
comp12159_c0_seq1.p1	sp|A3KPR5|CYAC3_DANRE_Cytochrome_b_ascorbate-dependent_protein_3_OS=Danio_rerio_GN=cybasc3_PE=2_SV=1	8.00E-26
comp12159_c0_seq1.p2		
comp12160_c0_seq1.p1	sp|Q6NU11|CHM6B_XENLA_Charged_multivesicular_body_protein_6-B_OS=Xenopus_laevis_GN=chmp6-b_PE=2_SV=3	3.00E-22
comp12162_c0_seq1.p1		
comp12165_c0_seq1.p1		
comp12166_c0_seq1.p1	sp|Q38950|2AAB_ARATH_Serine/threonine-protein_phosphatase_2A_65_kDa_regulatory_subunit_A_beta_isoform_OS=Arabidopsis_thaliana_GN=PP2AA2_PE=1_SV=2	4.00E-118
comp12167_c0_seq1.p1	sp|Q28BZ2|HINT3_XENTR_Histidine_triad_nucleotide-binding_protein_3_OS=Xenopus_tropicalis_GN=hint3_PE=2_SV=1	6.00E-22
comp12167_c0_seq1.p2		
comp12169_c0_seq1.p1		
comp12170_c0_seq1.p1	sp|Q6PC78|RN185_DANRE_E3_ubiquitin-protein_ligase_RNF185_OS=Danio_rerio_GN=rnf185_PE=2_SV=1	4.00E-29
comp12172_c0_seq1.p1		
comp12173_c0_seq1.p1	sp|P27659|RL3_MOUSE_60S_ribosomal_protein_L3_OS=Mus_musculus_GN=Rpl3_PE=2_SV=3	0
comp12174_c0_seq1.p2		
comp12175_c0_seq1.p1		
comp12176_c0_seq1.p1	sp|C5D8U8|RBGA_GEOSW_Ribosome_biogenesis_GTPase_A_OS=Geobacillus_sp._(strain_WCH70)_GN=rbgA_PE=3_SV=1	2.00E-36
comp12177_c0_seq1.p1	sp|Q5SMG8|MGTE_THET8_Magnesium_transporter_mgtE_OS=Thermus_thermophilus_(strain_HB8_/_ATCC_27634_/_DSM_579)_GN=TTHA1060_PE=1_SV=1	4.00E-29
comp12180_c0_seq1.p1		
comp12182_c0_seq1.p1	sp|P35815|PPM1B_RAT_Protein_phosphatase_1B_OS=Rattus_norvegicus_GN=Ppm1b_PE=2_SV=1	2.00E-72
comp12185_c0_seq1.p1		
comp12187_c0_seq1.p1		
comp12187_c0_seq1.p2		
comp12188_c0_seq1.p1	sp|Q42546|DPNP1_ARATH_SAL1_phosphatase_OS=Arabidopsis_thaliana_GN=SAL1_PE=1_SV=1	2.00E-67
comp12189_c0_seq1.p1		
comp12189_c0_seq1.p2		
comp12191_c0_seq2.p1		
comp12192_c0_seq1.p2	sp|Q5XGC9|SRFB1_XENTR_Serum_response_factor-binding_protein_1_OS=Xenopus_tropicalis_GN=srfbp1_PE=2_SV=1	4.00E-18
comp12193_c0_seq1.p1	sp|P34329|PDIA4_CAEEL_Probable_protein_disulfide-isomerase_A4_OS=Caenorhabditis_elegans_GN=C14B9.2_PE=2_SV=2	6.00E-45
comp12196_c0_seq1.p1		
comp12198_c0_seq1.p1	sp|Q9ULD4|BRPF3_HUMAN_Bromodomain_and_PHD_finger-containing_protein_3_OS=Homo_sapiens_GN=BRPF3_PE=1_SV=2	5.00E-12
comp12199_c0_seq1.p1		
comp12200_c0_seq1.p1		
comp12201_c0_seq1.p1		
comp12202_c0_seq1.p1		
comp12203_c0_seq1.p1	sp|Q9QXL7|NDK7_RAT_Nucleoside_diphosphate_kinase_7_OS=Rattus_norvegicus_GN=Nme7_PE=1_SV=1	6.00E-59
comp12203_c0_seq2.p1	sp|Q9Y5B8|NDK7_HUMAN_Nucleoside_diphosphate_kinase_7_OS=Homo_sapiens_GN=NME7_PE=1_SV=1	1.00E-22
comp12206_c0_seq1.p1	sp|Q54S38|RCL1_DICDI_Probable_RNA_3'-terminal_phosphate_cyclase-like_protein_OS=Dictyostelium_discoideum_GN=rcl1_PE=1_SV=2	1.00E-131
comp12207_c0_seq1.p1	sp|P50398|GDIA_RAT_Rab_GDP_dissociation_inhibitor_alpha_OS=Rattus_norvegicus_GN=Gdi1_PE=1_SV=1	3.00E-166
comp12207_c0_seq1.p2		
comp12208_c0_seq1.p1	sp|Q9LZA6|SDP1_ARATH_Triacylglycerol_lipase_SDP1_OS=Arabidopsis_thaliana_GN=SDP1_PE=1_SV=1	7.00E-63
comp12209_c0_seq1.p1	sp|Q58D06|WDR74_BOVIN_WD_repeat-containing_protein_74_OS=Bos_taurus_GN=WDR74_PE=2_SV=1	9.00E-31
comp12210_c0_seq1.p1	sp|Q9ZTS1|SYM_ORYSJ_Probable_methionine--tRNA_ligase_OS=Oryza_sativa_subsp._japonica_GN=Os06g0508700_PE=2_SV=2	2.00E-32
comp12211_c0_seq1.p1	sp|Q63507|RL14_RAT_60S_ribosomal_protein_L14_OS=Rattus_norvegicus_GN=Rpl14_PE=1_SV=3	2.00E-28
comp12212_c0_seq1.p1		
comp12214_c0_seq1.p1		
comp122151_c0_seq1.p1	sp|P77802|YAGX_ECOLI_Uncharacterized_protein_yagX_OS=Escherichia_coli_(strain_K12)_GN=yagX_PE=4_SV=1	5.00E-54
comp12216_c0_seq1.p1	sp|Q28E45|MCM10_XENTR_Protein_MCM10_homolog_OS=Xenopus_tropicalis_GN=mcm10_PE=2_SV=1	1.00E-29
comp12217_c0_seq1.p1	sp|P54887|P5CS1_ARATH_Delta-1-pyrroline-5-carboxylate_synthase_A_OS=Arabidopsis_thaliana_GN=P5CSA_PE=1_SV=1	0
comp12218_c0_seq1.p1		
comp12221_c0_seq1.p1	sp|Q0VA16|WDR70_XENTR_WD_repeat-containing_protein_70_OS=Xenopus_tropicalis_GN=wdr70_PE=2_SV=1	3.00E-85
comp12221_c0_seq1.p2	sp|Q96Q80|DERL3_HUMAN_Derlin-3_OS=Homo_sapiens_GN=DERL3_PE=1_SV=2	1.00E-14
comp12222_c0_seq1.p1	sp|Q5S1W2|BON2_ARATH_Protein_BONZAI_2_OS=Arabidopsis_thaliana_GN=BON2_PE=1_SV=2	1.00E-80
comp12223_c0_seq1.p1	sp|Q9K907|PRPE_BACHD_Bis(5'-nucleosyl)-tetraphosphatase_prpE_[asymmetrical]_OS=Bacillus_halodurans_(strain_ATCC_BAA-125_/_DSM_18197_/_FERM_7344_/_JCM_9153_/_C-125)_GN=prpE_PE=3_SV=1	2.00E-15
comp12224_c0_seq1.p1		
comp122249_c0_seq1.p1	sp|Q3Z4P8|FOLD_SHISS_Bifunctional_protein_FolD_OS=Shigella_sonnei_(strain_Ss046)_GN=folD_PE=3_SV=3	6.00E-72
comp12227_c0_seq1.p1	sp|Q0WSF1|AL221_ARATH_Aldehyde_dehydrogenase_22A1_OS=Arabidopsis_thaliana_GN=ALDH22A1_PE=2_SV=2	6.00E-151
comp122271_c0_seq1.p1		
comp12228_c0_seq2.p1	sp|Q8YXE4|SYW_NOSS1_Tryptophan--tRNA_ligase_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=trpS_PE=3_SV=1	4.00E-144
comp12229_c0_seq1.p1	sp|Q6CM00|NOG1_KLULA_Nucleolar_GTP-binding_protein_1_OS=Kluyveromyces_lactis_(strain_ATCC_8585_/_CBS_2359_/_DSM_70799_/_NBRC_1267_/_NRRL_Y-1140_/_WM37)_GN=NOG1_PE=3_SV=1	4.00E-24
comp12231_c0_seq1.p1		
comp12231_c0_seq1.p2		
comp12231_c0_seq2.p1		
comp12232_c0_seq1.p1	sp|P84675|PFM_CHAGB_Putative_fungistatic_metabolite_OS=Chaetomium_globosum_(strain_ATCC_6205_/_CBS_148.51_/_DSM_1962_/_NBRC_6347_/_NRRL_1970)_GN=CHGG_05463_PE=1_SV=2	4.00E-11
comp12233_c0_seq1.p1	sp|Q3SYU3|S39A1_BOVIN_Zinc_transporter_ZIP1_OS=Bos_taurus_GN=SLC39A1_PE=2_SV=1	8.00E-17
comp12234_c0_seq1.p1	sp|Q9UC06|ZNF70_HUMAN_Zinc_finger_protein_70_OS=Homo_sapiens_GN=ZNF70_PE=2_SV=2	5.00E-18
comp122347_c0_seq1.p1	sp|Q3YVI4|RHLB_SHISS_ATP-dependent_RNA_helicase_rhlB_OS=Shigella_sonnei_(strain_Ss046)_GN=rhlB_PE=3_SV=1	1.00E-70
comp12235_c0_seq1.p1		
comp12235_c1_seq1.p1		
comp12236_c0_seq1.p1	sp|P40421|RDGC_DROME_Serine/threonine-protein_phosphatase_rdgC_OS=Drosophila_melanogaster_GN=rdgC_PE=2_SV=1	2.00E-69
comp12237_c0_seq1.p1	sp|Q8YZH7|DER_NOSS1_GTPase_Der_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=der_PE=3_SV=1	3.00E-171
comp12238_c0_seq1.p1		
comp12239_c0_seq1.p1		
comp12241_c0_seq1.p1		
comp12242_c0_seq1.p1		
comp12243_c0_seq1.p1	sp|Q9FM19|HIR1_ARATH_Hypersensitive-induced_response_protein_1_OS=Arabidopsis_thaliana_GN=HIR1_PE=1_SV=1	3.00E-104
comp122438_c0_seq1.p1		
comp12244_c0_seq1.p1		
comp12248_c0_seq1.p1		
comp12249_c0_seq1.p2		
comp12250_c0_seq1.p1	sp|P47758|SRPRB_MOUSE_Signal_recognition_particle_receptor_subunit_beta_OS=Mus_musculus_GN=Srprb_PE=1_SV=1	4.00E-18
comp12253_c0_seq1.p1	sp|Q7T2P0|MX1_ICTPU_Interferon-induced_GTP-binding_protein_Mx1_OS=Ictalurus_punctatus_GN=mx1_PE=2_SV=1	2.00E-77
comp12254_c0_seq1.p1		
comp12255_c0_seq1.p1	sp|Q94AR8|LEUC_ARATH_3-isopropylmalate_dehydratase_OS=Arabidopsis_thaliana_GN=IIL1_PE=2_SV=1	0
comp12256_c0_seq1.p1	sp|Q9S795|BADH1_ARATH_Betaine_aldehyde_dehydrogenase_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=ALDH10A8_PE=2_SV=1	7.00E-147
comp12261_c0_seq1.p1	sp|Q9CX00|IST1_MOUSE_IST1_homolog_OS=Mus_musculus_GN=Ist1_PE=2_SV=1	2.00E-32
comp12263_c0_seq1.p1		
comp12264_c0_seq1.p1	sp|B2GUW6|AEN_RAT_Apoptosis-enhancing_nuclease_OS=Rattus_norvegicus_GN=Aen_PE=2_SV=1	5.00E-44
comp12267_c0_seq1.p1		
comp122715_c0_seq1.p1		
comp12273_c0_seq1.p1	sp|Q6PDU1|SRSF2_RAT_Serine/arginine-rich_splicing_factor_2_OS=Rattus_norvegicus_GN=Srsf2_PE=1_SV=3	4.00E-28

comp12273_c0_seq2.p1	sp|Q6PDU1|SRSF2_RAT_Serine/arginine-rich_splicing_factor_2_OS=Rattus_norvegicus_GN=Srsf2_PE=1_SV=3	5.00E-28	GO:0000166,GO:0003676,GO:0003723,GO:0005634,GO:0005634,GO:0005681,GO:0006397,GO:0008380,GO:0016607	nucleotide binding,nucleic acid binding,RNA binding,nucleus,nucleus,nucleus,spliceosomal complex,mRNA processing,RNA splicing,nuclear speck
comp12274_c0_seq1.p1				
comp122746_c0_seq1.p2	sp|Q8LPK2|AB2B_ARATH_ABC_transporter_B_family_member_2_OS=Arabidopsis_thaliana_GN=ABCB2_PE=1_SV=3	2.00E-37	GO:0000166,GO:0005524,GO:0005524,GO:0006200,GO:0006810,GO:0006810,GO:0010048,GO:0010315,GO:0010329,GO:0010540,GO:0010541,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016887,GO:0042626,GO:0042626,GO:0043481,GO:0048440,GO:0055085,GO:0055085	nucleotide binding,ATP binding,ATP binding,ATP catabolic process,transport,transport,vernalization response,auxin efflux,auxin efflux transmembrane transporter activity,basipetal auxin transport,acropetal auxin transport,membrane,membrane,membrane,integral component of membrane,integral component of membrane,integral component of membrane,ATPase activity,ATPase activity, coupled to transmembrane movement of substances,ATPase activity, coupled to transmembrane movement of substances,anthocyanin accumulation in tissues in response to UV light,carpel development,transmembrane transport,transmembrane transport
comp12277_c0_seq1.p1				
comp12278_c0_seq1.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	4.00E-37		
comp122785_c0_seq1.p1				
comp12279_c0_seq1.p1				
comp122809_c0_seq1.p1	sp|P46850|RTCB_ECOLI_RNA-splicing_ligase_RtcB_OS=Escherichia_coli_(strain_K12)_GN=rtcB_PE=1_SV=3	5.00E-84	GO:0003909,GO:0006266,GO:0006281,GO:0006281,GO:0006396,GO:0006396,GO:0006974,GO:0006974,GO:0008452,GO:0008452,GO:0016874,GO:0030145,GO:0030145,GO:0042245,GO:0042245,GO:0046872	DNA ligase activity,DNA ligation,DNA repair,DNA repair,RNA processing,RNA processing,cellular response to DNA damage stimulus,cellular response to DNA damage stimulus,RNA ligase activity,RNA ligase activity,ligase activity,manganese ion binding,manganese ion binding,RNA repair,RNA repair,metal ion binding
comp12281_c0_seq1.p2				
comp12283_c0_seq1.p1				
comp12284_c0_seq1.p1	sp|Q8BT14|CNOT4_MOUSE_CCR4-NOT_transcription_complex_subunit_4_OS=Mus_musculus_GN=Cnot4_PE=1_SV=2	3.00E-34	GO:0000166,GO:0003676,GO:0003723,GO:0004842,GO:0004842,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0008270,GO:0016567,GO:0016874,GO:0030014,GO:0044822,GO:0046872,GO:0046872,GO:0051865,GO:0051865,GO:0030014	nucleotide binding,nucleic acid binding,RNA binding,ubiquitin-protein transferase activity,ubiquitin-protein transferase activity,nucleus,nucleus,cytoplasm,cytoplasm,transcription, DNA-templated,regulation of transcription, DNA-templated,zinc ion binding,protein ubiquitination,ligase activity,CCR4-NOT complex,poly(A) RNA binding,metal ion binding,metal ion binding,protein autoubiquitination,protein autoubiquitination,CCR4-NOT complex
comp12286_c0_seq1.p1				
comp12287_c0_seq1.p1				
comp12288_c0_seq1.p1				
comp12291_c0_seq1.p1	sp|Q68EV5|CC026_XENLA_Uncharacterized_protein_C3orf26_homolog_OS=Xenopus_laevis_PE=2_SV=1	6.00E-16		
comp12292_c0_seq1.p1	sp|Q110D7|RF1_TRIEI_Peptide_chain_release_factor_1_OS=Trichodesmium_erythraeum_(strain_IMS101)_GN=prfA_PE=3_SV=1	2.00E-152	GO:0003747,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006415,GO:0006415,GO:0016149,GO:0016149	translation release factor activity,cytoplasm,cytoplasm,cytoplasm,cytoplasm,translation,translational termination,translational termination,translation release factor activity, codon specific,translation release factor activity, codon specific
comp12293_c0_seq1.p1	sp|Q09WE7|USP1_SOYBN_UDP-sugar_pyrophosphorylase_1_OS=Glycine_max_GN=USP1_PE=1_SV=1	5.00E-164	GO:0008152,GO:0016740,GO:0016779,GO:0051748,GO:0070569	metabolic process,transferase activity,nucleotidyltransferase activity,UTP-monosaccharide-1-phosphate uridylyltransferase activity,uridylyltransferase activity
comp12294_c0_seq1.p1				
comp12295_c0_seq2.p1	sp|Q80U30|CL16A_MOUSE_Protein_CLEC16A_OS=Mus_musculus_GN=Clec16a_PE=2_SV=2	4.00E-14	GO:0005515,GO:0005575,GO:0005764,GO:0005765,GO:0005768,GO:0006914,GO:0008150,GO:0010008,GO:0016020	protein binding,cellular_component,lysosome,lysosomal membrane,endosome,autophagy,biological_process,endosome membrane,membrane
comp122980_c0_seq1.p3				
comp12299_c0_seq1.p1				
comp12300_c0_seq1.p1	sp|Q6P806|SAM50_XENTR_Sorting_and_assembly_machinery_component_50_homolog_OS=Xenopus_tropicalis_GN=samm50_PE=2_SV=1	3.00E-23	GO:0005739,GO:0005741,GO:0005741,GO:0016020,GO:0016021,GO:0019867	mitochondrion,mitochondrial outer membrane,mitochondrial outer membrane,membrane,integral component of membrane,outer membrane
comp12301_c0_seq1.p1	sp|P0C1G8|PSA4A_ORYSJ_Proteasome_subunit_alpha_type-4-1_OS=Oryza_sativa_subsp._japonica_GN=PAC1_PE=2_SV=1	3.00E-48	GO:0000502,GO:0004175,GO:0004298,GO:0004298,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005839,GO:0006508,GO:0006511,GO:0008233,GO:0016787,GO:0019773,GO:0051603	proteasome complex,endopeptidase activity,threonine-type endopeptidase activity,threonine-type endopeptidase activity,nucleus,nucleus,cytoplasm,cytoplasm,proteasome core complex,proteolysis,ubiquitin-dependent protein catabolic process,peptidase activity,hydrolase activity,proteasome core complex, alpha-subunit complex,proteolysis involved in cellular protein catabolic process
comp123018_c0_seq1.p1	sp|Q32G88|ASTD_SHIDS_N-succinylglutamate_5-semialdehyde_dehydrogenase_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=astD_PE=3_SV=2	2.00E-84	GO:0006525,GO:0006527,GO:0008152,GO:0016491,GO:0016491,GO:0016491,GO:0016620,GO:0019544,GO:0019545,GO:0043824,GO:0043824,GO:0055114,GO:0055114	arginine metabolic process,arginine catabolic process,metabolic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor,arginine catabolic process to glutamate,arginine catabolic process to succinate,succinylglutamate-semialdehyde dehydrogenase activity,succinylglutamate-semialdehyde dehydrogenase activity,oxidation-reduction process,oxidation-reduction process
comp12302_c0_seq1.p1	sp|Q9ZUB3|SPD1_ARATH_Spermidine_synthase_1_OS=Arabidopsis_thaliana_GN=SPDSYN1_PE=1_SV=1	2.00E-99	GO:0003824,GO:0004766,GO:0005515,GO:0005515,GO:0006596,GO:0008295,GO:0008295,GO:0016740	catalytic activity,spermidine synthase activity,protein binding,protein binding,polyamine biosynthetic process,spermidine biosynthetic process,spermidine biosynthetic process,transferase activity
comp12302_c0_seq1.p2	sp|Q3AMP7|RL15_SYNSC_50S_ribosomal_protein_L15_OS=Synechococcus_sp._(strain_CC9605)_GN=rplO_PE=3_SV=1	2.00E-32	GO:0003723,GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0006412,GO:0015934,GO:0019843,GO:0019843,GO:0030529	RNA binding,structural constituent of ribosome,intracellular,ribosome,ribosome,translation,translation,large ribosomal subunit,rRNA binding,rRNA binding,ribonucleoprotein complex
comp12304_c0_seq1.p1	sp|Q3SZH6|TTLL9_BOVIN_Probable_tubulin_polyglutamylase_TTLL9_OS=Bos_taurus_GN=TTLL9_PE=2_SV=1	7.00E-136	GO:0005737,GO:0005856,GO:0005874,GO:0005929,GO:0006464,GO:0016874,GO:0042995	cytoplasm,cytoskeleton,cytoskeleton,microtubule,cilium,cellular protein modification process,ligase activity,cell projection
comp12305_c0_seq1.p1	sp|P38748|ETP1_YEAST_RING_finger_protein_ETP1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=ETP1_PE=1_SV=1	2.00E-19	GO:0005575,GO:0005737,GO:0005737,GO:0008139,GO:0008270,GO:0043130,GO:0045471,GO:0046872	cellular_component,cytoplasm,cytoplasm,nuclear localization sequence binding,zinc ion binding,ubiquitin binding,response to ethanol,metal ion binding
comp12307_c0_seq1.p1				
comp12308_c0_seq2.p1				
comp12308_c0_seq2.p3				
comp123082_c0_seq1.p1	sp|Q1RGC4|LEU3_ECOUT_3-isopropylmalate_dehydrogenase_OS=Escherichia_coli_(strain_UTI89_/_UPEC)_GN=leuB_PE=3_SV=1	1.00E-53	GO:0000287,GO:0003862,GO:0003862,GO:0003862,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0008652,GO:0009082,GO:0009098,GO:0009098,GO:0009098,GO:0009098,GO:0016491,GO:0016616,GO:0046872,GO:0051287,GO:0055114,GO:0055114	magnesium ion binding,3-isopropylmalate dehydrogenase activity,3-isopropylmalate dehydrogenase activity,3-isopropylmalate dehydrogenase activity,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cellular amino acid biosynthetic process,branched-chain amino acid biosynthetic process,leucine biosynthetic process,leucine biosynthetic process,leucine biosynthetic process,leucine biosynthetic process,oxidoreductase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,metal ion binding,NAD binding,oxidation-reduction process,oxidation-reduction process
comp12309_c0_seq1.p1	sp|Q9SSA5|CYP38_ARATH_Peptidyl-prolyl_cis-trans_isomerase_CYP38,_chloroplastic_OS=Arabidopsis_thaliana_GN=CYP38_PE=1_SV=1	1.00E-65	GO:0000165,GO:0000413,GO:0000413,GO:0003755,GO:0003755,GO:0003755,GO:0003755,GO:0006098,GO:0006364,GO:0006457,GO:0006612,GO:0006636,GO:0009409,GO:0009507,GO:0009507,GO:0009507,GO:0009534,GO:0009535,GO:0009536,GO:0009543,GO:0009570,GO:0009579,GO:0009579,GO:0009579,GO:0009595,GO:0009657,GO:0009697,GO:0009773,GO:0009814,GO:0009862,GO:0009867,GO:0009902,GO:0010027,GO:0010103,GO:0010200,GO:0010207,GO:0010310,GO:0010363,GO:0015995,GO:0016117,GO:0016853,GO:0019288,GO:0019684,GO:0031348,GO:0031977,GO:0035304,GO:0042742,GO:0042742,GO:0042793,GO:0043900,GO:0045893,GO:0050832	MAPK cascade,protein peptidyl-prolyl isomerization,protein peptidyl-prolyl isomerization,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,pentose-phosphate shunt,rRNA processing,protein folding,protein targeting to membrane,unsaturated fatty acid biosynthetic process,response to cold,chloroplast,chloroplast,chloroplast,chloroplast thylakoid membrane,plastid,chloroplast thylakoid lumen,chloroplast stroma,thylakoid,thylakoid,thylakoid,detection of biotic stimulus,plastid organization,salicylic acid biosynthetic process,photosynthetic electron transport in photosystem I,defense response, incompatible interaction,systemic acquired resistance, salicylic acid mediated signaling pathway,jasmonic acid mediated signaling pathway,chloroplast relocation,thylakoid membrane organization,stomatal complex morphogenesis,response to chitin,photosystem II assembly,regulation of hydrogen peroxide metabolic process,regulation of plant-type hypersensitive response,chlorophyll biosynthetic process,carotenoid biosynthetic process,isomerase activity,isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway,photosynthesis, light reaction,negative regulation of defense response,thylakoid lumen,regulation of protein dephosphorylation,defense response to bacterium,defense response to bacterium,transcription from plastid promoter,regulation of multi-organism process,positive regulation of transcription, DNA-templated,defense response to fungus
comp12310_c0_seq1.p1	sp|Q3T095|ING4_BOVIN_Inhibitor_of_growth_protein_4_OS=Bos_taurus_GN=ING4_PE=2_SV=1	2.00E-13	GO:0000123,GO:0003713,GO:0005634,GO:0005634,GO:0005634,GO:0006978,GO:0007049,GO:0008270,GO:0008285,GO:0016568,GO:0016573,GO:0035064,GO:0043065,GO:0043065,GO:0043966,GO:0043981,GO:0043982,GO:0043983,GO:0046872,GO:1903506,GO:0043984	histone acetyltransferase complex,transcription coactivator activity,nucleus,nucleus,nucleus,DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator,cell cycle,zinc ion binding,negative regulation of cell proliferation,chromatin modification,chromatin modification,histone acetylation,methylated histone binding,positive regulation of apoptotic process,positive regulation of apoptotic process,histone H3 acetylation,histone H4-K5 acetylation,histone H4-K8 acetylation,histone H4-K12 acetylation,metal ion binding,regulation of nucleic acid-templated transcription,histone H4-K16 acetylation
comp123101_c0_seq1.p1				
comp12311_c0_seq1.p1	sp|Q8CHY3|DYM_MOUSE_Dymeclin_OS=Mus_musculus_GN=Dym_PE=2_SV=1	1.00E-18	GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005794,GO:0005794,GO:0005794,GO:0005794,GO:0007030,GO:0007030,GO:0019899,GO:0060348,GO:0060348	cytoplasm,cytoplasm,cytoplasm,cytoplasm,Golgi apparatus,Golgi apparatus,Golgi apparatus,Golgi apparatus,Golgi organization,Golgi organization,enzyme binding,bone development,bone development
comp12312_c0_seq1.p1				
comp12313_c0_seq1.p1	sp|O23365|C97B3_ARATH_Cytochrome_P450_97B3,_chloroplastic_OS=Arabidopsis_thaliana_GN=CYP97B3_PE=1_SV=2	0	GO:0004497,GO:0005506,GO:0009507,GO:0009507,GO:0009536,GO:0009570,GO:0009941,GO:0016020,GO:0016117,GO:0016491,GO:0016705,GO:0019288,GO:0020037,GO:0031969,GO:0046872,GO:0055114,GO:0055114	monooxygenase activity,iron ion binding,chloroplast,chloroplast,plastid,chloroplast stroma,chloroplast envelope,membrane,carotenoid biosynthetic process,oxidoreductase activity,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway,heme binding,chloroplast membrane,metal ion binding,oxidation-reduction process,oxidation-reduction process
comp123136_c0_seq1.p1				
comp12314_c0_seq1.p1				
comp12314_c0_seq2.p1				
comp12315_c0_seq1.p1				
comp12316_c0_seq1.p1				
comp12317_c0_seq1.p1				

comp12607_c0_seq1.p1	sp|Q96ST3|SIN3A_HUMAN_Paired_amphipathic_helix_protein_Sin3a_OS=Homo_sapiens_GN=SIN3A_PE=1_SV=2	7.00E-28
comp12608_c0_seq1.p1		
comp12610_c0_seq1.p1		
comp12613_c0_seq1.p1		
comp12614_c0_seq2.p1		
comp12616_c0_seq2.p1		
comp12620_c0_seq1.p1		
comp12621_c0_seq1.p1	sp|Q9CY21|WBS22_MOUSE_Uncharacterized_methyltransferase_WBSCR22_OS=Mus_musculus_GN=Wbscr22_PE=2_SV=1	6.00E-91
comp12625_c0_seq1.p1		
comp12625_c0_seq2.p1		
comp126266_c0_seq1.p1	sp|Q3Z257|BTUD_SHISS_Vitamin_B12_import_ATP-binding_protein_BtuD_OS=Shigella_sonnei_(strain_Ss046)_GN=btuD_PE=3_SV=1	3.00E-72
comp12627_c0_seq1.p1		
comp12628_c0_seq1.p1	sp|B1ZW79|TRPC_OPITP_Indole-3-glycerol_phosphate_synthase_OS=Opitutus_terrae_(strain_DSM_11246_/_PB90-1)_GN=trpC_PE=3_SV=1	1.00E-25
comp12629_c0_seq1.p1	sp|Q5ZJ06|MAGT1_CHICK_Magnesium_transporter_protein_1_OS=Gallus_gallus_GN=MAGT1_PE=2_SV=1	3.00E-17
comp126325_c0_seq1.p1		
comp12634_c0_seq1.p1		
comp12638_c0_seq1.p1	sp|P20606|SAR1_YEAST_Small_COPII_coat_GTPase_SAR1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=SAR1_PE=1_SV=1	4.00E-42
comp12639_c0_seq1.p1		
comp12641_c0_seq1.p1	sp|Q5M843|CQ101_RAT_PKHD_domain-containing_transmembrane_protein_C17orf101_homolog_OS=Rattus_norvegicus_PE=2_SV=1	1.00E-38
comp12642_c0_seq1.p1	sp|P45482|FTSZ_NOSS1_Cell_division_protein_FtsZ_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=ftsZ_PE=3_SV=2	1.00E-73
comp12642_c1_seq1.p2	sp|O82533|FTZ21_ARATH_Cell_division_protein_FtsZ_homolog_2-1,_chloroplastic_OS=Arabidopsis_thaliana_GN=FTSZ2-1_PE=1_SV=2	2.00E-22
comp126420_c0_seq1.p1	sp|Q3Z5W2|KEFC_SHISS_Glutathione-regulated_potassium-efflux_system_protein_kefC_OS=Shigella_sonnei_(strain_Ss046)_GN=kefC_PE=3_SV=1	4.00E-59
comp12645_c0_seq1.p2		
comp12645_c0_seq2.p1		
comp12646_c0_seq1.p1	sp|Q9MB58|F26_ARATH_6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase_OS=Arabidopsis_thaliana_GN=FKFBP_PE=1_SV=1	2.00E-95
comp12647_c0_seq1.p1		
comp12647_c0_seq1.p3		
comp12647_c0_seq2.p1		
comp12651_c0_seq1.p1	sp|P38838|WSS1_YEAST_DNA_damage_response_protein_WSS1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=WSS1_PE=1_SV=1	5.00E-11
comp12654_c0_seq1.p3		
comp12655_c0_seq1.p1		
comp12656_c0_seq1.p1	sp|Q14562|DHX8_HUMAN_ATP-dependent_RNA_helicase_DHX8_OS=Homo_sapiens_GN=DHX8_PE=1_SV=1	3.00E-17
comp12656_c0_seq2.p1	sp|Q14562|DHX8_HUMAN_ATP-dependent_RNA_helicase_DHX8_OS=Homo_sapiens_GN=DHX8_PE=1_SV=1	8.00E-18
comp12657_c0_seq1.p1		
comp12657_c1_seq1.p1		
comp12659_c0_seq1.p1		
comp12660_c0_seq2.p1		
comp12661_c0_seq1.p1	sp|F4JMJ1|HSP7R_ARATH_Heat_shock_70_kDa_protein_17_OS=Arabidopsis_thaliana_GN=HSP70-17_PE=2_SV=1	2.00E-27
comp12662_c0_seq1.p1		
comp12666_c0_seq1.p1		
comp12666_c0_seq2.p1		
comp12671_c0_seq1.p1		
comp12671_c1_seq1.p1	sp|O94901|SUN1_HUMAN_SUN_domain-containing_protein_1_OS=Homo_sapiens_GN=SUN1_PE=1_SV=3	3.00E-27
comp12674_c0_seq1.p1		
comp12680_c0_seq1.p2		
comp126817_c0_seq1.p2	sp|P21345|GLTP_ECOLI_Proton_glutamate_symport_protein_OS=Escherichia_coli_(strain_K12)_GN=gltP_PE=1_SV=2	2.00E-64
comp12682_c0_seq1.p1	sp|Q6EPN8|FACE1_ORYSJ_CAAX_prenyl_protease_1_homolog_OS=Oryza_sativa_subsp._japonica_GN=FACE1_PE=2_SV=1	9.00E-131
comp12684_c0_seq1.p1	sp|Q58D20|NLE1_BOVIN_Notchless_protein_homolog_1_OS=Bos_taurus_GN=NLE1_PE=2_SV=2	0
comp12687_c0_seq1.p1		
comp12691_c0_seq1.p1	sp|P59668|FAD12_MORIS_Delta(12)_fatty_acid_desaturase_OS=Mortierella_isabellina_PE=2_SV=1	9.00E-125
comp12692_c0_seq2.p1		
comp126944_c0_seq1.p1		
comp12696_c0_seq1.p3		
comp12696_c0_seq3.p2		
comp12697_c0_seq1.p1	sp|Q56X52|AOX4_ARATH_Alternative_oxidase_4,_chloroplastic/chromoplastic_OS=Arabidopsis_thaliana_GN=AOX4_PE=1_SV=2	5.00E-60
comp126973_c0_seq1.p2	sp|Q31WE3|PHYDA_SHIBS_D-phenylhydantoinase_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=hyuA_PE=3_SV=2	3.00E-47
comp12698_c0_seq1.p2		
comp12699_c0_seq1.p1	sp|Q962R9|RS10_SPOFR_40S_ribosomal_protein_S10_OS=Spodoptera_frugiperda_GN=RpS10_PE=2_SV=1	2.00E-39
comp12702_c0_seq1.p1		
comp12704_c0_seq1.p1	sp|O31680|YKVO_BACSU_Uncharacterized_oxidoreductase_ykvO_OS=Bacillus_subtilis_GN=ykvO_PE=3_SV=1	2.00E-18
comp12705_c0_seq1.p1	sp|Q5ZLX5|ZRAB2_CHICK_Zinc_finger_Ran-binding_domain-containing_protein_2_OS=Gallus_gallus_GN=ZRANB2_PE=2_SV=1	8.00E-12
comp12710_c0_seq1.p1		
comp12711_c0_seq2.p1		
comp12713_c0_seq1.p1		
comp12713_c0_seq2.p1		
comp12715_c0_seq1.p1		
comp12715_c0_seq2.p1		
comp12723_c0_seq1.p1	sp|P38166|SFT2_YEAST_Protein_transport_protein_SFT2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=SFT2_PE=1_SV=1	2.00E-17
comp12724_c0_seq2.p1		
comp12724_c0_seq3.p3		
comp12727_c0_seq1.p1		
comp12729_c0_seq1.p1	sp|P84239|H3_URECA_Histone_H3_OS=Urechis_caupo_PE=1_SV=2	2.00E-87
comp12730_c0_seq1.p1		
comp12731_c0_seq1.p3		
comp12731_c1_seq1.p2		
comp12735_c0_seq1.p2		
comp12740_c0_seq1.p1		
comp12741_c0_seq1.p1		
comp12741_c0_seq2.p1	sp|P50198|LINX_PSEPA_2,5-dichloro-2,5-cyclohexadiene-1,4-diol_dehydrogenase_OS=Pseudomonas_paucimobilis_GN=linX_PE=3_SV=1	4.00E-14
comp12748_c0_seq1.p1		
comp12752_c0_seq1.p1		
comp12752_c0_seq2.p1		
comp12754_c0_seq1.p1		
comp12756_c0_seq1.p1	sp|Q5VNN5|DEF1B_ORYSJ_Peptide_deformylase_1B,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=PDF1B_PE=2_SV=1	7.00E-25
comp12756_c0_seq2.p1	sp|Q5VNN5|DEF1B_ORYSJ_Peptide_deformylase_1B,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=PDF1B_PE=2_SV=1	1.00E-33
comp12758_c0_seq1.p1	sp|P85200|PRS6B_HELAN_26S_protease_regulatory_subunit_6B_homolog_OS=Helianthus_annuus_PE=1_SV=1	0
comp12762_c0_seq1.p1	sp|Q31N27|ZDS_SYNE7_Probable_zeta-carotene_desaturase_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=zds_PE=3_SV=1	2.00E-29
comp12763_c0_seq1.p1		
comp12766_c1_seq1.p1	sp|P45432|CSN1_ARATH_COP9_signalosome_complex_subunit_1_OS=Arabidopsis_thaliana_GN=CSN1_PE=1_SV=2	3.00E-120
comp12767_c0_seq2.p1		
comp12770_c0_seq1.p1	sp|P36411|RAB7A_DICDI_Ras-related_protein_Rab-7A_OS=Dictyostelium_discoideum_GN=rab7A_PE=1_SV=1	3.00E-71
comp12771_c0_seq2.p1		
comp12773_c0_seq1.p1		
comp127739_c0_seq1.p1		
comp12774_c0_seq1.p1	sp|Q96252|ATP4_ARATH_ATP_synthase_subunit_delta',_mitochondrial_OS=Arabidopsis_thaliana_GN=At5g47030_PE=1_SV=1	8.00E-25
comp127745_c0_seq1.p1	sp|P53451|TCPD_TAKRU_T-complex_protein_1_subunit_delta_OS=Takifugu_rubripes_GN=cct4_PE=2_SV=1	9.00E-39
comp127756_c0_seq1.p1	sp|P33235|FLGK_ECOLI_Flagellar_hook-associated_protein_1_OS=Escherichia_coli_(strain_K12)_GN=flgK_PE=3_SV=3	5.00E-77
comp12776_c0_seq1.p1	sp|O55201|SPT5H_MOUSE_Transcription_elongation_factor_SPT5_OS=Mus_musculus_GN=Supt5h_PE=1_SV=1	3.00E-94
comp12777_c0_seq1.p1		
comp12778_c0_seq1.p1		
comp12779_c0_seq1.p1		
comp12780_c0_seq1.p1		
comp12782_c0_seq2.p1		
comp127820_c0_seq1.p1		
comp12783_c0_seq1.p1	sp|Q3UFF7|LYPL1_MOUSE_Lysophospholipase-like_protein_1_OS=Mus_musculus_GN=Lyplal1_PE=1_SV=3	2.00E-30
comp127832_c0_seq1.p2		
comp12785_c0_seq1.p1		
comp127866_c0_seq1.p2		
comp12787_c0_seq1.p1		
comp12787_c1_seq1.p1		
comp12788_c0_seq1.p2	sp|O13842|CDA1_SCHPO_Chitin_deacetylase_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=cda1_PE=1_SV=1	9.00E-81
comp12789_c0_seq1.p1		
comp12790_c0_seq1.p1		
comp12791_c0_seq1.p1	sp|Q9PTY0|ATPB_CYPCA_ATP_synthase_subunit_beta,_mitochondrial_OS=Cyprinus_carpio_GN=atp5b_PE=2_SV=1	0
comp127962_c0_seq1.p1	sp|P31126|YDEE_ECOLI_Uncharacterized_MFS-type_transporter_ydeE_OS=Escherichia_coli_(strain_K12)_GN=ydeE_PE=3_SV=2	5.00E-60
comp12799_c0_seq1.p1	sp|Q28EW0|TM87A_XENTR_Transmembrane_protein_87A_OS=Xenopus_tropicalis_GN=tmem87a_PE=2_SV=1	1.00E-41
comp12800_c0_seq1.p1		
comp12801_c0_seq1.p1		
comp12804_c0_seq1.p1	sp|O13853|ITS3_SCHPO_Phosphatidylinositol_4-phosphate_5-kinase_its3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=its3_PE=1_SV=1	6.00E-46
comp12806_c0_seq1.p1		
comp12807_c0_seq1.p1		
comp12809_c0_seq1.p2		
comp12811_c0_seq2.p1	sp|Q7XPW5|PMM_ORYSJ_Phosphomannomutase_OS=Oryza_sativa_subsp._japonica_GN=PMM_PE=2_SV=2	3.00E-122
comp12813_c0_seq2.p1	sp|P0A962|ASPG1_ECOLI_L-asparaginase_1_OS=Escherichia_coli_(strain_K12)_GN=ansA_PE=1_SV=1	2.00E-84
comp12814_c0_seq1.p1	sp|Q28I39|IMP1L_XENTR_Mitochondrial_inner_membrane_protease_subunit_1_OS=Xenopus_tropicalis_GN=immp1l_PE=2_SV=1	2.00E-36
comp12815_c0_seq1.p1		
comp12816_c0_seq1.p1	sp|O15145|ARPC3_HUMAN_Actin-related_protein_2/3_complex_subunit_3_OS=Homo_sapiens_GN=ARPC3_PE=1_SV=3	9.00E-44
comp128167_c0_seq1.p1	sp|P64507|YEBY_SHIFL_Uncharacterized_protein_yebY_OS=Shigella_flexneri_GN=yebY_PE=4_SV=1	3.00E-60
comp12817_c0_seq1.p2		
comp12818_c0_seq1.p1	sp|Q4KLI2|RG9D2_RAT_RNA_(guanine-9-)-methyltransferase_domain-containing_protein_2_OS=Rattus_norvegicus_GN=Rg9mtd2_PE=2_SV=1	5.00E-31
comp12819_c0_seq1.p1		
comp128213_c0_seq1.p1	sp|P0A961|ALAA_SHIFL_Glutamate-pyruvate_aminotransferase_AlaA_OS=Shigella_flexneri_GN=alaA_PE=3_SV=1	3.00E-91
comp12823_c0_seq1.p1		
comp12824_c0_seq1.p1	sp|Q1AU63|RL13_RUBXD_50S_ribosomal_protein_L13_OS=Rubrobacter_xylanophilus_(strain_DSM_9941_/_NBRC_16129)_GN=rplM_PE=3_SV=2	2.00E-45
comp12825_c0_seq1.p1	sp|Q641C9|CD123_XENLA_Cell_division_cycle_protein_123_homolog_OS=Xenopus_laevis_GN=cdc123_PE=2_SV=1	1.00E-59
comp12826_c0_seq1.p1		
comp12827_c0_seq1.p1		
comp12829_c0_seq1.p1	sp|Q54N38|UCHL5_DICDI_Ubiquitin_carboxyl-terminal_hydrolase_isozyme_L5_OS=Dictyostelium_discoideum_GN=uch2_PE=3_SV=1	3.00E-97
comp12830_c0_seq1.p1		
comp128315_c0_seq1.p1		
comp12832_c0_seq1.p1		
comp12834_c0_seq1.p1	sp|Q0QLE4|DML_EUBBA_2,3-dimethylmalate_lyase_OS=Eubacterium_barkeri_GN=Dml_PE=1_SV=1	4.00E-64
comp12834_c0_seq1.p2		
comp128349_c0_seq1.p1		
comp12835_c0_seq1.p1	sp|Q6AXC6|DDX11_MOUSE_Probable_ATP-dependent_RNA_helicase_DDX11_OS=Mus_musculus_GN=Ddx11_PE=2_SV=1	9.00E-49
comp12836_c0_seq1.p1		
comp12838_c0_seq1.p1		
comp12840_c0_seq1.p2		
comp12841_c0_seq1.p1		
comp12842_c0_seq1.p3	sp|Q9UYV6|Y1401_PYRAB_Putative_phosphate_permease_PYRAB14010_OS=Pyrococcus_abyssi_(strain_GE5_/_Orsay)_GN=PYRAB14010_PE=3_SV=1	8.00E-15
comp12845_c0_seq1.p1		
comp12846_c0_seq1.p1	sp|Q9ZUI0|Y2241_ARATH_Putative_leucine-rich_repeat_receptor-like_serine/threonine-protein_kinase_At2g24130_OS=Arabidopsis_thaliana_GN=At2g24130_PE=2_SV=1	8.00E-18
comp12847_c0_seq1.p1		
comp12847_c0_seq2.p1		
comp12848_c0_seq1.p1		
comp12848_c0_seq2.p1		
comp128482_c0_seq1.p2		
comp12849_c0_seq1.p1	sp|O60999|CUL1_DICDI_Cullin-1_OS=Dictyostelium_discoideum_GN=culA_PE=1_SV=1	8.00E-61
comp12852_c0_seq1.p1		
comp12853_c0_seq1.p1		
comp12854_c0_seq1.p1		
comp12856_c0_seq1.p1		
comp12858_c0_seq1.p1	sp|P27626|DIN1_RAPSA_Senescence-associated_protein_DIN1_OS=Raphanus_sativus_GN=DIN1_PE=2_SV=1	2.00E-20
comp12860_c0_seq1.p1	sp|A6H791|TRM61_BOVIN_tRNA_(adenine(58)-N(1))-methyltransferase_catalytic_subunit_TRMT61A_OS=Bos_taurus_GN=TRMT61A_PE=2_SV=1	3.00E-57
comp128609_c0_seq1.p1	sp|P30015|LHR_ECOLI_Probable_ATP-dependent_helicase_lhr_OS=Escherichia_coli_(strain_K12)_GN=lhr_PE=3_SV=2	8.00E-58
comp12861_c0_seq2.p1	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	2.00E-16
comp128613_c0_seq1.p1		
comp12863_c0_seq1.p1	sp|Q63450|KCC1A_RAT_Calcium/calmodulin-dependent_protein_kinase_type_1_OS=Rattus_norvegicus_GN=Camk1_PE=1_SV=1	8.00E-64
comp12864_c0_seq1.p1		
comp12866_c0_seq1.p2	sp|Q5E9K0|PSB2_BOVIN_Proteasome_subunit_beta_type-2_OS=Bos_taurus_GN=PSMB2_PE=1_SV=1	1.00E-32
comp12869_c0_seq1.p1	sp|O04202|EIF3F_ARATH_Eukaryotic_translation_initiation_factor_3_subunit_F_OS=Arabidopsis_thaliana_GN=TIF3F1_PE=2_SV=1	5.00E-66
comp12871_c0_seq1.p1	sp|O82392|THIC_ARATH_Phosphomethylpyrimidine_synthase,_chloroplastic_OS=Arabidopsis_thaliana_GN=THIC_PE=1_SV=1	0
comp12872_c0_seq1.p1	sp|P31692|ADT_PARKE_ADP,ATP_carrier_protein_OS=Parachlorella_kessleri_PE=3_SV=1	7.00E-112
comp12872_c0_seq1.p4		
comp12873_c0_seq1.p2	sp|Q5XGC9|SRFB1_XENTR_Serum_response_factor-binding_protein_1_OS=Xenopus_tropicalis_GN=srfbp1_PE=2_SV=1	7.00E-22
comp12874_c0_seq1.p1	sp|Q9WVD5|ORNT1_MOUSE_Mitochondrial_ornithine_transporter_1_OS=Mus_musculus_GN=Slc25a15_PE=2_SV=1	1.00E-42
comp12876_c0_seq1.p1	sp|P73714|Y1821_SYNY3_Putative_zinc_metalloprotease_slr1821_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr1821_PE=3_SV=1	8.00E-47
comp12877_c0_seq1.p1		
comp12878_c0_seq1.p1		
comp12879_c0_seq1.p3		
comp12880_c0_seq1.p1	sp|P42765|THIM_HUMAN_3-ketoacyl-CoA_thiolase,_mitochondrial_OS=Homo_sapiens_GN=ACAA2_PE=1_SV=2	2.00E-141
comp128803_c0_seq1.p2		
comp12881_c0_seq1.p1		
comp12882_c0_seq1.p2		
comp12883_c0_seq1.p1		
comp12884_c0_seq1.p1		
comp12885_c0_seq1.p1		
comp12886_c0_seq1.p1		
comp12887_c0_seq1.p1	sp|P45127|Y1252_HAEIN_Uncharacterized_ABC_transporter_ATP-binding_protein_HI_1252_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=HI_1252_PE=1_SV=1	0
comp128873_c0_seq1.p2		
comp12890_c0_seq1.p1	sp|Q9ZPV8|COAD_ARATH_Phosphopantetheine_adenylyltransferase_OS=Arabidopsis_thaliana_GN=COAD_PE=1_SV=1	5.00E-24
comp12891_c0_seq1.p1		
comp12894_c0_seq1.p1		
comp12894_c0_seq2.p1		
comp12895_c0_seq2.p1		
comp12897_c0_seq1.p1	sp|Q869Q0|Y4527_DICDI_COBW_domain-containing_protein_DDB_G0274527_OS=Dictyostelium_discoideum_GN=DDB_G0274527_PE=3_SV=1	5.00E-19
comp12898_c0_seq1.p1		
comp12900_c0_seq1.p1	sp|Q8L716|U2A2B_ARATH_Splicing_factor_U2af_large_subunit_B_OS=Arabidopsis_thaliana_GN=U2AF65B_PE=2_SV=2	2.00E-71
comp12901_c0_seq1.p1		
comp12902_c0_seq1.p1	sp|Q54ZX5|PX24A_DICDI_PXMP2/4_family_protein_1_OS=Dictyostelium_discoideum_GN=DDB_G0277335_PE=3_SV=1	1.00E-19
comp12902_c0_seq1.p2	sp|Q9BRX9|WDR83_HUMAN_WD_repeat_domain-containing_protein_83_OS=Homo_sapiens_GN=WDR83_PE=1_SV=1	7.00E-76
comp12903_c0_seq1.p1	sp|Q8R173|ZDHC3_MOUSE_Palmitoyltransferase_ZDHHC3_OS=Mus_musculus_GN=Zdhhc3_PE=1_SV=1	1.00E-24
comp12904_c0_seq1.p1	sp|A6NKF1|SAC31_HUMAN_SAC3_domain-containing_protein_1_OS=Homo_sapiens_GN=SAC3D1_PE=1_SV=2	7.00E-12
comp12906_c0_seq2.p1		
comp12906_c0_seq3.p2	sp|P70805|ALGG_AZOVI_Poly(beta-D-mannuronate)_C5_epimerase_OS=Azotobacter_vinelandii_GN=algG_PE=2_SV=1	1.00E-11
comp129065_c0_seq1.p1	sp|P59293|ARGA_SHIFL_Amino-acid_acetyltransferase_OS=Shigella_flexneri_GN=argA_PE=3_SV=1	2.00E-93
comp12908_c0_seq1.p1		
comp12909_c0_seq1.p1	sp|Q9JMK8|VPS54_RAT_Vacuolar_protein_sorting-associated_protein_54_OS=Rattus_norvegicus_GN=Vps54_PE=2_SV=1	3.00E-24
comp12910_c0_seq1.p1	sp|P23651|RBL_PYLLI_Ribulose_bisphosphate_carboxylase_large_chain_OS=Pylaiella_littoralis_GN=rbcL_PE=3_SV=1	0
comp12912_c0_seq2.p1		
comp12913_c0_seq1.p1		
comp12913_c0_seq2.p1		
comp12914_c0_seq1.p1		
comp12915_c0_seq1.p1	sp|Q9LQK0|DRG1_ARATH_Developmentally_regulated_G-protein_1_OS=Arabidopsis_thaliana_GN=DRG1_PE=1_SV=1	7.00E-135
comp12916_c0_seq1.p1		
comp12917_c0_seq1.p1	sp|Q9Z1G3|VATC1_MOUSE_V-type_proton_ATPase_subunit_C_1_OS=Mus_musculus_GN=Atp6v1c1_PE=1_SV=4	2.00E-56
comp12918_c0_seq2.p1	sp|Q9M2P7|PAP9_ARATH_Probable_plastid-lipid-associated_protein_9,_chloroplastic_OS=Arabidopsis_thaliana_GN=PAP9_PE=1_SV=1	5.00E-14
comp12919_c0_seq1.p1	sp|Q9FLF0|RS92_ARATH_40S_ribosomal_protein_S9-2_OS=Arabidopsis_thaliana_GN=RPS9C_PE=2_SV=1	2.00E-86
comp12921_c0_seq1.p1		
comp12922_c0_seq1.p1	sp|Q10099|SEH1_SCHPO_Nucleoporin_seh1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=seh1_PE=1_SV=1	7.00E-28
comp12922_c0_seq2.p1	sp|Q4FZW5|SEH1A_XENLA_Nucleoporin_seh1-A_OS=Xenopus_laevis_GN=seh1l-a_PE=2_SV=1	2.00E-42
comp129224_c0_seq1.p1	sp|P0ABH9|CLPA_ECOLI_ATP-dependent_Clp_protease_ATP-binding_subunit_ClpA_OS=Escherichia_coli_(strain_K12)_GN=clpA_PE=1_SV=1	2.00E-83
comp12923_c0_seq1.p1		
comp12925_c0_seq2.p1	sp|Q91WA1|TIPIN_MOUSE_TIMELESS-interacting_protein_OS=Mus_musculus_GN=Tipin_PE=1_SV=2	2.00E-13
comp12927_c0_seq1.p1	sp|Q01667|CAB6_ARATH_Chlorophyll_a-b_binding_protein_6,_chloroplastic_OS=Arabidopsis_thaliana_GN=LHCA1_PE=1_SV=1	4.00E-16
comp12929_c0_seq2.p1		
comp12930_c0_seq1.p1	sp|P62243|RS8_RAT_40S_ribosomal_protein_S8_OS=Rattus_norvegicus_GN=Rps8_PE=1_SV=2	3.00E-72
comp12931_c0_seq1.p1	sp|O80800|ACPM2_ARATH_Acyl_carrier_protein_2,_mitochondrial_OS=Arabidopsis_thaliana_GN=MTACP2_PE=1_SV=1	8.00E-22
comp129325_c0_seq1.p1	sp|P08506|DACC_ECOLI_D-alanyl-D-alanine_carboxypeptidase_dacC_OS=Escherichia_coli_(strain_K12)_GN=dacC_PE=1_SV=2	3.00E-34
comp12933_c0_seq1.p1	sp|P0C8M8|CCR1_MAIZE_Probable_serine/threonine-protein_kinase_CCRP1_OS=Zea_mays_GN=CCRP1_PE=1_SV=1	5.00E-91
comp12934_c0_seq1.p1		
comp12937_c0_seq1.p1		
comp12938_c0_seq1.p1		
comp12939_c0_seq1.p1	sp|Q6NUA0|CHRD1_XENLA_Cysteine_and_histidine-rich_domain-containing_protein_1_OS=Xenopus_laevis_GN=chordc1_PE=2_SV=1	6.00E-24
comp12939_c0_seq2.p1	sp|Q6NUA0|CHRD1_XENLA_Cysteine_and_histidine-rich_domain-containing_protein_1_OS=Xenopus_laevis_GN=chordc1_PE=2_SV=1	9.00E-28
comp12946_c0_seq1.p1	sp|Q923K9|A1CF_RAT_APOBEC1_complementation_factor_OS=Rattus_norvegicus_GN=A1cf_PE=1_SV=1	2.00E-15
comp12948_c0_seq1.p1		
comp12952_c0_seq1.p2		
comp12953_c0_seq1.p1		
comp12953_c0_seq2.p1		
comp12953_c0_seq2.p3		
comp12954_c0_seq1.p1		
comp12955_c0_seq1.p1		
comp12955_c0_seq1.p3		
comp12956_c0_seq1.p1		
comp12959_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	1.00E-25
comp12960_c0_seq1.p1	sp|Q55DM5|S35B2_DICDI_Adenosine_3'-phospho_5'-phosphosulfate_transporter_1_OS=Dictyostelium_discoideum_GN=slc35b2_PE=3_SV=1	1.00E-11
comp12960_c0_seq2.p1	sp|P78383|S35B1_HUMAN_Solute_carrier_family_35_member_B1_OS=Homo_sapiens_GN=SLC35B1_PE=2_SV=1	4.00E-43
comp12961_c0_seq1.p1	sp|P39598|YWBO_BACSU_Uncharacterized_protein_ywbO_OS=Bacillus_subtilis_GN=ywbO_PE=4_SV=1	3.00E-13
comp12962_c0_seq1.p1		
comp12964_c0_seq1.p1		
comp12965_c0_seq1.p1		
comp12967_c0_seq1.p1	sp|Q5PQR5|IMP4_RAT_U3_small_nucleolar_ribonucleoprotein_protein_IMP4_OS=Rattus_norvegicus_GN=Imp4_PE=2_SV=1	4.00E-108
comp12970_c0_seq1.p1		
comp12971_c0_seq1.p1		
comp12971_c0_seq2.p1		
comp12972_c0_seq1.p1		
comp12972_c0_seq2.p1		
comp12973_c0_seq1.p1	sp|Q650T9|RH7_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_7_OS=Oryza_sativa_subsp._japonica_GN=Os09g0520700_PE=2_SV=1	1.00E-99
comp129737_c0_seq1.p2	sp|Q6JWW5|RL5_OIKDI_60S_ribosomal_protein_L5_OS=Oikopleura_dioica_GN=RPL5_PE=3_SV=1	2.00E-27
comp12974_c0_seq1.p2		
comp12975_c0_seq1.p1		
comp129775_c0_seq1.p2		
comp12980_c0_seq1.p1		
comp12981_c0_seq1.p1	sp|Q117I4|HEM1_TRIEI_Glutamyl-tRNA_reductase_OS=Trichodesmium_erythraeum_(strain_IMS101)_GN=hemA_PE=3_SV=1	6.00E-109
comp12982_c0_seq1.p1		
comp129830_c0_seq1.p2		
comp12985_c0_seq1.p1		
comp12986_c0_seq1.p1		
comp12986_c0_seq2.p1		
comp12988_c0_seq1.p1		
comp12989_c0_seq1.p1	sp|Q94IR2|CCD1_PHAVU_Carotenoid_9,10(9',10')-cleavage_dioxygenase_1_OS=Phaseolus_vulgaris_GN=CCD1_PE=1_SV=1	8.00E-115
comp12992_c0_seq1.p1		
comp12994_c0_seq1.p1	sp|P24726|PSBA_ECTSI_Photosystem_Q(B)_protein_OS=Ectocarpus_siliculosus_GN=psbA_PE=3_SV=1	4.00E-169
comp12995_c0_seq2.p1		
comp12997_c0_seq1.p1	sp|Q0WPX9|P4KB2_ARATH_Phosphatidylinositol_4-kinase_2_OS=Arabidopsis_thaliana_GN=PI4KBETA2_PE=2_SV=1	8.00E-64
comp13000_c0_seq1.p1	sp|Q96KR6|F210B_HUMAN_Protein_FAM210B_OS=Homo_sapiens_GN=FAM210B_PE=1_SV=2	4.00E-12
comp13001_c0_seq1.p1	sp|P22793|TRHY_SHEEP_Trichohyalin_OS=Ovis_aries_GN=TCHH_PE=2_SV=1	3.00E-11
comp13002_c0_seq1.p1		
comp130022_c0_seq1.p1	sp|Q83QT2|NUON_SHIFL_NADH-quinone_oxidoreductase_subunit_N_OS=Shigella_flexneri_GN=nuoN_PE=3_SV=3	4.00E-68
comp13004_c0_seq1.p1	sp|P37879|SYK_CRIGR_Lysine--tRNA_ligase_OS=Cricetulus_griseus_GN=KARS_PE=1_SV=1	0
comp13006_c0_seq1.p1	sp|P82887|H2B_OLILU_Histone_H2B_OS=Olisthodiscus_luteus_PE=1_SV=2	1.00E-51
comp13012_c0_seq1.p1	sp|Q65050|RL15A_PICMA_60S_ribosomal_protein_L15-1_OS=Picea_mariana_GN=SB61_PE=2_SV=1	1.00E-91
comp13017_c0_seq1.p1	sp|Q0VCH8|TMM65_BOVIN_Transmembrane_protein_65_OS=Bos_taurus_GN=TMEM65_PE=2_SV=1	4.00E-36
comp130199_c0_seq1.p1	sp|P06709|BIRA_ECOLI_Bifunctional_protein_BirA_OS=Escherichia_coli_(strain_K12)_GN=birA_PE=1_SV=1	9.00E-64
comp13021_c0_seq1.p1		
comp130216_c0_seq1.p1		
comp130237_c0_seq1.p2		
comp13031_c0_seq1.p1		
comp13032_c0_seq1.p1	sp|Q8DK30|DXR_THEEB_1-deoxy-D-xylulose_5-phosphate_reductoisomerase_OS=Thermosynechococcus_elongatus_(strain_BP-1)_GN=dxr_PE=3_SV=1	9.00E-167
comp13032_c0_seq2.p1	sp|C0ZF60|DXR_BREBN_1-deoxy-D-xylulose_5-phosphate_reductoisomerase_OS=Brevibacillus_brevis_(strain_47_/_JCM_6285_/_NBRC_100599)_GN=dxr_PE=3_SV=1	1.00E-12
comp13033_c0_seq1.p2		
comp13035_c0_seq1.p1	sp|Q84Y18|CXIP4_ARATH_CAX-interacting_protein_4_OS=Arabidopsis_thaliana_GN=CXIP4_PE=1_SV=2	3.00E-19
comp13035_c0_seq2.p1	sp|Q84Y18|CXIP4_ARATH_CAX-interacting_protein_4_OS=Arabidopsis_thaliana_GN=CXIP4_PE=1_SV=2	3.00E-19
comp13037_c0_seq1.p1	sp|Q500W7|PIGM_ARATH_GPI_mannosyltransferase_1_OS=Arabidopsis_thaliana_GN=PIGM_PE=2_SV=1	4.00E-84
comp13037_c0_seq1.p2	sp|O73672|PSA2_CARAU_Proteasome_subunit_alpha_type-2_OS=Carassius_auratus_GN=psma2_PE=2_SV=3	2.00E-40
comp130370_c0_seq1.p1	sp|P0ABM4|CCMC_SHIFL_Heme_exporter_protein_C_OS=Shigella_flexneri_GN=ccmC_PE=3_SV=1	3.00E-76
comp13040_c0_seq1.p1	sp|O04059|DHBK_SOLLC_Putative_3,4-dihydroxy-2-butanone_kinase_OS=Solanum_lycopersicum_GN=DHBK_PE=2_SV=1	2.00E-95
comp130402_c0_seq1.p1	sp|P33570|TKT2_ECOLI_Transketolase_2_OS=Escherichia_coli_(strain_K12)_GN=tktB_PE=1_SV=1	4.00E-71
comp13041_c0_seq1.p1		
comp13044_c0_seq1.p1		
comp13046_c0_seq1.p1	sp|Q2VEX9|CRTSO_DAUCA_Prolycopene_isomerase,_chloroplastic_OS=Daucus_carota_GN=CRTISO_PE=2_SV=1	9.00E-35
comp130478_c0_seq1.p2	sp|P37659|YHJU_ECOLI_Uncharacterized_protein_yhjU_OS=Escherichia_coli_(strain_K12)_GN=yhjU_PE=4_SV=1	1.00E-62
comp13048_c0_seq1.p1	sp|P00255|FER_SYNLI_Ferredoxin_OS=Synechococcus_lividus_PE=1_SV=2	6.00E-15
comp130481_c0_seq1.p1		
comp13049_c0_seq1.p1	sp|P34091|RL6_MESCR_60S_ribosomal_protein_L6_OS=Mesembryanthemum_crystallinum_GN=RPL6_PE=2_SV=1	3.00E-45
comp13049_c0_seq2.p1	sp|P34091|RL6_MESCR_60S_ribosomal_protein_L6_OS=Mesembryanthemum_crystallinum_GN=RPL6_PE=2_SV=1	1.00E-57
comp13050_c0_seq1.p1	sp|O13883|PIGU_SCHPO_GPI_transamidase_component_GAB1_homolog_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC1952.01_PE=2_SV=2	2.00E-21
comp13051_c0_seq1.p1		
comp13055_c0_seq1.p2		
comp13056_c0_seq1.p1	sp|O13396|MSH2_NEUCR_DNA_mismatch_repair_protein_msh-2_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=msh-2_PE=3_SV=1	7.00E-160
comp13059_c0_seq1.p1		
comp13060_c0_seq1.p1	sp|Q54MI3|SUN2_DICDI_SUN_domain-containing_protein_2_OS=Dictyostelium_discoideum_GN=sun2_PE=3_SV=1	3.00E-28
comp13061_c0_seq1.p1		
comp13063_c0_seq1.p1	sp|Q9LFQ3|SNL2_ARATH_Paired_amphipathic_helix_protein_Sin3-like_2_OS=Arabidopsis_thaliana_GN=SNL2_PE=1_SV=2	1.00E-16
comp13064_c0_seq1.p1	sp|Q5R788|ISCA2_PONAB_Iron-sulfur_cluster_assembly_2_homolog,_mitochondrial_OS=Pongo_abelii_GN=ISCA2_PE=2_SV=1	2.00E-20
comp13068_c0_seq1.p2	sp|Q9BMX5|RS6_APLCA_40S_ribosomal_protein_S6_OS=Aplysia_californica_GN=RPS6_PE=2_SV=1	2.00E-77
comp13069_c0_seq1.p1		
comp13070_c0_seq1.p2	sp|O23968|GPX4_HELAN_Probable_phospholipid_hydroperoxide_glutathione_peroxidase_OS=Helianthus_annuus_GN=GPXHA-2_PE=2_SV=1	2.00E-33
comp13071_c0_seq1.p1		
comp13071_c0_seq2.p1		
comp13072_c0_seq1.p3		
comp13073_c0_seq1.p1	sp|Q9USI5|STI1_SCHPO_Heat_shock_protein_sti1_homolog_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=sti1_PE=2_SV=1	3.00E-15
comp13075_c0_seq1.p1		
comp130765_c0_seq1.p1		
comp13077_c0_seq1.p1		
comp13077_c0_seq2.p1		

comp13078_c0_seq1.p1				
comp13080_c0_seq1.p1	sp|Q505D7|OPA3_MOUSE_Optic_atrophy_3_protein_homolog_OS=Mus_musculus_GN=Opa3_PE=1_SV=1	9.00E-12	[illegible]	[illegible]
comp13081_c0_seq1.p1	sp|Q7D8I1|PKS18_MYCTU_Alpha-pyrone_synthesis_polyketide_synthase-like_Pks18_OS=Mycobacterium_tuberculosis_GN=pks18_PE=1_SV=1	2.00E-73		
comp13083_c0_seq1.p1				
comp13084_c0_seq1.p1				
comp13085_c0_seq1.p2				
comp13087_c0_seq1.p1				
comp13088_c0_seq1.p1	sp|O13985|YEG3_SCHPO_Uncharacterized_WD_repeat-containing_protein_C26H5.03_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC26H5.03_PE=1_SV=2	4.00E-37	[illegible]	[illegible]
comp130880_c0_seq1.p1				
comp13090_c0_seq1.p1				
comp13091_c0_seq1.p1				
comp13092_c0_seq1.p1				
comp13092_c0_seq2.p1	sp|A8LVF4|KMO_SALAI_Kynurenine_3-monooxygenase_OS=Salinispora_arenicola_(strain_CNS-205)_GN=kmo_PE=3_SV=1	6.00E-35	[illegible]	[illegible]
comp13093_c0_seq1.p1	sp|Q9URM2|TKT_SCHPO_Probable_transketolase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC2G5.05_PE=2_SV=1	4.00E-48	[illegible]	[illegible]
comp13095_c0_seq1.p1				
comp13098_c0_seq2.p1	sp|Q54TL0|KIF7_DICDI_Kinesin-related_protein_7_OS=Dictyostelium_discoideum_GN=kif7_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp13101_c0_seq1.p1				
comp13102_c0_seq2.p1				
comp13103_c0_seq1.p1				
comp131059_c0_seq1.p2				
comp13106_c0_seq1.p1	sp|Q5RJF7|CA2D4_MOUSE_Voltage-dependent_calcium_channel_subunit_alpha-2/delta-4_OS=Mus_musculus_GN=Cacna2d4_PE=2_SV=1	4.00E-25	[illegible]	[illegible]
comp13108_c0_seq1.p1				
comp13110_c0_seq1.p1				
comp13112_c0_seq1.p1	sp|Q6GL41|MCM4_XENTR_DNA_replication_licensing_factor_mcm4_OS=Xenopus_tropicalis_GN=mcm4_PE=2_SV=1	1.00E-67	[illegible]	[illegible]
comp13114_c0_seq1.p1				
comp13115_c0_seq1.p1				
comp13116_c0_seq1.p1				
comp13117_c0_seq2.p1	sp|Q6PE01|SNR40_MOUSE_U5_small_nuclear_ribonucleoprotein_40_kDa_protein_OS=Mus_musculus_GN=Snrnp40_PE=2_SV=1	4.00E-120	[illegible]	[illegible]
comp13117_c0_seq2.p2	sp|Q114R5|GRPE_TRIEI_Protein_grpE_OS=Trichodesmium_erythraeum_(strain_IMS101)_GN=grpE_PE=3_SV=1	2.00E-20	[illegible]	[illegible]
comp13118_c0_seq1.p1				
comp13118_c0_seq2.p1				
comp13119_c0_seq1.p1	sp|Q982V6|CLPP2_RHILO_ATP-dependent_Clp_protease_proteolytic_subunit_2_OS=Rhizobium_loti_(strain_MAFF303099)_GN=clpP2_PE=3_SV=1	3.00E-79	[illegible]	[illegible]
comp13120_c0_seq1.p1				
comp13120_c0_seq2.p1				
comp13122_c0_seq1.p1				
comp13122_c0_seq1.p3				
comp13124_c0_seq1.p1	sp|P64956|Y2253_MYCBO_Uncharacterized_protein_Mb2253c_OS=Mycobacterium_bovis_GN=Mb2253c_PE=4_SV=1	6.00E-22	[illegible]	[illegible]
comp13126_c0_seq1.p1	sp|Q8NDA2|HMCN2_HUMAN_Hemicentin-2_OS=Homo_sapiens_GN=HMCN2_PE=2_SV=2	6.00E-12	[illegible]	[illegible]
comp13127_c0_seq1.p1	sp|P16120|THRC_YEAST_Threonine_synthase_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=THR4_PE=1_SV=1	1.00E-133	[illegible]	[illegible]
comp13128_c0_seq1.p1	sp|Q5R9N7|L2HDH_PONAB_L-2-hydroxyglutarate_dehydrogenase,_mitochondrial_OS=Pongo_abelii_GN=L2HGDH_PE=2_SV=1	2.00E-47	[illegible]	[illegible]
comp13131_c0_seq1.p1				
comp13132_c0_seq1.p1	sp|O88788|AG10B_RAT_Putative_Dol-P-Glc:Glc(2)Man(9)GlcNAc(2)-PP-Dol_alpha-1,2-glucosyltransferase_OS=Rattus_norvegicus_GN=Alg10b_PE=1_SV=1	5.00E-28	[illegible]	[illegible]
comp13133_c0_seq1.p1	sp|Q5EA97|S38AB_BOVIN_Putative_sodium-coupled_neutral_amino_acid_transporter_11_OS=Bos_taurus_GN=SLC38A11_PE=2_SV=1	6.00E-15	[illegible]	[illegible]
comp13137_c0_seq1.p1				
comp131370_c0_seq1.p1				
comp13138_c0_seq2.p1	sp|Q51342|PUR1_PSEAE_Amidophosphoribosyltransferase_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=purF_PE=3_SV=3	2.00E-159	[illegible]	[illegible]
comp13139_c0_seq1.p1	sp|Q9LFT9|RAH1E_ARATH_Ras-related_protein_RABH1e_OS=Arabidopsis_thaliana_GN=RABH1E_PE=2_SV=1	8.00E-101	[illegible]	[illegible]
comp13142_c0_seq2.p1				
comp13144_c0_seq1.p2				
comp13145_c0_seq1.p1	sp|Q5UP39|YR873_MIMIV_Putative_ankyrin_repeat_protein_R873_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R873_PE=4_SV=1	1.00E-19		
comp13146_c0_seq2.p1				
comp13150_c0_seq1.p1				
comp131574_c0_seq1.p1				
comp13159_c0_seq1.p1				
comp131613_c0_seq1.p1				
comp13166_c0_seq1.p1				
comp13167_c1_seq1.p1	sp|Q9Y5N5|HEMK2_HUMAN_HemK_methyltransferase_family_member_2_OS=Homo_sapiens_GN=N6AMT1_PE=1_SV=3	1.00E-44	[illegible]	[illegible]
comp13170_c0_seq2.p1				
comp13205_c0_seq1.p2				
comp13205_c0_seq2.p2				
comp13213_c0_seq1.p1				
comp13213_c0_seq1.p3				
comp13220_c0_seq1.p2	sp|P46575|RL40_EIMBO_Ubiquitin-60S_ribosomal_protein_L40_OS=Eimeria_bovis_PE=2_SV=2	5.00E-65	[illegible]	[illegible]
comp132298_c0_seq1.p1				
comp13234_c0_seq1.p1				
comp13239_c0_seq1.p1				
comp132403_c0_seq1.p1	sp|P38035|RTCR_ECOLI_Transcriptional_regulatory_protein_rtcR_OS=Escherichia_coli_(strain_K12)_GN=rtcR_PE=4_SV=2	1.00E-77	[illegible]	[illegible]
comp13246_c0_seq1.p1				
comp13248_c0_seq1.p1	sp|Q3TX08|TRM1_MOUSE_tRNA_(guanine(26)-N(2))-dimethyltransferase_OS=Mus_musculus_GN=Trmt1_PE=1_SV=2	3.00E-11	[illegible]	[illegible]
comp13250_c0_seq1.p2				
comp132519_c0_seq1.p1				
comp13252_c0_seq1.p1	sp|P51293|RPOA_PORPU_DNA-directed_RNA_polymerase_subunit_alpha_OS=Porphyra_purpurea_GN=rpoA_PE=3_SV=1	4.00E-57	[illegible]	[illegible]
comp13256_c0_seq1.p1				
comp132564_c0_seq1.p5				
comp13263_c0_seq1.p1				
comp13265_c0_seq1.p1	sp|Q5R573|RBL2A_PONAB_Rab-like_protein_2A_OS=Pongo_abelii_GN=RABL2A_PE=2_SV=1	5.00E-48	[illegible]	[illegible]
comp13276_c0_seq1.p1	sp|P14882|PCCA_RAT_Propionyl-CoA_carboxylase_alpha_chain,_mitochondrial_OS=Rattus_norvegicus_GN=Pcca_PE=1_SV=3	8.00E-55	[illegible]	[illegible]
comp13286_c0_seq1.p1				
comp13291_c0_seq1.p1				
comp13295_c0_seq1.p2				
comp13295_c0_seq1.p3	sp|Q9LHG9|NACA1_ARATH_Nascent_polypeptide-associated_complex_subunit_alpha-like_protein_1_OS=Arabidopsis_thaliana_GN=At3g12390_PE=1_SV=1	1.00E-27	[illegible]	[illegible]
comp132990_c0_seq1.p2				
comp13321_c0_seq1.p1				
comp13324_c0_seq1.p1	sp|P25696|ENO2_ARATH_Bifunctional_enolase_2/transcriptional_activator_OS=Arabidopsis_thaliana_GN=ENO2_PE=1_SV=1	0	[illegible]	[illegible]
comp133252_c0_seq1.p3	sp|Q15YB0|RPOC_PSEA6_DNA-directed_RNA_polymerase_subunit_beta'_OS=Pseudoalteromonas_atlantica_(strain_T6c_/_ATCC_BAA-1087)_GN=rpoC_PE=3_SV=1	1.00E-40	[illegible]	[illegible]
comp13326_c0_seq1.p1	sp|Q9C099|LRCC1_HUMAN_Leucine-rich_repeat_and_coiled-coil_domain-containing_protein_1_OS=Homo_sapiens_GN=LRRCC1_PE=2_SV=2	1.00E-11	[illegible]	[illegible]
comp13328_c0_seq1.p2				
comp13329_c0_seq1.p2	sp|P84239|H3_URECA_Histone_H3_OS=Urechis_caupo_PE=1_SV=2	1.00E-75	[illegible]	[illegible]
comp13353_c0_seq1.p1				
comp13369_c0_seq1.p2				
comp13370_c0_seq1.p1				
comp13375_c0_seq1.p1				
comp133762_c0_seq1.p2				
comp13393_c0_seq2.p1				
comp13426_c0_seq1.p1				
comp13434_c0_seq1.p1				
comp13440_c0_seq2.p1	sp|Q9JKK8|ATR_MOUSE_Serine/threonine-protein_kinase_ATR_OS=Mus_musculus_GN=Atr_PE=1_SV=2	3.00E-11	[illegible]	[illegible]
comp13442_c0_seq1.p1				
comp13445_c0_seq1.p1	sp|Q9JLI7|SPAG6_MOUSE_Sperm-associated_antigen_6_OS=Mus_musculus_GN=Spag6_PE=1_SV=1	0	[illegible]	[illegible]
comp13447_c0_seq1.p1	sp|P23641|MPCP_YEAST_Mitochondrial_phosphate_carrier_protein_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=MIR1_PE=1_SV=1	1.00E-81	[illegible]	[illegible]
comp13450_c0_seq1.p1				
comp13453_c0_seq2.p1				
comp13457_c0_seq1.p2				
comp13458_c0_seq1.p1				
comp13477_c0_seq1.p1	sp|Q9ULJ7|ANR50_HUMAN_Ankyrin_repeat_domain-containing_protein_50_OS=Homo_sapiens_GN=ANKRD50_PE=1_SV=4	8.00E-14	GO:0005515	[illegible]
comp13477_c0_seq1.p2				
comp13502_c0_seq1.p1				
comp13504_c0_seq2.p1				
comp13524_c0_seq1.p1				
comp13529_c0_seq2.p1				
comp135302_c0_seq1.p1	sp|B7NH49|DEOC_ECOLU_Deoxyribose-phosphate_aldolase_OS=Escherichia_coli_O17:K52:H18_(strain_UMN026_/_ExPEC)_GN=deoC_PE=3_SV=1	2.00E-56	[illegible]	[illegible]
comp135303_c0_seq1.p1				
comp13540_c0_seq1.p2				
comp13546_c0_seq1.p1	sp|P0DJ18|RL18A_TETTH_60S_ribosomal_protein_L18a_OS=Tetrahymena_thermophila_GN=RPL18A_PE=1_SV=1	2.00E-34	[illegible]	[illegible]
comp13549_c0_seq1.p1	sp|Q9LVA7|ICLN_ARATH_Chloride_conductance_regulatory_protein_ICln_OS=Arabidopsis_thaliana_GN=At5g62290_PE=2_SV=1	1.00E-20	[illegible]	[illegible]
comp13549_c0_seq2.p1	sp|Q9LVA7|ICLN_ARATH_Chloride_conductance_regulatory_protein_ICln_OS=Arabidopsis_thaliana_GN=At5g62290_PE=2_SV=1	1.00E-20	[illegible]	[illegible]
comp13555_c0_seq1.p1				
comp13565_c0_seq1.p2	sp|Q8LGG0|FKB12_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP12_OS=Arabidopsis_thaliana_GN=FKBP12_PE=1_SV=2	7.00E-52	[illegible]	[illegible]
comp13568_c0_seq2.p1	sp|Q55BF2|NMD3_DICDI_60S_ribosomal_export_protein_NMD3_OS=Dictyostelium_discoideum_GN=nmd3_PE=3_SV=1	1.00E-86	[illegible]	[illegible]
comp135711_c0_seq1.p2	sp|Q5RCH2|PDIA2_PONAB_Protein_disulfide-isomerase_A2_OS=Pongo_abelii_GN=PDIA2_PE=2_SV=1	2.00E-15	[illegible]	[illegible]
comp13576_c0_seq1.p1				
comp13580_c0_seq1.p1				
comp13586_c0_seq1.p1	sp|O80800|ACPM2_ARATH_Acyl_carrier_protein_2,_mitochondrial_OS=Arabidopsis_thaliana_GN=MTACP2_PE=1_SV=1	5.00E-20	[illegible]	[illegible]
comp13588_c0_seq1.p1	sp|O82171|AGD10_ARATH_ADP-ribosylation_factor_GTPase-activating_protein_AGD10_OS=Arabidopsis_thaliana_GN=AGD10_PE=2_SV=1	1.00E-38	[illegible]	[illegible]
comp13588_c0_seq2.p1	sp|O82171|AGD10_ARATH_ADP-ribosylation_factor_GTPase-activating_protein_AGD10_OS=Arabidopsis_thaliana_GN=AGD10_PE=2_SV=1	1.00E-38	[illegible]	[illegible]
comp135888_c0_seq1.p2	sp|Q54DU9|TP4AA_DICDI_Probable_protein_tyrosine_phosphatase_type_IVA_A_OS=Dictyostelium_discoideum_GN=DDB_G0292024_PE=3_SV=1	2.00E-24	[illegible]	[illegible]
comp13591_c0_seq1.p1				
comp13594_c0_seq1.p1				
comp13601_c0_seq1.p1				
comp13604_c0_seq1.p1				
comp13610_c0_seq1.p1				
comp13618_c0_seq1.p1	sp|Q8VC51|WAP53_MOUSE_Telomerase_Cajal_body_protein_1_OS=Mus_musculus_GN=Wrap53_PE=2_SV=1	6.00E-88	[illegible]	[illegible]
comp13618_c0_seq2.p3				
comp13621_c0_seq1.p1				
comp13623_c0_seq1.p1				
comp13627_c0_seq1.p1				
comp13637_c0_seq1.p1				
comp13643_c0_seq1.p1				
comp13653_c0_seq1.p1				
comp13656_c0_seq1.p1				
comp13662_c0_seq1.p1				
comp13669_c0_seq1.p1				
comp13670_c0_seq1.p1				
comp13674_c0_seq1.p1				
comp13675_c0_seq1.p1				
comp13675_c1_seq1.p1				
comp13689_c0_seq1.p1	sp|Q9LF30|RS192_ARATH_40S_ribosomal_protein_S19-2_OS=Arabidopsis_thaliana_GN=RPS19B_PE=2_SV=1	2.00E-49	[illegible]	[illegible]
comp13691_c0_seq1.p1				
comp13693_c0_seq1.p1	sp|P54280|PMS1_SCHPO_DNA_mismatch_repair_protein_pms1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=pms1_PE=2_SV=1	1.00E-16	[illegible]	[illegible]
comp13709_c0_seq2.p1				
comp13711_c0_seq1.p1				
comp13713_c0_seq1.p1				
comp13718_c0_seq1.p1				
comp13729_c0_seq1.p2	sp|P22738|RL32_ARATH_60S_ribosomal_protein_L3-2_OS=Arabidopsis_thaliana_GN=ARP2_PE=2_SV=4	1.00E-176	[illegible]	[illegible]
comp13735_c0_seq1.p1				
comp13743_c0_seq1.p1				
comp13750_c0_seq2.p1				
comp13764_c0_seq1.p1				
comp13764_c0_seq1.p2	sp|Q9LR64|Y1360_ARATH_Thylakoid_lumenal_protein_At1g03610,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g03600_PE=1_SV=1	3.00E-18	[illegible]	[illegible]
comp13783_c0_seq1.p1	sp|Q96IU4|ABHEB_HUMAN_Abhydrolase_domain-containing_protein_14B_OS=Homo_sapiens_GN=ABHD14B_PE=1_SV=1	3.00E-39	[illegible]	[illegible]
comp13791_c0_seq1.p2				
comp13792_c0_seq1.p1	sp|Q23K29|TTL3D_TETTS_Tubulin_glycylase_3D_OS=Tetrahymena_thermophila_(strain_SB210)_GN=TTLL3D_PE=3_SV=1	2.00E-62	[illegible]	[illegible]
comp13797_c0_seq1.p1				
comp13803_c0_seq1.p1				
comp13804_c0_seq2.p1				
comp13810_c0_seq1.p1				
comp13820_c0_seq1.p1	sp|Q5ZJN4|UBP10_CHICK_Ubiquitin_carboxyl-terminal_hydrolase_10_OS=Gallus_gallus_GN=USP10_PE=2_SV=1	1.00E-12	[illegible]	[illegible]
comp13836_c0_seq1.p2				
comp13838_c0_seq1.p1				
comp13849_c0_seq1.p1				
comp13852_c0_seq1.p1	sp|Q26481|RL5_STYCL_60S_ribosomal_protein_L5_OS=Styela_clava_GN=RPL5_PE=3_SV=3	6.00E-117	[illegible]	[illegible]
comp13864_c0_seq1.p1				
comp13864_c0_seq2.p1				
comp13867_c0_seq2.p1	sp|Q54NM6|MOCS1_DICDI_Molybdenum_cofactor_biosynthesis_protein_1_OS=Dictyostelium_discoideum_GN=mocs1_PE=3_SV=1	5.00E-118	[illegible]	[illegible]
comp13881_c0_seq1.p1				
comp13884_c0_seq1.p1				
comp13889_c0_seq2.p1				
comp138891_c0_seq1.p1				
comp13904_c0_seq1.p1				
comp13904_c1_seq1.p1				
comp13913_c0_seq1.p1	sp|Q69TY4|PR2E1_ORYSJ_Peroxiredoxin-2E-1,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=PRXIIE-1_PE=2_SV=1	3.00E-33	[illegible]	[illegible]
comp13913_c0_seq2.p1	sp|Q69TY4|PR2E1_ORYSJ_Peroxiredoxin-2E-1,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=PRXIIE-1_PE=2_SV=1	3.00E-33	[illegible]	[illegible]
comp13916_c0_seq1.p1				
comp13924_c0_seq1.p1				
comp13930_c0_seq2.p3				
comp13930_c0_seq3.p1				
comp13931_c0_seq2.p1	sp|Q8LBP4|ALB3_ARATH_Inner_membrane_protein_ALBINO3,_chloroplastic_OS=Arabidopsis_thaliana_GN=ALB3_PE=1_SV=2	6.00E-60	[illegible]	[illegible]
comp13938_c1_seq1.p1	sp|Q8K3X3|GMDS_CRIGR_GDP-mannose_4,6_dehydratase_OS=Cricetulus_griseus_GN=GMDS_PE=2_SV=1	5.00E-21	[illegible]	[illegible]
comp13948_c0_seq1.p1				
comp13963_c0_seq1.p1				
comp13980_c0_seq2.p1				
comp139822_c0_seq1.p1				
comp13984_c0_seq1.p1				
comp13989_c0_seq1.p1	sp|Q7LHG5|YI31B_YEAST_Transposon_Ty3-I_Gag-Pol_polyprotein_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TY3B-I_PE=3_SV=2	2.00E-18	[illegible]	[illegible]
comp14025_c0_seq1.p1				
comp14048_c0_seq1.p1	sp|Q7PRH1|AKTIP_ANOGA_Protein_crossbronx_homolog_OS=Anopheles_gambiae_GN=AGAP010478_PE=3_SV=3	2.00E-28	GO:0008152,GO:0016881	[illegible]
comp14049_c1_seq1.p1	sp|P30131|HYPF_ECOLI_Carbamoyltransferase_hypF_OS=Escherichia_coli_(strain_K12)_GN=hypF_PE=1_SV=2	0	[illegible]	[illegible]
comp14054_c0_seq1.p2	sp|P65835|RLUD_SHIFL_Ribosomal_large_subunit_pseudouridine_synthase_D_OS=Shigella_flexneri_GN=rluD_PE=3_SV=2	5.00E-50	[illegible]	[illegible]
comp14054_c1_seq1.p1	sp|P0AC02|YFIO_ECOLI_UPF0169_lipoprotein_yfiO_OS=Escherichia_coli_(strain_K12)_GN=yfiO_PE=1_SV=1	2.00E-124	[illegible]	[illegible]
comp14056_c0_seq1.p2				
comp14064_c0_seq1.p1	sp|B4K892|EI3D1_DROMO_Eukaryotic_translation_initiation_factor_3_subunit_D-1_OS=Drosophila_mojavensis_GN=eIF-3p66_PE=3_SV=1	1.00E-144	[illegible]	[illegible]
comp14074_c0_seq1.p1	sp|O76756|RS8_APIME_40S_ribosomal_protein_S8_OS=Apis_mellifera_GN=RpS8_PE=2_SV=2	3.00E-62	[illegible]	[illegible]
comp14075_c0_seq1.p1	sp|Q3Z5Q5|GUAC_SHISS_GMP_reductase_OS=Shigella_sonnei_(strain_Ss046)_GN=guaC_PE=3_SV=1	5.00E-129	[illegible]	[illegible]
comp14077_c0_seq2.p1	sp|Q8L5Y9|PANK2_ARATH_Pantothenate_kinase_2_OS=Arabidopsis_thaliana_GN=At4g32180_PE=1_SV=2	5.00E-68	[illegible]	[illegible]
comp14079_c0_seq1.p2				
comp140838_c0_seq1.p1				
comp14087_c0_seq1.p1	sp|Q8VYP0|SCO11_ARATH_Protein_SCO1_homolog_1,_mitochondrial_OS=Arabidopsis_thaliana_GN=HCC1_PE=2_SV=1	2.00E-46	[illegible]	[illegible]
comp14090_c0_seq2.p1	sp|P20285|ODP2_NEUCR_Dihydrolipoyllysine-residue_acetyltransferase_component_of_pyruvate_dehydrogenase_complex,_mitochondrial_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=mrp-3_PE=1_SV=2	3.00E-22	[illegible]	[illegible]
comp14095_c0_seq1.p1				
comp14098_c0_seq1.p1				
comp14098_c0_seq2.p1				
comp14104_c0_seq1.p1	sp|Q08277|HSP82_MAIZE_Heat_shock_protein_82_OS=Zea_mays_GN=HSP82_PE=3_SV=1	2.00E-49	[illegible]	[illegible]
comp14105_c0_seq1.p1				
comp14108_c0_seq1.p1	sp|Q8LPL6|AP2A1_ARATH_AP-2_complex_subunit_alpha-1_OS=Arabidopsis_thaliana_GN=ALPHA-ADR_PE=1_SV=1	3.00E-177	[illegible]	[illegible]
comp14111_c0_seq1.p1				
comp14120_c0_seq1.p1				
comp14122_c0_seq1.p1				
comp14123_c1_seq1.p1	sp|P77364|GLXK1_ECOLI_Glycerate_kinase_1_OS=Escherichia_coli_(strain_K12)_GN=glxK_PE=2_SV=1	0	[illegible]	[illegible]
comp14127_c0_seq1.p1	sp|P0AF10|MTLR_ECOLI_Mannitol_operon_repressor_OS=Escherichia_coli_(strain_K12)_GN=mtlR_PE=1_SV=1	2.00E-70	[illegible]	[illegible]
comp14128_c0_seq1.p1	sp|Q05CL8|LARP7_MOUSE_La-related_protein_7_OS=Mus_musculus_GN=Larp7_PE=1_SV=2	4.00E-11	[illegible]	[illegible]
comp14129_c0_seq1.p1	sp|Q769K2|NAPEP_RAT_N-acyl-phosphatidylethanolamine-hydrolyzing_phospholipase_D_OS=Rattus_norvegicus_GN=Napepld_PE=1_SV=1	2.00E-82	[illegible]	[illegible]
comp14129_c0_seq2.p1	sp|Q769K2|NAPEP_RAT_N-acyl-phosphatidylethanolamine-hydrolyzing_phospholipase_D_OS=Rattus_norvegicus_GN=Napepld_PE=1_SV=1	4.00E-87	[illegible]	[illegible]
comp14132_c0_seq1.p1	sp|Q01890|YPT1_PHYIN_Ras-like_GTP-binding_protein_YPT1_OS=Phytophthora_infestans_GN=YPT1_PE=3_SV=1	5.00E-110	[illegible]	[illegible]
comp14142_c0_seq1.p1				
comp14148_c0_seq1.p1	sp|P0ABX1|FLGB_SHIFL_Flagellar_basal_body_rod_protein_FlgB_OS=Shigella_flexneri_GN=flgB_PE=3_SV=2	7.00E-85	[illegible]	[illegible]
comp14157_c0_seq1.p1	sp|P0ACB3|HEM2_SHIFL_Delta-aminolevulinic_acid_dehydratase_OS=Shigella_flexneri_GN=hemB_PE=3_SV=2	3.00E-84	[illegible]	[illegible]
comp141613_c0_seq1.p1	sp|P0ABP6|DEDA_ECOLI_Protein_dedA_OS=Escherichia_coli_(strain_K12)_GN=dedA_PE=1_SV=1	3.00E-81	[illegible]	[illegible]
comp14167_c0_seq1.p1	sp|Q63164|DYH1_RAT_Dynein_heavy_chain_1,_axonemal_OS=Rattus_norvegicus_GN=Dnah1_PE=2_SV=2	4.00E-118	[illegible]	[illegible]
comp14169_c0_seq1.p1	sp|P0AEY3|MAZG_ECOLI_Nucleoside_triphosphate_pyrophosphohydrolase_OS=Escherichia_coli_(strain_K12)_GN=mazG_PE=1_SV=1	6.00E-87	[illegible]	[illegible]
comp14184_c0_seq1.p1	sp|P77747|OMPN_ECOLI_Outer_membrane_protein_N_OS=Escherichia_coli_(strain_K12)_GN=ompN_PE=1_SV=1	7.00E-45	[illegible]	[illegible]
comp14186_c0_seq1.p1	sp|P26795|RLA3_TRYCR_60S_acidic_ribosomal_protein_P2-B_OS=Trypanosoma_cruzi_PE=3_SV=1	5.00E-12	[illegible]	[illegible]
comp14188_c0_seq1.p1	sp|P0AF44|YJBB_SHIFL_Uncharacterized_protein_yjbB_OS=Shigella_flexneri_GN=yjbB_PE=4_SV=1	2.00E-165	[illegible]	[illegible]
comp14188_c1_seq1.p1	sp|P0AF44|YJBB_SHIFL_Uncharacterized_protein_yjbB_OS=Shigella_flexneri_GN=yjbB_PE=4_SV=1	1.00E-50	[illegible]	[illegible]
comp14191_c0_seq1.p1				
comp14191_c0_seq2.p1				
comp14196_c0_seq1.p1				
comp14199_c0_seq2.p1				
comp14200_c0_seq1.p1	sp|P93028|UBE11_ARATH_Ubiquitin-activating_enzyme_E1_1_OS=Arabidopsis_thaliana_GN=UBA1_PE=1_SV=1	9.00E-27	[illegible]	[illegible]
comp14203_c0_seq1.p2	sp|P15651|ACADS_RAT_Short-chain_specific_acyl-CoA_dehydrogenase,_mitochondrial_OS=Rattus_norvegicus_GN=Acads_PE=1_SV=2	1.00E-57	[illegible]	[illegible]
comp14212_c0_seq1.p2				
comp14213_c0_seq1.p1				
comp14218_c0_seq1.p1				
comp14228_c0_seq1.p3				
comp14228_c0_seq2.p2				
comp142281_c0_seq1.p1	sp|P0AF16|MURJ_ECOLI_Probable_peptidoglycan_biosynthesis_protein_MurJ_OS=Escherichia_coli_(strain_K12)_GN=murJ_PE=1_SV=1	3.00E-66	[illegible]	[illegible]
comp14231_c0_seq1.p1				
comp14232_c0_seq1.p2				
comp14232_c0_seq2.p1	sp|Q8R1E7|TM234_MOUSE_Transmembrane_protein_234_OS=Mus_musculus_GN=Tmem234_PE=2_SV=1	9.00E-15	[illegible]	[illegible]
comp14239_c0_seq1.p1	sp|Q7UBI7|GLNE_SHIFL_Glutamate-ammonia-ligase_adenylyltransferase_OS=Shigella_flexneri_GN=glnE_PE=3_SV=1	2.00E-71	[illegible]	[illegible]
comp14247_c0_seq1.p1	sp|P14868|SYDC_HUMAN_Aspartate--tRNA_ligase,_cytoplasmic_OS=Homo_sapiens_GN=DARS_PE=1_SV=2	1.00E-132	[illegible]	[illegible]
comp14258_c0_seq1.p1	sp|P37647|KDGK_ECOLI_2-dehydro-3-deoxygluconokinase_OS=Escherichia_coli_(strain_K12)_GN=kdgK_PE=3_SV=1	7.00E-100	[illegible]	[illegible]
comp14262_c0_seq1.p2				
comp14263_c0_seq1.p1	sp|Q759R7|RL3_ASHGO_60S_ribosomal_protein_L3_OS=Ashbya_gossypii_(strain_ATCC_10895_/_CBS_109.51_/_FGSC_9923_/_NRRL_Y-1056)_GN=RPL3_PE=3_SV=1	3.00E-56	[illegible]	[illegible]
comp14277_c0_seq1.p2				
comp14281_c0_seq2.p1	sp|A4IJ21|MNS1_XENTR_Meiosis-specific_nuclear_structural_protein_1_OS=Xenopus_tropicalis_GN=mns1_PE=2_SV=1	6.00E-24	[illegible]	[illegible]
comp14283_c0_seq1.p1	sp|Q31UK2|RHAT_SHIBS_L-rhamnose-proton_symporter_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=rhaT_PE=3_SV=1	1.00E-103	[illegible]	[illegible]
comp14285_c0_seq1.p1	sp|B7LVB9|END4_ESCF3_Probable_endonuclease_4_OS=Escherichia_fergusonii_(strain_ATCC_35469_/_DSM_13698_/_CDC_0568-73)_GN=nfo_PE=3_SV=1	4.00E-61	[illegible]	[illegible]
comp14291_c0_seq1.p2				
comp14292_c0_seq1.p1	sp|P77416|HYFD_ECOLI_Hydrogenase-4_component_D_OS=Escherichia_coli_(strain_K12)_GN=hyfD_PE=3_SV=1	2.00E-86	[illegible]	[illegible]
comp14292_c0_seq1.p2	sp|P0AEW3|HYFE_SHIFL_Hydrogenase-4_component_E_OS=Shigella_flexneri_GN=hyfE_PE=3_SV=1	2.00E-54	[illegible]	[illegible]
comp14311_c0_seq1.p1	sp|Q3YUH3|MUTL_SHISS_DNA_mismatch_repair_protein_mutL_OS=Shigella_sonnei_(strain_Ss046)_GN=mutL_PE=3_SV=1	7.00E-143	[illegible]	[illegible]
comp14321_c0_seq1.p1	sp|Q3Z375|OPGG_SHISS_Glucans_biosynthesis_protein_G_OS=Shigella_sonnei_(strain_Ss046)_GN=mdoG_PE=3_SV=1	2.00E-64	[illegible]	[illegible]
comp14323_c0_seq1.p1				
comp14326_c0_seq1.p1	sp|P15038|HELD_ECOLI_Helicase_IV_OS=Escherichia_coli_(strain_K12)_GN=helD_PE=1_SV=2	6.00E-81	[illegible]	[illegible]
comp14329_c0_seq1.p2				
comp14332_c0_seq2.p1				
comp14334_c0_seq1.p1				
comp14337_c0_seq1.p2	sp|P21169|DCOR_ECOLI_Ornithine_decarboxylase,_constitutive_OS=Escherichia_coli_(strain_K12)_GN=speC_PE=1_SV=2	3.00E-71	[illegible]	[illegible]
comp14337_c1_seq1.p1	sp|P21169|DCOR_ECOLI_Ornithine_decarboxylase,_constitutive_OS=Escherichia_coli_(strain_K12)_GN=speC_PE=1_SV=2	1.00E-64	[illegible]	[illegible]
comp14340_c0_seq1.p1				
comp143488_c0_seq1.p1	sp|P75770|YBHN_ECOLI_Inner_membrane_protein_ybhN_OS=Escherichia_coli_(strain_K12)_GN=ybhN_PE=1_SV=1	6.00E-66	[illegible]	[illegible]
comp14353_c0_seq1.p1	sp|P37776|GALF_SHIFL_UTP--glucose-1-phosphate_uridylyltransferase_OS=Shigella_flexneri_GN=galF_PE=3_SV=2	1.00E-72	[illegible]	[illegible]
comp143676_c0_seq1.p1				
comp14368_c0_seq1.p1	sp|Q46908|YGCR_ECOLI_Putative_electron_transfer_flavoprotein_subunit_ygcR_OS=Escherichia_coli_(strain_K12)_GN=ygcR_PE=3_SV=2	9.00E-98	GO:0009055,GO:0055114	[illegible]
comp14370_c0_seq1.p1	sp|P0ABH7|CISY_ECOLI_Citrate_synthase_OS=Escherichia_coli_(strain_K12)_GN=gltA_PE=1_SV=1	5.00E-111	[illegible]	[illegible]
comp14379_c0_seq2.p1	sp|Q9SBN4|PGKH_VOLCA_Phosphoglycerate_kinase,_chloroplastic_OS=Volvox_carteri_GN=PGK_PE=2_SV=1	0	[illegible]	[illegible]
comp14379_c0_seq2.p2	sp|Q9PVQ1|PSA7B_XENLA_Proteasome_subunit_alpha_type-7-B_OS=Xenopus_laevis_GN=psma7-b_PE=2_SV=1	2.00E-32	[illegible]	[illegible]
comp14380_c0_seq1.p1	sp|Q68WT3|TRXB_RICTY_Thioredoxin_reductase_OS=Rickettsia_typhi_(strain_ATCC_VR-144_/_Wilmington)_GN=trxB_PE=3_SV=1	4.00E-55	[illegible]	[illegible]
comp14393_c0_seq1.p1				
comp14394_c0_seq1.p2	sp|P46222|RL11_DROME_60S_ribosomal_protein_L11_OS=Drosophila_melanogaster_GN=RpL11_PE=1_SV=2	1.00E-80	[illegible]	[illegible]
comp14400_c0_seq1.p1				
comp14400_c1_seq1.p1				
comp14402_c0_seq1.p1	sp|Q8X7P1|MANC1_ECO57_Mannose-1-phosphate_guanylyltransferase_1_OS=Escherichia_coli_O157:H7_GN=manC1_PE=1_SV=1	5.00E-100	[illegible]	[illegible]
comp14406_c0_seq1.p1	sp|Q3Z5U2|SGRR_SHISS_HTH-type_transcriptional_regulator_sgrR_OS=Shigella_sonnei_(strain_Ss046)_GN=sgrR_PE=3_SV=1	3.00E-106	[illegible]	[illegible]
comp14408_c0_seq1.p1	sp|Q59385|COPA_ECOLI_Copper-exporting_P-type_ATPase_A_OS=Escherichia_coli_(strain_K12)_GN=copA_PE=1_SV=4	0	[illegible]	[illegible]
comp14410_c0_seq1.p2	sp|P23538|PPSA_ECOLI_Phosphoenolpyruvate_synthase_OS=Escherichia_coli_(strain_K12)_GN=ppsA_PE=1_SV=5	6.00E-125	[illegible]	[illegible]
comp14422_c0_seq1.p1				
comp14426_c0_seq1.p2	sp|P37306|ARCC_ECOLI_Carbamate_kinase_OS=Escherichia_coli_(strain_K12)_GN=arcC_PE=3_SV=2	3.00E-109	[illegible]	[illegible]
comp14447_c0_seq1.p1	sp|A8A3I8|NORW_ECOHS_Nitric_oxide_reductase_FlRd-NAD(+)_reductase_OS=Escherichia_coli_O9:H4_(strain_HS)_GN=norW_PE=3_SV=1	2.00E-76	[illegible]	[illegible]
comp14448_c0_seq1.p1				
comp14449_c0_seq1.p1				
comp14449_c0_seq2.p1				
comp14454_c0_seq1.p2	sp|Q2HJ51|RA51D_BOVIN_DNA_repair_protein_RAD51_homolog_4_OS=Bos_taurus_GN=RAD51D_PE=2_SV=1	2.00E-12	[illegible]	[illegible]
comp14454_c0_seq2.p1	sp|Q2HJ51|RA51D_BOVIN_DNA_repair_protein_RAD51_homolog_4_OS=Bos_taurus_GN=RAD51D_PE=2_SV=1	1.00E-29	[illegible]	[illegible]
comp14456_c0_seq1.p1	sp|Q90YS3|RS2_ICTPU_40S_ribosomal_protein_S2_OS=Ictalurus_punctatus_GN=rps2_PE=2_SV=1	9.00E-31	[illegible]	[illegible]
comp144767_c0_seq1.p1				
comp14478_c0_seq1.p2				
comp14479_c0_seq1.p1				
comp14483_c0_seq1.p1				
comp14490_c0_seq1.p1				
comp14493_c0_seq1.p2				
comp14496_c0_seq1.p1	sp|P73627|Y1770_SYNY3_Uncharacterized_protein_sll1770_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll1770_PE=3_SV=1	5.00E-107	[illegible]	[illegible]
comp14499_c0_seq1.p1	sp|Q3YYC9|MUTS_SHISS_DNA_mismatch_repair_protein_MutS_OS=Shigella_sonnei_(strain_Ss046)_GN=mutS_PE=3_SV=1	7.00E-94	[illegible]	[illegible]
comp14511_c0_seq1.p1	sp|P0AFM4|PSIF_ECOLI_Phosphate_starvation-inducible_protein_psiF_OS=Escherichia_coli_(strain_K12)_GN=psiF_PE=1_SV=1	5.00E-55		
comp14519_c0_seq1.p1	sp|Q3YWW3|RS4_SHISS_30S_ribosomal_protein_S4_OS=Shigella_sonnei_(strain_Ss046)_GN=rpsD_PE=3_SV=1	2.00E-72	[illegible]	[illegible]
comp14522_c0_seq1.p1				
comp14523_c0_seq1.p1				
comp14536_c0_seq1.p1				
comp14537_c0_seq1.p1	sp|P08142|ILVB_ECOLI_Acetolactate_synthase_isozyme_1_large_subunit_OS=Escherichia_coli_(strain_K12)_GN=ilvB_PE=1_SV=1	1.00E-129	[illegible]	[illegible]
comp14549_c0_seq1.p1				
comp14557_c0_seq1.p1	sp|P76558|MAO2_ECOLI_NADP-dependent_malic_enzyme_OS=Escherichia_coli_(strain_K12)_GN=maeB_PE=1_SV=1	5.00E-69	[illegible]	[illegible]
comp14558_c0_seq1.p2	sp|P0ACP9|PURR_SHIFL_HTH-type_transcriptional_repressor_PurR_OS=Shigella_flexneri_GN=purR_PE=3_SV=2	1.00E-87	[illegible]	[illegible]
comp14559_c0_seq1.p1				
comp14561_c0_seq1.p1				
comp14572_c0_seq1.p1				
comp14575_c0_seq1.p1	sp|P75892|RUTG_ECOLI_Putative_pyrimidine_permease_RutG_OS=Escherichia_coli_(strain_K12)_GN=rutG_PE=1_SV=2	3.00E-100	[illegible]	[illegible]
comp14586_c0_seq1.p1	sp|P76464|YFAS_ECOLI_Putative_UPF0192_protein_yfaS_OS=Escherichia_coli_(strain_K12)_GN=yfaS_PE=5_SV=2	2.00E-98	GO:0004866,GO:0010951	[illegible]
comp14596_c0_seq1.p1	sp|P59741|FADL_SHIFL_Long-chain_fatty_acid_transport_protein_OS=Shigella_flexneri_GN=fadL_PE=3_SV=2	3.00E-175	[illegible]	[illegible]
comp14598_c0_seq1.p1				
comp14611_c0_seq1.p1	sp|P38097|YEGE_ECOLI_Probable_diguanylate_cyclase_YegE_OS=Escherichia_coli_(strain_K12)_GN=yegE_PE=2_SV=2	2.00E-91	[illegible]	[illegible]
comp14614_c0_seq1.p1				
comp14621_c0_seq1.p1				
comp146229_c0_seq1.p2				
comp14623_c0_seq1.p1				
comp14623_c0_seq2.p1				
comp14626_c0_seq1.p1				
comp14634_c0_seq1.p1				
comp14638_c0_seq1.p1				
comp14638_c0_seq2.p1				
comp14639_c0_seq1.p1				
comp14639_c0_seq1.p2				
comp14645_c0_seq1.p2	sp|P36889|SAHH_LEIDO_Adenosylhomocysteinase_OS=Leishmania_donovani_PE=3_SV=2	5.00E-75	[illegible]	[illegible]
comp14659_c0_seq1.p2	sp|O76756|RS8_APIME_40S_ribosomal_protein_S8_OS=Apis_mellifera_GN=RpS8_PE=2_SV=2	8.00E-48	[illegible]	[illegible]
comp14670_c0_seq1.p1	sp|Q9SEI4|PRS6B_ARATH_26S_protease_regulatory_subunit_6B_homolog_OS=Arabidopsis_thaliana_GN=RPT3_PE=1_SV=1	3.00E-93	[illegible]	[illegible]
comp14672_c0_seq1.p1	sp|P41095|RLA0_ORYSJ_60S_acidic_ribosomal_protein_P0_OS=Oryza_sativa_subsp._japonica_GN=Os08g0130500_PE=1_SV=3	2.00E-40	[illegible]	[illegible]
comp14680_c0_seq1.p1				
comp14688_c0_seq1.p1				
comp14690_c0_seq1.p1				
comp14691_c0_seq1.p2				
comp14695_c0_seq1.p1				
comp14700_c0_seq1.p1	sp|P36178|CTRB2_LITVA_Chymotrypsin_BII_OS=Litopenaeus_vannamei_PE=1_SV=1	9.00E-70	[illegible]	[illegible]
comp14704_c0_seq1.p1				
comp14719_c0_seq1.p1	sp|P39285|YJEP_ECOLI_Uncharacterized_MscS_family_protein_YjeP_OS=Escherichia_coli_(strain_K12)_GN=yjeP_PE=3_SV=3	9.00E-65	[illegible]	[illegible]
comp14721_c0_seq2.p1				
comp14726_c0_seq2.p1	sp|P83877|TXN4A_MOUSE_Thioredoxin-like_protein_4A_OS=Mus_musculus_GN=Txnl4a_PE=2_SV=1	1.00E-84	[illegible]	[illegible]
comp14728_c0_seq1.p1				
comp14728_c0_seq1.p2				
comp14728_c0_seq2.p1				
comp14763_c0_seq1.p2				
comp14767_c0_seq1.p1				
comp14794_c0_seq1.p1	sp|P09546|PUTA_ECOLI_Bifunctional_protein_putA_OS=Escherichia_coli_(strain_K12)_GN=putA_PE=1_SV=3	2.00E-85	[illegible]	[illegible]
comp14807_c0_seq1.p1				

comp14823_c0_seq1.p1				
comp14824_c0_seq1.p1				
comp14836_c0_seq1.p1				
comp14841_c0_seq1.p2	sp|P75828|YBJD_ECOLI_Uncharacterized_protein_ybjD_OS=Escherichia_coli_(strain_K12)_GN=ybjD_PE=4_SV=1	4.00E-69	GO:0000166,GO:0005524	nucleotide binding,ATP binding
comp14849_c1_seq1.p2	sp|Q3Z601|DNAK_SHISS_Chaperone_protein_DnaK_OS=Shigella_sonnei_(strain_Ss046)_GN=dnaK_PE=3_SV=1	1.00E-96	GO:0000166,GO:0005524,GO:0005524,GO:0005524,GO:0006457,GO:0051082	nucleotide binding,ATP binding,ATP binding,ATP binding,protein folding,unfolded protein binding
comp14859_c0_seq1.p1	sp|P25718|AMY1_ECOLI_Alpha-amylase_OS=Escherichia_coli_(strain_K12)_GN=malS_PE=1_SV=1	9.00E-162	GO:0003824,GO:0004556,GO:0004556,GO:0004556,GO:0004556,GO:0005509,GO:0005509,GO:0005975,GO:0005975,GO:0008152,GO:0016787,GO:0016798,GO:0030288,GO:0030980,GO:0030980,GO:0042597,GO:0042597,GO:0042597,GO:0042597,GO:0043169,GO:0046872,GO:0051692,GO:0051692	[illegible]
comp14862_c0_seq1.p2				
comp14875_c0_seq1.p2	sp|P16926|MREC_ECOLI_Rod_shape-determining_protein_mreC_OS=Escherichia_coli_(strain_K12)_GN=mreC_PE=3_SV=1	1.00E-122	GO:0005515,GO:0005515,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0008360,GO:0016020,GO:0016021,GO:0043621,GO:0071963,GO:0071963	[illegible]
comp14876_c0_seq1.p1	sp|Q60809|CNOT7_MOUSE_CCR4-NOT_transcription_complex_subunit_7_OS=Mus_musculus_GN=Cnot7_PE=1_SV=1	5.00E-103	GO:0000175,GO:0000175,GO:0000289,GO:0000290,GO:0000290,GO:0000932,GO:0000932,GO:0003676,GO:0003723,GO:0004518,GO:0004527,GO:0004532,GO:0004532,GO:0004535,GO:0004535,GO:0004535,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0006417,GO:0008284,GO:0008284,GO:0008285,GO:0008285,GO:0016020,GO:0016787,GO:0030014,GO:0030014,GO:0031047,GO:0031047,GO:0033962,GO:0043928,GO:0043928,GO:0045944,GO:0046872,GO:0060213,GO:0060213,GO:0090305,GO:0090305,GO:0090503,GO:0090503,GO:0090503,GO:0090503,GO:1900153,GO:1900153,GO:1900153	[illegible]
comp14876_c0_seq2.p1				
comp14884_c0_seq1.p1				
comp14887_c0_seq1.p1	sp|P23865|PRC_ECOLI_Tail-specific_protease_OS=Escherichia_coli_(strain_K12)_GN=prc_PE=1_SV=2	3.00E-81	GO:0004175,GO:0005886,GO:0005886,GO:0005886,GO:0006508,GO:0006508,GO:0006508,GO:0008233,GO:0008236,GO:0008236,GO:0016020,GO:0016787,GO:0030163,GO:0030288,GO:0042493	[illegible]
comp14888_c0_seq1.p1	sp|Q9HC24|LFG4_HUMAN_Protein_lifeguard_4_OS=Homo_sapiens_GN=TMBIM4_PE=1_SV=3	5.00E-39	GO:0000139,GO:0005515,GO:0005794,GO:0005795,GO:0006915,GO:0016020,GO:0016021,GO:0043066,GO:0050848	[illegible]
comp14888_c0_seq2.p1				
comp14898_c0_seq1.p2	sp|P09030|EX3_ECOLI_Exodeoxyribonuclease_III_OS=Escherichia_coli_(strain_K12)_GN=xthA_PE=1_SV=4	3.00E-72	GO:0000737,GO:0000738,GO:0000738,GO:0000738,GO:0003677,GO:0003906,GO:0004518,GO:0004518,GO:0004519,GO:0004527,GO:0004527,GO:0005622,GO:0006281,GO:0006281,GO:0006284,GO:0006974,GO:0006974,GO:0008311,GO:0008853,GO:0008853,GO:0016787,GO:0046872,GO:0090305,GO:0090305,GO:0090305,GO:0090305,GO:0090305	[illegible]
comp14899_c0_seq1.p1				
comp14899_c0_seq2.p1				
comp14900_c0_seq1.p1				
comp14909_c0_seq1.p1	sp|P0ABN0|CCMH_SHIFL_Cytochrome_c-type_biogenesis_protein_CcmH_OS=Shigella_flexneri_GN=ccmH_PE=3_SV=1	2.00E-78	GO:0005886,GO:0005886,GO:0005886,GO:0016020,GO:0016021,GO:0017004,GO:0046872	[illegible]
comp14910_c0_seq1.p1	sp|Q54U44|ABCCC_DICDI_ABC_transporter_C_family_member_12_OS=Dictyostelium_discoideum_GN=abcC12_PE=3_SV=1	2.00E-40	GO:0000166,GO:0005215,GO:0005524,GO:0005524,GO:0006200,GO:0006810,GO:0006810,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016887,GO:0042626,GO:0042626,GO:0055085	[illegible]
comp14912_c0_seq1.p1	sp|Q9ET30|TM9S3_MOUSE_Transmembrane_9_superfamily_member_3_OS=Mus_musculus_GN=Tm9sf3_PE=1_SV=1	1.00E-167	GO:0003674,GO:0005575,GO:0008150,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021	[illegible]
comp14913_c0_seq1.p1	sp|A4RW83|SECA_OSTLU_Protein_translocase_subunit_SecA,_chloroplastic_OS=Ostreococcus_lucimarinus_(strain_CCE9901)_GN=secA_PE=3_SV=1	0	GO:0000166,GO:0000166,GO:0005524,GO:0005524,GO:0005524,GO:0006605,GO:0006605,GO:0006810,GO:0006810,GO:0006810,GO:0006886,GO:0006886,GO:0009507,GO:0009535,GO:0009536,GO:0009570,GO:0009579,GO:0015031,GO:0015031,GO:0016020,GO:0016020,GO:0016020,GO:0017038,GO:0017038	[illegible]
comp14916_c0_seq1.p1				
comp14918_c0_seq1.p1	sp|Q99956|DUS9_HUMAN_Dual_specificity_protein_phosphatase_9_OS=Homo_sapiens_GN=DUSP9_PE=1_SV=1	5.00E-22	GO:0000188,GO:0000188,GO:0004721,GO:0004721,GO:0004721,GO:0004725,GO:0005515,GO:0005515,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006470,GO:0006470,GO:0006470,GO:0007254,GO:0008138,GO:0008138,GO:0016311,GO:0016787,GO:0016791,GO:0017017,GO:0017017,GO:0035335	[illegible]
comp14920_c0_seq1.p1				
comp14923_c0_seq2.p1				
comp14933_c0_seq1.p1	sp|P57760|STK16_RAT_Serine/threonine-protein_kinase_16_OS=Rattus_norvegicus_GN=Stk16_PE=2_SV=2	3.00E-56	GO:0000166,GO:0001077,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004715,GO:0005524,GO:0005524,GO:0005737,GO:0005798,GO:0006468,GO:0006468,GO:0016020,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0018108,GO:0045944,GO:0046777,GO:0046777,GO:0046777,GO:0048471,GO:0071560	[illegible]
comp14933_c0_seq2.p1	sp|P57760|STK16_RAT_Serine/threonine-protein_kinase_16_OS=Rattus_norvegicus_GN=Stk16_PE=2_SV=2	3.00E-56	GO:0000166,GO:0001077,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004715,GO:0005524,GO:0005524,GO:0005737,GO:0005798,GO:0006468,GO:0006468,GO:0016020,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0018108,GO:0045944,GO:0046777,GO:0046777,GO:0046777,GO:0048471,GO:0071560	[illegible]
comp14935_c0_seq1.p1	sp|Q944B0|FK161_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP16-1,_chloroplastic_OS=Arabidopsis_thaliana_GN=FKBP16-1_PE=2_SV=1	6.00E-20	GO:0000413,GO:0003755,GO:0003755,GO:0003755,GO:0005528,GO:0006457,GO:0009507,GO:0009507,GO:0009536,GO:0009543,GO:0009579,GO:0016853,GO:0061077	[illegible]
comp14936_c0_seq1.p1				
comp14938_c0_seq1.p1	sp|Q9SMH3|DYH1A_CHLRE_Dynein-1-alpha_heavy_chain,_flagellar_inner_arm_I1_complex_OS=Chlamydomonas_reinhardtii_GN=DHC1_PE=1_SV=1	4.00E-26	GO:0000166,GO:0003774,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005874,GO:0005929,GO:0006200,GO:0007018,GO:0008152,GO:0008152,GO:0016887,GO:0030030,GO:0030286,GO:0030286,GO:0031514,GO:0042995	[illegible]
comp14943_c0_seq1.p2	sp|Q3YV01|RL11_SHISS_50S_ribosomal_protein_L11_OS=Shigella_sonnei_(strain_Ss046)_GN=rplK_PE=3_SV=3	3.00E-78	GO:0003723,GO:0003735,GO:0005840,GO:0005840,GO:0006412,GO:0006412,GO:0019843,GO:0030529,GO:0070180	[illegible]
comp14947_c0_seq1.p1	sp|Q01474|SAR1B_ARATH_GTP-binding_protein_SAR1B_OS=Arabidopsis_thaliana_GN=SAR1B_PE=2_SV=1	6.00E-80	GO:0000166,GO:0005515,GO:0005525,GO:0005525,GO:0005525,GO:0005622,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005794,GO:0005794,GO:0005829,GO:0005829,GO:0005886,GO:0005886,GO:0006094,GO:0006810,GO:0006886,GO:0006888,GO:0007010,GO:0010498,GO:0015031,GO:0016192,GO:0019898	[illegible]
comp14969_c0_seq1.p1				
comp14969_c0_seq2.p1	sp|Q6ZMV9|KIF6_HUMAN_Kinesin-like_protein_KIF6_OS=Homo_sapiens_GN=KIF6_PE=1_SV=3	4.00E-18	GO:0000166,GO:0001673,GO:0003777,GO:0003777,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005871,GO:0005874,GO:0006200,GO:0007018,GO:0007018,GO:0008017,GO:0008152,GO:0008152,GO:0016887	[illegible]
comp14980_c0_seq1.p1				
comp14981_c0_seq1.p1	sp|Q5UAS2|RL17_BOMMO_60S_ribosomal_protein_L17_OS=Bombyx_mori_GN=RpL17_PE=2_SV=1	8.00E-33	[illegible]	[illegible]
comp14984_c0_seq1.p1				
comp14989_c0_seq1.p2	sp|P42825|DNAJ2_ARATH_Chaperone_protein_dnaJ_2_OS=Arabidopsis_thaliana_GN=ATJ2_PE=1_SV=2	5.00E-25	[illegible]	[illegible]
comp14995_c0_seq1.p1	sp|Q3Z4W5|CLPX_SHISS_ATP-dependent_Clp_protease_ATP-binding_subunit_ClpX_OS=Shigella_sonnei_(strain_Ss046)_GN=clpX_PE=3_SV=1	5.00E-76	[illegible]	[illegible]
comp14996_c0_seq1.p1	sp|P92966|RSP41_ARATH_Arginine/serine-rich-splicing_factor_RSP41_OS=Arabidopsis_thaliana_GN=RSP41_PE=1_SV=2	3.00E-20	[illegible]	[illegible]
comp15003_c0_seq1.p1				
comp15007_c0_seq2.p1	sp|P14938|FER3_RAPSA_Ferredoxin,_leaf_L-A_OS=Raphanus_sativus_PE=1_SV=1	2.00E-11	[illegible]	[illegible]
comp15012_c0_seq1.p1				
comp15016_c0_seq1.p1				
comp15016_c0_seq2.p1				
comp15019_c0_seq1.p1	sp|O00303|EIF3F_HUMAN_Eukaryotic_translation_initiation_factor_3_subunit_F_OS=Homo_sapiens_GN=EIF3F_PE=1_SV=1	5.00E-20	[illegible]	[illegible]
comp15024_c0_seq1.p1	sp|P32670|PTFX2_ECOLI_Multiphosphoryl_transfer_protein_2_OS=Escherichia_coli_(strain_K12)_GN=ptsA_PE=3_SV=2	3.00E-74	[illegible]	[illegible]
comp15026_c0_seq1.p1				
comp15026_c0_seq2.p1				
comp15031_c0_seq1.p2	sp|Q9SJ44|UEV1C_ARATH_Ubiquitin-conjugating_enzyme_E2_variant_1C_OS=Arabidopsis_thaliana_GN=UEV1C_PE=1_SV=1	1.00E-34	[illegible]	[illegible]
comp15033_c0_seq1.p1	sp|P02919|PBPB_ECOLI_Penicillin-binding_protein_1B_OS=Escherichia_coli_(strain_K12)_GN=mrcB_PE=1_SV=2	1.00E-67	[illegible]	[illegible]
comp15041_c0_seq1.p1	sp|P06612|TOP1_ECOLI_DNA_topoisomerase_1_OS=Escherichia_coli_(strain_K12)_GN=topA_PE=1_SV=2	4.00E-79	[illegible]	[illegible]
comp15045_c0_seq1.p1				
comp15046_c0_seq1.p1				
comp15051_c0_seq1.p1	sp|Q6ZDY8|DHSA_ORYSJ_Succinate_dehydrogenase_[ubiquinone]_flavoprotein_subunit,_mitochondrial_OS=Oryza_sativa_subsp._japonica_GN=SDH1_PE=2_SV=1	1.00E-70	[illegible]	[illegible]
comp15053_c1_seq1.p1	sp|P0AEZ7|MLTD_ECOLI_Membrane-bound_lytic_murein_transglycosylase_D_OS=Escherichia_coli_(strain_K12)_GN=mltD_PE=1_SV=1	7.00E-118	[illegible]	[illegible]
comp15062_c0_seq1.p1				
comp15066_c0_seq1.p1				
comp15091_c0_seq1.p1				
comp15092_c0_seq1.p1	sp|P39270|YJDF_ECOLI_Inner_membrane_protein_yjdF_OS=Escherichia_coli_(strain_K12)_GN=yjdF_PE=1_SV=1	2.00E-72	GO:0005886,GO:0005886,GO:0005886,GO:0016020,GO:0016021	[illegible]
comp15098_c0_seq1.p2				
comp15103_c0_seq1.p2				
comp15104_c0_seq1.p1	sp|P0A3D3|FER1_SYNP6_Ferredoxin-1_OS=Synechococcus_sp._(strain_ATCC_27144_/_PCC_6301_/_SAUG_1402/1)_GN=petF1_PE=1_SV=2	7.00E-24	[illegible]	[illegible]
comp15125_c0_seq1.p1				
comp15128_c0_seq1.p1	sp|O04996|SODC_SOLCS_Superoxide_dismutase_[Cu-Zn]_OS=Solidago_canadensis_var._scabra_GN=SODCC_PE=2_SV=3	1.00E-50	[illegible]	[illegible]
comp15128_c0_seq2.p1	sp|P11418|SODC_PRIGL_Superoxide_dismutase_[Cu-Zn]_OS=Prionace_glauca_GN=sod1_PE=1_SV=1	8.00E-38	[illegible]	[illegible]
comp15129_c0_seq1.p1	sp|Q54NZ6|ISC1A_DICDI_Isochorismatase_family_protein_1A_OS=Dictyostelium_discoideum_GN=DDB_G0285041_PE=3_SV=1	9.00E-43	GO:0003824,GO:0008152	[illegible]
comp15129_c0_seq2.p1	sp|Q54NZ8|ISC1B_DICDI_Isochorismatase_family_protein_1B_OS=Dictyostelium_discoideum_GN=DDB_G0284901_PE=3_SV=1	1.00E-51	GO:0003824,GO:0008152	[illegible]
comp15136_c0_seq1.p2	sp|Q3YVN4|GLMU_SHISS_Bifunctional_protein_GlmU_OS=Shigella_sonnei_(strain_Ss046)_GN=glmU_PE=3_SV=1	2.00E-61	[illegible]	[illegible]
comp15138_c0_seq2.p1	sp|Q80YA7|DPP8_MOUSE_Dipeptidyl_peptidase_8_OS=Mus_musculus_GN=Dpp8_PE=1_SV=1	1.00E-76	[illegible]	[illegible]
comp15141_c0_seq1.p2				
comp15141_c0_seq2.p1	sp|Q5RCZ7|RCBT2_PONAB_RCC1_and_BTB_domain-containing_protein_2_OS=Pongo_abelii_GN=RCBTB2_PE=2_SV=1	3.00E-13	GO:0001669	[illegible]
comp15142_c0_seq1.p1	sp|Q7NFE9|CLPB_GLOVI_Chaperone_protein_ClpB_OS=Gloeobacter_violaceus_(strain_PCC_7421)_GN=clpB_PE=3_SV=1	5.00E-145	[illegible]	[illegible]
comp151431_c0_seq1.p1	sp|P39369|YJHR_ECOLI_Putative_uncharacterized_protein_yjhR_OS=Escherichia_coli_(strain_K12)_GN=yjhR_PE=5_SV=1	2.00E-73	GO:0003824,GO:0008152,GO:0016787	[illegible]
comp15147_c0_seq1.p1	sp|P00634|PPB_ECOLI_Alkaline_phosphatase_OS=Escherichia_coli_(strain_K12)_GN=phoA_PE=1_SV=1	2.00E-75	[illegible]	[illegible]
comp15147_c1_seq1.p1	sp|P00634|PPB_ECOLI_Alkaline_phosphatase_OS=Escherichia_coli_(strain_K12)_GN=phoA_PE=1_SV=1	1.00E-92	[illegible]	[illegible]
comp15161_c0_seq1.p1				
comp15161_c1_seq1.p1				
comp15165_c0_seq1.p1	sp|Q3YZ35|RLMN_SHISS_Ribosomal_RNA_large_subunit_methyltransferase_N_OS=Shigella_sonnei_(strain_Ss046)_GN=rlmN_PE=3_SV=1	3.00E-119	[illegible]	[illegible]
comp15177_c0_seq1.p1	sp|Q3Z409|BIOB_SHISS_Biotin_synthase_OS=Shigella_sonnei_(strain_Ss046)_GN=bioB_PE=3_SV=1	6.00E-86	[illegible]	[illegible]
comp151785_c0_seq1.p1				
comp15184_c0_seq1.p1				
comp15189_c0_seq1.p1	sp|Q9SIP7|RS31_ARATH_40S_ribosomal_protein_S3-1_OS=Arabidopsis_thaliana_GN=RPS3A_PE=1_SV=1	2.00E-115	[illegible]	[illegible]
comp15197_c0_seq2.p1				
comp15204_c0_seq1.p1				
comp15206_c0_seq2.p1	sp|Q54QQ0|IMDH_DICDI_Inosine-5'-monophosphate_dehydrogenase_OS=Dictyostelium_discoideum_GN=impdh_PE=1_SV=1	0	[illegible]	[illegible]
comp15217_c0_seq1.p1	sp|Q6PE15|ABHDA_MOUSE_Abhydrolase_domain-containing_protein_10,_mitochondrial_OS=Mus_musculus_GN=Abhd10_PE=2_SV=1	2.00E-25	[illegible]	[illegible]
comp15217_c0_seq2.p1	sp|Q5I0K5|ABHDA_RAT_Abhydrolase_domain-containing_protein_10,_mitochondrial_OS=Rattus_norvegicus_GN=Abhd10_PE=1_SV=2	3.00E-28	[illegible]	[illegible]
comp15223_c0_seq1.p1	sp|Q0VD48|VPS4B_BOVIN_Vacuolar_protein_sorting-associated_protein_4B_OS=Bos_taurus_GN=VPS4B_PE=2_SV=1	2.00E-25	[illegible]	[illegible]
comp15235_c0_seq1.p1				
comp15236_c0_seq1.p1				
comp15237_c0_seq2.p1	sp|Q6NNI8|SAP1_ARATH_Zinc_finger_A20_and_AN1_domain-containing_stress-associated_protein_1_OS=Arabidopsis_thaliana_GN=SAP1_PE=1_SV=1	2.00E-14	GO:0003677,GO:0008150,GO:0008270,GO:0046872	[illegible]
comp152385_c0_seq1.p1				
comp15239_c0_seq1.p1	sp|P22524|MUKE_ECOLI_Chromosome_partition_protein_mukE_OS=Escherichia_coli_(strain_K12)_GN=mukE_PE=1_SV=5	2.00E-121	[illegible]	[illegible]
comp15249_c0_seq1.p1				
comp15253_c0_seq1.p1	sp|Q84MN7|HFA2A_ORYSJ_Heat_stress_transcription_factor_A-2a_OS=Oryza_sativa_subsp._japonica_GN=HSFA2A_PE=2_SV=1	7.00E-14	[illegible]	[illegible]
comp15264_c0_seq1.p1	sp|P64429|YPFJ_ECOLI_Uncharacterized_protein_ypfJ_OS=Escherichia_coli_(strain_K12)_GN=ypfJ_PE=4_SV=1	3.00E-44	GO:0016020,GO:0016020,GO:0016021	[illegible]
comp15267_c0_seq1.p1	sp|Q39610|DYHA_CHLRE_Dynein_alpha_chain,_flagellar_outer_arm_OS=Chlamydomonas_reinhardtii_GN=ODA11_PE=3_SV=2	2.00E-17	[illegible]	[illegible]
comp15269_c0_seq1.p1	sp|Q4R502|IDHP_MACFA_Isocitrate_dehydrogenase_[NADP],_mitochondrial_OS=Macaca_fascicularis_GN=IDH2_PE=2_SV=1	0	[illegible]	[illegible]
comp152755_c0_seq1.p1	sp|P45469|YRAR_ECOLI_Uncharacterized_protein_yraR_OS=Escherichia_coli_(strain_K12)_GN=yraR_PE=4_SV=2	1.00E-68		
comp15281_c0_seq1.p1				
comp152849_c0_seq1.p1	sp|P0AD65|PBP2_ECOLI_Penicillin-binding_protein_2_OS=Escherichia_coli_(strain_K12)_GN=mrdA_PE=3_SV=1	1.00E-66	[illegible]	[illegible]
comp15288_c0_seq1.p1				
comp152924_c0_seq1.p1				
comp15301_c0_seq1.p1	sp|P46474|YHDP_ECOLI_Uncharacterized_protein_yhdP_OS=Escherichia_coli_(strain_K12)_GN=yhdP_PE=4_SV=4	9.00E-71		
comp15322_c0_seq1.p1				
comp15323_c0_seq1.p1	sp|P0AEJ0|EMRB_ECOLI_Multidrug_resistance_protein_B_OS=Escherichia_coli_(strain_K12)_GN=emrB_PE=1_SV=1	1.00E-42	[illegible]	[illegible]
comp15326_c0_seq1.p2				
comp15334_c0_seq1.p1	sp|Q9LD57|PGKH1_ARATH_Phosphoglycerate_kinase_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=PGK1_PE=1_SV=1	5.00E-101	[illegible]	[illegible]
comp15335_c0_seq1.p1				
comp153414_c0_seq1.p2				
comp15347_c0_seq1.p1				
comp15362_c0_seq2.p1	sp|Q9WTN0|GGPPS_MOUSE_Geranylgeranyl_pyrophosphate_synthase_OS=Mus_musculus_GN=Ggps1_PE=2_SV=1	6.00E-111	[illegible]	[illegible]
comp15375_c0_seq1.p2				
comp153978_c0_seq1.p1				
comp15404_c0_seq1.p1				
comp15406_c0_seq1.p1				
comp15412_c0_seq1.p1	sp|P77277|EUTJ_ECOLI_Ethanolamine_utilization_protein_eutJ_OS=Escherichia_coli_(strain_K12)_GN=eutJ_PE=4_SV=1	4.00E-107	GO:0046336	[illegible]
comp15415_c0_seq1.p1	sp|P31459|DGOK_ECOLI_2-dehydro-3-deoxygalactonokinase_OS=Escherichia_coli_(strain_K12)_GN=dgoK_PE=4_SV=1	6.00E-63	[illegible]	[illegible]
comp15426_c0_seq1.p2				
comp15436_c0_seq1.p1	sp|O49318|Y2317_ARATH_Probable_leucine-rich_repeat_receptor-like_protein_kinase_At2g33170_OS=Arabidopsis_thaliana_GN=At2g33170_PE=2_SV=1	2.00E-34	[illegible]	[illegible]
comp15445_c0_seq1.p1				
comp15448_c0_seq1.p1				
comp15450_c0_seq1.p1	sp|Q0QEL7|CISY_MESAU_Citrate_synthase,_mitochondrial_(Fragment)_OS=Mesocricetus_auratus_GN=CS_PE=1_SV=1	2.00E-87	[illegible]	[illegible]
comp15459_c0_seq1.p2	sp|Q61151|2A5E_MOUSE_Serine/threonine-protein_phosphatase_2A_56_kDa_regulatory_subunit_epsilon_isoform_OS=Mus_musculus_GN=Ppp2r5e_PE=2_SV=3	5.00E-24	[illegible]	[illegible]
comp15459_c0_seq2.p1	sp|O04376|2A5B_ARATH_Serine/threonine-protein_phosphatase_2A_57_kDa_regulatory_subunit_B'_beta_isoform_OS=Arabidopsis_thaliana_GN=B'BETA_PE=1_SV=1	3.00E-56	GO:0000159,GO:0007165,GO:0008601,GO:0050790	[illegible]
comp15462_c0_seq1.p1	sp|Q5RGV1|IMDH3_DANRE_Inosine-5'-monophosphate_dehydrogenase_1b_OS=Danio_rerio_GN=impdh1b_PE=2_SV=1	6.00E-48	[illegible]	[illegible]
comp1547_c0_seq1.p1				
comp15479_c0_seq1.p1				
comp15481_c0_seq1.p1				
comp15501_c0_seq1.p1				
comp15501_c0_seq2.p2				
comp15526_c0_seq1.p1	sp|Q55AI5|SUCB1_DICDI_Succinyl-CoA_ligase_[ADP-forming]_subunit_beta,_mitochondrial_OS=Dictyostelium_discoideum_GN=scsC_PE=3_SV=1	1.00E-30	[illegible]	[illegible]
comp15545_c0_seq1.p1	sp|P39831|YDFG_ECOLI_NADP-dependent_3-hydroxy_acid_dehydrogenase_YdfG_OS=Escherichia_coli_(strain_K12)_GN=ydfG_PE=1_SV=2	9.00E-77	[illegible]	[illegible]
comp15550_c0_seq1.p1	sp|Q46863|YGIS_ECOLI_Putative_binding_protein_ygiS_OS=Escherichia_coli_(strain_K12)_GN=ygiS_PE=1_SV=1	3.00E-135	GO:0005215,GO:0006810,GO:0006810,GO:0042597,GO:0042597	[illegible]
comp155545_c0_seq1.p1	sp|P30958|MFD_ECOLI_Transcription-repair-coupling_factor_OS=Escherichia_coli_(strain_K12)_GN=mfd_PE=1_SV=2	8.00E-67	[illegible]	[illegible]
comp15556_c0_seq1.p1	sp|Q3YXK1|ZUPT_SHISS_Zinc_transporter_ZupT_OS=Shigella_sonnei_(strain_Ss046)_GN=zupT_PE=3_SV=1	1.00E-83	[illegible]	[illegible]
comp15557_c0_seq1.p1				
comp155574_c0_seq1.p1				
comp15559_c0_seq1.p1	sp|P0ADJ2|YHHN_SHIFL_Uncharacterized_membrane_protein_yhhN_OS=Shigella_flexneri_GN=yhhN_PE=3_SV=1	1.00E-80	GO:0005886,GO:0005886,GO:0016020,GO:0016021,GO:0016021	[illegible]
comp15561_c0_seq1.p1	sp|Q54BF6|MCFN_DICDI_Mitochondrial_substrate_carrier_family_protein_N_OS=Dictyostelium_discoideum_GN=mcfN_PE=1_SV=2	3.00E-38	[illegible]	[illegible]
comp15561_c0_seq2.p1				
comp15572_c0_seq1.p1				
comp15577_c0_seq2.p2				
comp15588_c0_seq1.p2	sp|P36938|PGM_ECOLI_Phosphoglucomutase_OS=Escherichia_coli_(strain_K12)_GN=pgm_PE=1_SV=1	6.00E-165	[illegible]	[illegible]
comp15591_c0_seq1.p1	sp|P28904|TREC_ECOLI_Trehalose-6-phosphate_hydrolase_OS=Escherichia_coli_(strain_K12)_GN=treC_PE=3_SV=3	9.00E-173	[illegible]	[illegible]
comp15591_c0_seq2.p1	sp|P30131|HYPF_ECOLI_Carbamoyltransferase_hypF_OS=Escherichia_coli_(strain_K12)_GN=hypF_PE=1_SV=2	1.00E-88	[illegible]	[illegible]
comp15593_c0_seq1.p1	sp|P0CK95|ACFD_ECOLI_Putative_lipoprotein_AcfD_homolog_OS=Escherichia_coli_(strain_K12)_GN=yghJ_PE=4_SV=1	3.00E-88	GO:0005886,GO:0005886,GO:0016020	[illegible]
comp15595_c1_seq1.p1	sp|Q3Z5R1|SECA_SHISS_Protein_translocase_subunit_SecA_OS=Shigella_sonnei_(strain_Ss046)_GN=secA_PE=3_SV=1	2.00E-78	[illegible]	[illegible]
comp15597_c0_seq2.p1				
comp15614_c0_seq1.p1				
comp15675_c0_seq2.p1				
comp15677_c0_seq1.p1	sp|P0A9H3|LDCI_ECOLI_Lysine_decarboxylase,_inducible_OS=Escherichia_coli_(strain_K12)_GN=cadA_PE=1_SV=1	1.00E-95	[illegible]	[illegible]
comp15684_c0_seq1.p1				
comp15698_c0_seq1.p1				
comp15700_c0_seq1.p1	sp|O80763|NRX1_ARATH_Probable_nucleoredoxin_1_OS=Arabidopsis_thaliana_GN=At1g60420_PE=1_SV=1	5.00E-23	[illegible]	[illegible]
comp15702_c1_seq1.p1	sp|P28635|METQ_ECOLI_D-methionine-binding_lipoprotein_metQ_OS=Escherichia_coli_(strain_K12)_GN=metQ_PE=1_SV=2	3.00E-95	GO:0005886,GO:0005886,GO:0006810,GO:0006865,GO:0016020	[illegible]
comp15709_c0_seq1.p2	sp|P54399|PDI_DROME_Protein_disulfide-isomerase_OS=Drosophila_melanogaster_GN=Pdi_PE=2_SV=1	1.00E-47	[illegible]	[illegible]
comp15712_c0_seq1.p1	sp|P21169|DCOR_ECOLI_Ornithine_decarboxylase,_constitutive_OS=Escherichia_coli_(strain_K12)_GN=speC_PE=1_SV=2	5.00E-167	[illegible]	[illegible]
comp157205_c0_seq1.p1				
comp15722_c0_seq1.p1	sp|P00946|MANA_ECOLI_Mannose-6-phosphate_isomerase_OS=Escherichia_coli_(strain_K12)_GN=manA_PE=1_SV=1	4.00E-86	[illegible]	[illegible]
comp15726_c0_seq1.p1	sp|P0AG33|RHO_SHIFL_Transcription_termination_factor_Rho_OS=Shigella_flexneri_GN=rho_PE=3_SV=1	4.00E-102	[illegible]	[illegible]
comp15731_c0_seq1.p1	sp|B6EIM4|FOLD_ALISL_Bifunctional_protein_FolD_OS=Aliivibrio_salmonicida_(strain_LFI1238)_GN=folD_PE=3_SV=1	5.00E-56	[illegible]	[illegible]
comp15741_c0_seq1.p1				
comp15748_c0_seq1.p1	sp|P21893|RECJ_ECOLI_Single-stranded-DNA-specific_exonuclease_recJ_OS=Escherichia_coli_(strain_K12)_GN=recJ_PE=1_SV=2	3.00E-62	[illegible]	[illegible]
comp15750_c0_seq1.p1	sp|P04993|EX5A_ECOLI_Exodeoxyribonuclease_V_alpha_chain_OS=Escherichia_coli_(strain_K12)_GN=recD_PE=1_SV=2	6.00E-65	[illegible]	[illegible]
comp15752_c0_seq1.p1				
comp15753_c0_seq1.p1	sp|P0A9A6|FTSZ_ECOLI_Cell_division_protein_FtsZ_OS=Escherichia_coli_(strain_K12)_GN=ftsZ_PE=1_SV=1	1.00E-106	[illegible]	[illegible]
comp15761_c0_seq1.p1	sp|P36562|COBT_ECOLI_Nicotinate-nucleotide--dimethylbenzimidazole_phosphoribosyltransferase_OS=Escherichia_coli_(strain_K12)_GN=cobT_PE=3_SV=3	3.00E-112	[illegible]	[illegible]
comp15766_c0_seq1.p1				
comp15768_c0_seq1.p1				
comp15769_c0_seq1.p1				
comp15770_c0_seq1.p1				
comp157729_c0_seq1.p1				
comp15779_c0_seq1.p1	sp|P53028|RL10A_TRYBR_60S_ribosomal_protein_L10a_OS=Trypanosoma_brucei_rhodesiense_GN=RPL10A_PE=2_SV=1	2.00E-45	[illegible]	[illegible]
comp15786_c0_seq1.p1	sp|Q90YR6|RS8_ICTPU_40S_ribosomal_protein_S8_OS=Ictalurus_punctatus_GN=rps8_PE=2_SV=3	9.00E-79	[illegible]	[illegible]
comp15800_c0_seq1.p1				
comp15800_c0_seq2.p1				
comp15801_c0_seq2.p1				
comp15802_c0_seq1.p1				
comp15806_c0_seq1.p1	sp|Q83JF9|IF2_SHIFL_Translation_initiation_factor_IF-2_OS=Shigella_flexneri_GN=infB_PE=3_SV=1	1.00E-100	[illegible]	[illegible]
comp15817_c1_seq1.p1				
comp15824_c0_seq1.p1	sp|O76577|PSDE_CAEEL_26S_proteasome_non-ATPase_regulatory_subunit_14_OS=Caenorhabditis_elegans_GN=rpn-11_PE=1_SV=1	7.00E-65	[illegible]	[illegible]
comp15830_c0_seq1.p2	sp|Q9P2D7|DYH1_HUMAN_Dynein_heavy_chain_1,_axonemal_OS=Homo_sapiens_GN=DNAH1_PE=1_SV=4	2.00E-30	[illegible]	[illegible]
comp15830_c1_seq1.p1	sp|Q9P2D7|DYH1_HUMAN_Dynein_heavy_chain_1,_axonemal_OS=Homo_sapiens_GN=DNAH1_PE=1_SV=4	1.00E-79	[illegible]	[illegible]
comp158369_c0_seq1.p2	sp|P36683|ACON2_ECOLI_Aconitate_hydratase_2_OS=Escherichia_coli_(strain_K12)_GN=acnB_PE=1_SV=3	6.00E-58	[illegible]	[illegible]
comp15839_c0_seq1.p1				
comp15842_c0_seq1.p1				
comp15848_c0_seq1.p1	sp|P33231|LLDP_ECOLI_L-lactate_permease_OS=Escherichia_coli_(strain_K12)_GN=lldP_PE=1_SV=1	3.00E-88	[illegible]	[illegible]
comp15848_c1_seq1.p1	sp|P33231|LLDP_ECOLI_L-lactate_permease_OS=Escherichia_coli_(strain_K12)_GN=lldP_PE=1_SV=1	3.00E-120	[illegible]	[illegible]
comp15849_c0_seq1.p1				
comp15855_c0_seq1.p1	sp|Q8W5S1|CCH11_ARATH_Cyclin-H1-1_OS=Arabidopsis_thaliana_GN=CYCH1-1_PE=1_SV=1	2.00E-29	[illegible]	[illegible]
comp15874_c0_seq1.p1	sp|P0A9S3|GATD_ECOLI_Galactitol-1-phosphate_5-dehydrogenase_OS=Escherichia_coli_(strain_K12)_GN=gatD_PE=3_SV=1	4.00E-86	[illegible]	[illegible]
comp15882_c0_seq1.p2				
comp15893_c0_seq1.p1	sp|Q84WL9|AP2S_ARATH_AP-2_complex_subunit_sigma_OS=Arabidopsis_thaliana_GN=AP17_PE=2_SV=1	9.00E-58	[illegible]	[illegible]
comp15919_c0_seq1.p1				
comp15921_c0_seq1.p1				
comp15928_c0_seq1.p1	sp|Q9V853|SMUF1_DROME_E3_ubiquitin-protein_ligase_Smurf1_OS=Drosophila_melanogaster_GN=lack_PE=1_SV=3	1.00E-11	[illegible]	[illegible]
comp15929_c0_seq1.p1	sp|Q9FK28|MEM12_ARATH_Membrin-12_OS=Arabidopsis_thaliana_GN=MEMB12_PE=2_SV=1	2.00E-17	[illegible]	[illegible]
comp15942_c0_seq1.p1				
comp15942_c0_seq2.p1				
comp15944_c0_seq1.p1	sp|Q32BQ3|GCP_SHIDS_Probable_tRNA_threonylcarbamoyladenosine_biosynthesis_protein_Gcp_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=gcp_PE=3_SV=1	1.00E-148	[illegible]	[illegible]
comp15964_c1_seq1.p1	sp|Q3Z504|QUEA_SHISS_S-adenosylmethionine:tRNA_ribosyltransferase-isomerase_OS=Shigella_sonnei_(strain_Ss046)_GN=queA_PE=3_SV=1	2.00E-67	[illegible]	[illegible]
comp159640_c0_seq1.p1	sp|P57266|KPRS_BUCAI_Ribose-phosphate_pyrophosphokinase_OS=Buchnera_aphidicola_subsp._Acyrthosiphon_pisum_(strain_APS)_GN=prs_PE=3_SV=1	3.00E-32	[illegible]	[illegible]
comp15979_c0_seq1.p2	sp|Q3YVP8|ASNA_SHISS_Aspartate--ammonia_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=asnA_PE=3_SV=1	1.00E-34	[illegible]	[illegible]
comp15986_c0_seq1.p1				
comp15990_c0_seq1.p2	sp|P58234|RS19A_SCHPO_40S_ribosomal_protein_S19-A_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rps19a_PE=2_SV=1	3.00E-32	[illegible]	[illegible]
comp16023_c0_seq1.p1	sp|P0A699|UVRA_SHIFL_UvrABC_system_protein_A_OS=Shigella_flexneri_GN=uvrA_PE=3_SV=1	6.00E-64	[illegible]	[illegible]
comp16025_c0_seq2.p1				
comp16026_c0_seq1.p1	sp|P26459|APPC_ECOLI_Cytochrome_bd-II_oxidase_subunit_1_OS=Escherichia_coli_(strain_K12)_GN=appC_PE=1_SV=1	3.00E-149	[illegible]	[illegible]
comp16029_c0_seq1.p1	sp|O59790|ARK1_SCHPO_Serine/threonine-protein_kinase_ark1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ark1_PE=1_SV=2	2.00E-55	[illegible]	[illegible]
comp160361_c0_seq1.p1	sp|P0AG84|YGHA_ECOLI_Uncharacterized_oxidoreductase_yghA_OS=Escherichia_coli_(strain_K12)_GN=yghA_PE=1_SV=1	8.00E-61	GO:0008152,GO:0016491,GO:0016491,GO:0055114	[illegible]
comp16056_c0_seq1.p1	sp|P52903|ODPA_SOLTU_Pyruvate_dehydrogenase_E1_component_subunit_alpha,_mitochondrial_OS=Solanum_tuberosum_PE=1_SV=1	4.00E-112	[illegible]	[illegible]
comp16070_c0_seq1.p2	sp|B0JW23|DNAJ_MICAN_Chaperone_protein_DnaJ_OS=Microcystis_aeruginosa_(strain_NIES-843)_GN=dnaJ_PE=3_SV=1	5.00E-17	[illegible]	[illegible]
comp16076_c0_seq1.p1	sp|Q9NYU2|UGGG1_HUMAN_UDP-glucose:glycoprotein_glucosyltransferase_1_OS=Homo_sapiens_GN=UGGT1_PE=1_SV=3	7.00E-144	[illegible]	[illegible]
comp16081_c0_seq2.p1				
comp16102_c0_seq1.p2				
comp16102_c0_seq2.p1				
comp16103_c0_seq1.p1				
comp16106_c1_seq1.p1	sp|P76558|MAO2_ECOLI_NADP-dependent_malic_enzyme_OS=Escherichia_coli_(strain_K12)_GN=maeB_PE=1_SV=1	1.00E-126	[illegible]	[illegible]
comp16113_c0_seq1.p1	sp|P16682|PHND_ECOLI_Phosphonates-binding_periplasmic_protein_OS=Escherichia_coli_(strain_K12)_GN=phnD_PE=4_SV=2	4.00E-80	[illegible]	[illegible]
comp16115_c0_seq1.p1	sp|P77378|YDIR_ECOLI_Putative_electron_transfer_flavoprotein_subunit_ydiR_OS=Escherichia_coli_(strain_K12)_GN=ydiR_PE=3_SV=1	2.00E-87	GO:0009055,GO:0050660,GO:0055114	[illegible]
comp16116_c0_seq1.p1				
comp16118_c0_seq2.p1				
comp16120_c0_seq1.p1	sp|P0AF97|TABA_SHIFL_Toxin-antitoxin_biofilm_protein_TabA_homolog_OS=Shigella_flexneri_GN=tabA_PE=3_SV=1	1.00E-105		
comp16134_c0_seq1.p2	sp|P42604|UXAA_ECOLI_Altronate_hydrolase_OS=Escherichia_coli_(strain_K12)_GN=uxaA_PE=2_SV=3	1.00E-84	GO:0008198,GO:0008789,GO:0016829,GO:0016836,GO:0019698	[illegible]
comp16134_c1_seq1.p1	sp|P42604|UXAA_ECOLI_Altronate_hydrolase_OS=Escherichia_coli_(strain_K12)_GN=uxaA_PE=2_SV=3	4.00E-87	GO:0008198,GO:0008789,GO:0016829,GO:0016836,GO:0019698	[illegible]
comp16147_c0_seq1.p1	sp|Q3YV16|ARLY_SHISS_Argininosuccinate_lyase_OS=Shigella_sonnei_(strain_Ss046)_GN=argH_PE=3_SV=1	8.00E-73	[illegible]	[illegible]
comp16147_c1_seq1.p1	sp|Q3YV16|ARLY_SHISS_Argininosuccinate_lyase_OS=Shigella_sonnei_(strain_Ss046)_GN=argH_PE=3_SV=1	1.00E-134	[illegible]	[illegible]
comp16162_c0_seq2.p2	sp|O80873|PHF5_ARATH_Uncharacterized_protein_At1g07170/At2g30000_OS=Arabidopsis_thaliana_GN=At1g07170_PE=2_SV=1	8.00E-80		
comp16168_c0_seq1.p1	sp|Q3YZ26|HSCA_SHISS_Chaperone_protein_hscA_OS=Shigella_sonnei_(strain_Ss046)_GN=hscA_PE=3_SV=1	9.00E-57	[illegible]	[illegible]
comp16182_c0_seq1.p1	sp|Q664U6|RPOA_YERPS_DNA-directed_RNA_polymerase_subunit_alpha_OS=Yersinia_pseudotuberculosis_GN=rpoA_PE=1_SV=1	1.00E-66	[illegible]	[illegible]
comp16194_c0_seq1.p1	sp|P27254|ARGK_ECOLI_Probable_GTPase_ArgK_OS=Escherichia_coli_(strain_K12)_GN=argK_PE=1_SV=2	4.00E-92	[illegible]	[illegible]
comp16198_c0_seq1.p1				
comp16204_c0_seq1.p1	sp|Q96M98|PACRG_HUMAN_Parkin_coregulated_gene_protein_OS=Homo_sapiens_GN=PACRG_PE=1_SV=2	2.00E-35	[illegible]	[illegible]
comp16205_c0_seq1.p1	sp|Q39575|DYHG_CHLRE_Dynein_gamma_chain,_flagellar_outer_arm_OS=Chlamydomonas_reinhardtii_GN=ODA2_PE=1_SV=1	5.00E-47	[illegible]	[illegible]
comp16218_c0_seq1.p1	sp|P39099|DEGQ_ECOLI_Periplasmic_pH-dependent_serine_endoprotease_DegQ_OS=Escherichia_coli_(strain_K12)_GN=degQ_PE=1_SV=1	3.00E-57	[illegible]	[illegible]
comp16224_c0_seq1.p1				
comp16225_c0_seq1.p1				
comp16230_c0_seq1.p1	sp|Q3YX86|YHBQ_SHISS_UPF0213_protein_yhbQ_OS=Shigella_sonnei_(strain_Ss046)_GN=yhbQ_PE=3_SV=1	4.00E-65	GO:0090305	[illegible]
comp16236_c0_seq1.p1	sp|P0A699|UVRA_SHIFL_UvrABC_system_protein_A_OS=Shigella_flexneri_GN=uvrA_PE=3_SV=1	1.00E-76	[illegible]	[illegible]
comp16238_c0_seq1.p1	sp|Q3YU98|OTC_SHISS_Ornithine_carbamoyltransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=argI_PE=3_SV=1	5.00E-98	[illegible]	[illegible]
comp16240_c0_seq1.p1				
comp16251_c0_seq1.p1				
comp16254_c0_seq1.p1				
comp16255_c0_seq1.p1				
comp16260_c0_seq1.p1	sp|A7H3B9|PCKA_CAMJD_Phosphoenolpyruvate_carboxykinase_[ATP]_OS=Campylobacter_jejuni_subsp._doylei_(strain_ATCC_BAA-1458_/_RM4099_/_269.97)_GN=pckA_PE=3_SV=1	0	[illegible]	[illegible]
comp16263_c0_seq1.p1				
comp16266_c0_seq1.p1				
comp16276_c0_seq1.p1	sp|Q10BT5|PP2A2_ORYSJ_Serine/threonine-protein_phosphatase_PP2A-2_catalytic_subunit_OS=Oryza_sativa_subsp._japonica_GN=PP2A2_PE=2_SV=1	2.00E-78	[illegible]	[illegible]
comp16284_c0_seq2.p1	sp|P36183|ENPL_HORVU_Endoplasmin_homolog_OS=Hordeum_vulgare_PE=2_SV=1	0	[illegible]	[illegible]
comp16297_c0_seq1.p2				
comp16308_c0_seq2.p1	sp|P36618|CDC16_SCHPO_Cell_division_control_protein_16_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=cdc16_PE=1_SV=1	2.00E-38	[illegible]	[illegible]
comp16308_c0_seq2.p2				
comp16314_c0_seq1.p1				
comp16327_c0_seq1.p1	sp|P27795|H2B_TRYCR_Histone_H2B_OS=Trypanosoma_cruzi_PE=3_SV=1	6.00E-32	[illegible]	[illegible]
comp16330_c0_seq1.p1	sp|P34519|TXTP_CAEEL_Putative_tricarboxylate_transport_protein,_mitochondrial_OS=Caenorhabditis_elegans_GN=K11H3.3_PE=2_SV=1	2.00E-67	[illegible]	[illegible]
comp16354_c0_seq1.p1	sp|Q9SB58|ZDH19_ARATH_Probable_S-acyltransferase_At4g24630_OS=Arabidopsis_thaliana_GN=At4g24630_PE=1_SV=2	2.00E-12	[illegible]	[illegible]
comp16355_c0_seq1.p1	sp|Q63170|DYH7_RAT_Dynein_heavy_chain_7,_axonemal_OS=Rattus_norvegicus_GN=Dnah7_PE=2_SV=2	4.00E-30	[illegible]	[illegible]
comp16361_c0_seq1.p1				
comp16362_c0_seq1.p1	sp|Q3YW96|GLGA_SHISS_Glycogen_synthase_OS=Shigella_sonnei_(strain_Ss046)_GN=glgA_PE=3_SV=1	3.00E-176	[illegible]	[illegible]
comp16367_c0_seq1.p1	sp|P0AEG1|DPPC_ECOLI_Dipeptide_transport_system_permease_protein_dppC_OS=Escherichia_coli_(strain_K12)_GN=dppC_PE=1_SV=1	2.00E-169	[illegible]	[illegible]
comp16367_c0_seq1.p3	sp|P0AAG2|DPPD_SHIFL_Dipeptide_transport_ATP-binding_protein_DppD_OS=Shigella_flexneri_GN=dppD_PE=3_SV=1	5.00E-68	[illegible]	[illegible]
comp16376_c0_seq1.p1				
comp16376_c1_seq1.p1				
comp16380_c0_seq1.p1				
comp16389_c0_seq1.p1				
comp16391_c0_seq1.p1	sp|P0AEW4|CPDA_ECOLI_3',5'-cyclic_adenosine_monophosphate_phosphodiesterase_CpdA_OS=Escherichia_coli_(strain_K12)_GN=cpdA_PE=1_SV=1	1.00E-88	[illegible]	[illegible]
comp16397_c0_seq1.p1	sp|P30843|BASR_ECOLI_Transcriptional_regulatory_protein_BasR_OS=Escherichia_coli_(strain_K12)_GN=basR_PE=1_SV=3	6.00E-76	[illegible]	[illegible]
comp16398_c0_seq1.p1	sp|Q91W90|TXND5_MOUSE_Thioredoxin_domain-containing_protein_5_OS=Mus_musculus_GN=Txndc5_PE=1_SV=2	2.00E-28	[illegible]	[illegible]
comp16401_c0_seq1.p1	sp|Q3Z035|EFPL_SHISS_Elongation_factor_P-like_protein_OS=Shigella_sonnei_(strain_Ss046)_GN=yeiP_PE=3_SV=2	9.00E-83	[illegible]	[illegible]
comp16407_c0_seq1.p1	sp|P04825|AMPN_ECOLI_Aminopeptidase_N_OS=Escherichia_coli_(strain_K12)_GN=pepN_PE=1_SV=2	2.00E-117	[illegible]	[illegible]
comp16416_c0_seq1.p1	sp|P45758|GSPD_ECOLI_Putative_general_secretion_pathway_protein_D_OS=Escherichia_coli_(strain_K12)_GN=gspD_PE=2_SV=2	1.00E-46	[illegible]	[illegible]
comp16419_c0_seq1.p2				
comp16419_c1_seq1.p1				
comp16448_c0_seq1.p1	sp|O05519|YDIF_BACSU_Uncharacterized_ABC_transporter_ATP-binding_protein_YdiF_OS=Bacillus_subtilis_GN=ydiF_PE=3_SV=2	3.00E-69	[illegible]	[illegible]
comp16449_c1_seq1.p1				
comp16460_c0_seq1.p1				
comp16462_c0_seq1.p1				
comp16478_c0_seq1.p1				
comp16480_c0_seq1.p1				
comp16495_c1_seq1.p1				
comp16496_c0_seq1.p1	sp|Q3YVY1|TDH_SHISS_L-threonine_3-dehydrogenase_OS=Shigella_sonnei_(strain_Ss046)_GN=tdh_PE=3_SV=1	1.00E-87	[illegible]	[illegible]
comp16498_c0_seq1.p1	sp|Q0T208|DER_SHIF8_GTPase_Der_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=der_PE=3_SV=1	3.00E-101	GO:0000166,GO:0005525,GO:0005525,GO:0005525,GO:0042254	[illegible]
comp16499_c0_seq1.p1	sp|Q3YV11|TRMA_SHISS_tRNA_(uracil(54)-C(5))-methyltransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=trmA_PE=3_SV=1	4.00E-101	[illegible]	[illegible]
comp16502_c0_seq1.p1	sp|P21893|RECJ_ECOLI_Single-stranded-DNA-specific_exonuclease_recJ_OS=Escherichia_coli_(strain_K12)_GN=recJ_PE=1_SV=2	7.00E-155	[illegible]	[illegible]
comp16502_c0_seq1.p2	sp|P0AEG6|DSBC_ECOLI_Thiol:disulfide_interchange_protein_DsbC_OS=Escherichia_coli_(strain_K12)_GN=dsbC_PE=1_SV=1	2.00E-67	[illegible]	[illegible]
comp16515_c0_seq1.p1				
comp16520_c0_seq1.p1				
comp16523_c0_seq2.p1				
comp16525_c0_seq1.p1				
comp16528_c0_seq1.p1				
comp16531_c0_seq2.p1	sp|B2RY56|RBM25_MOUSE_RNA-binding_protein_25_OS=Mus_musculus_GN=Rbm25_PE=1_SV=1	2.00E-21	[illegible]	[illegible]
comp16539_c0_seq1.p1				
comp16540_c0_seq1.p1				
comp16544_c0_seq2.p1	sp|P37339|LHGO_ECOLI_L-2-hydroxyglutarate_oxidase_LhgO_OS=Escherichia_coli_(strain_K12)_GN=lhgO_PE=1_SV=3	2.00E-64	[illegible]	[illegible]
comp16557_c0_seq2.p1	sp|Q9Y1W0|FAD5A_DICDI_Delta(5)_fatty_acid_desaturase_A_OS=Dictyostelium_discoideum_GN=fadA_PE=1_SV=1	1.00E-105	[illegible]	[illegible]

comp16567_c0_seq1.p1				
comp16572_c0_seq1.p1	sp|P32681|YJAH_ECOLI_Uncharacterized_protein_yjaH_OS=Escherichia_coli_(strain_K12)_GN=yjaH_PE=4_SV=1	1.00E-81		
comp16574_c0_seq1.p1				
comp16585_c1_seq1.p1	sp|P09980|REP_ECOLI_ATP-dependent_DNA_helicase_rep_OS=Escherichia_coli_(strain_K12)_GN=rep_PE=1_SV=3	3.00E-69	[illegible]	[illegible]
comp16588_c0_seq1.p1				
comp16588_c0_seq2.p1				
comp16589_c0_seq1.p1	sp|P65807|YGEY_ECOLI_Uncharacterized_protein_ygeY_OS=Escherichia_coli_(strain_K12)_GN=ygeY_PE=3_SV=1	1.00E-175	[illegible]	[illegible]
comp16609_c0_seq1.p1				
comp16636_c0_seq1.p1	sp|P0AFU5|QSEF_ECO57_Transcriptional_regulatory_protein_QseF_OS=Escherichia_coli_O157:H7_GN=qseF_PE=1_SV=1	4.00E-81	[illegible]	[illegible]
comp16637_c0_seq1.p1	sp|Q3Z3H3|RLML_SHISS_Ribosomal_RNA_large_subunit_methyltransferase_L_OS=Shigella_sonnei_(strain_Ss046)_GN=rlmL_PE=3_SV=1	2.00E-70	[illegible]	[illegible]
comp16637_c1_seq1.p1	sp|Q1RDR6|RLML_ECOUT_Ribosomal_RNA_large_subunit_methyltransferase_L_OS=Escherichia_coli_(strain_UTI89_/_UPEC)_GN=rlmL_PE=3_SV=1	2.00E-167	[illegible]	[illegible]
comp16643_c0_seq1.p2				
comp16657_c0_seq1.p1	sp|Q09927|PPR1_SCHPO_L-azetidine-2-carboxylic_acid_acetyltransferase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ppr1_PE=1_SV=1	3.00E-32	[illegible]	[illegible]
comp16657_c0_seq2.p1	sp|Q09927|PPR1_SCHPO_L-azetidine-2-carboxylic_acid_acetyltransferase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ppr1_PE=1_SV=1	4.00E-29	[illegible]	[illegible]
comp16660_c0_seq1.p1	sp|P21437|GLPX2_ECOLI_Fructose-1,6-bisphosphatase_2_class_2_OS=Escherichia_coli_(strain_K12)_GN=yggF_PE=1_SV=2	2.00E-113	[illegible]	[illegible]
comp16660_c0_seq2.p1	sp|P21437|GLPX2_ECOLI_Fructose-1,6-bisphosphatase_2_class_2_OS=Escherichia_coli_(strain_K12)_GN=yggF_PE=1_SV=2	8.00E-71	[illegible]	[illegible]
comp16667_c0_seq1.p1	sp|P32784|GPT1_YEAST_Glycerol-3-phosphate_O-acyltransferase_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=SCT1_PE=1_SV=3	2.00E-22	[illegible]	[illegible]
comp16671_c0_seq1.p1	sp|P58931|BCSA_PSEFS_Cellulose_synthase_catalytic_subunit_[UDP-forming]_OS=Pseudomonas_fluorescens_(strain_SBW25)_GN=bcsA_PE=3_SV=2	9.00E-25	[illegible]	[illegible]
comp16677_c0_seq1.p1	sp|Q47208|FDRA_ECOLI_Protein_FdrA_OS=Escherichia_coli_(strain_K12)_GN=fdrA_PE=1_SV=1	3.00E-60	[illegible]	[illegible]
comp16678_c0_seq1.p1				
comp16693_c1_seq1.p1	sp|Q3Z323|ACP_SHISS_Acyl_carrier_protein_OS=Shigella_sonnei_(strain_Ss046)_GN=acpP_PE=3_SV=1	5.00E-34	[illegible]	[illegible]
comp16698_c0_seq1.p1				
comp16702_c0_seq1.p1	sp|P08400|PHOR_ECOLI_Phosphate_regulon_sensor_protein_phoR_OS=Escherichia_coli_(strain_K12)_GN=phoR_PE=1_SV=1	2.00E-146	[illegible]	[illegible]
comp16707_c0_seq1.p1	sp|P67444|XANQ_ECOLI_Xanthine_permease_XanQ_OS=Escherichia_coli_(strain_K12)_GN=xanQ_PE=1_SV=2	0	[illegible]	[illegible]
comp16709_c0_seq1.p2	sp|P36934|VPS_BPP2_Tail_completion_protein_S_OS=Enterobacteria_phage_P2_GN=S_PE=4_SV=1	9.00E-18		
comp16712_c0_seq1.p2				
comp16712_c0_seq2.p1				
comp16714_c0_seq1.p1				
comp16715_c0_seq1.p1	sp|P00561|AK1H_ECOLI_Bifunctional_aspartokinase/homoserine_dehydrogenase_1_OS=Escherichia_coli_(strain_K12)_GN=thrA_PE=1_SV=2	0	[illegible]	[illegible]
comp16719_c1_seq1.p1	sp|P0AG23|RELA_SHIFL_GTP_pyrophosphokinase_OS=Shigella_flexneri_GN=relA_PE=3_SV=1	2.00E-106	[illegible]	[illegible]
comp16725_c0_seq1.p2	sp|Q3Z601|DNAK_SHISS_Chaperone_protein_DnaK_OS=Shigella_sonnei_(strain_Ss046)_GN=dnaK_PE=3_SV=1	9.00E-100	[illegible]	[illegible]
comp16738_c0_seq1.p1	sp|Q3YYB7|TRUD_SHISS_tRNA_pseudouridine_synthase_D_OS=Shigella_sonnei_(strain_Ss046)_GN=truD_PE=3_SV=1	1.00E-102	[illegible]	[illegible]
comp16738_c1_seq1.p1	sp|Q3YYB7|TRUD_SHISS_tRNA_pseudouridine_synthase_D_OS=Shigella_sonnei_(strain_Ss046)_GN=truD_PE=3_SV=1	1.00E-112	[illegible]	[illegible]
comp16740_c0_seq1.p1				
comp16744_c0_seq1.p1	sp|A4W964|OPGH_ENT38_Glucans_biosynthesis_glucosyltransferase_H_OS=Enterobacter_sp._(strain_638)_GN=mdoH_PE=3_SV=1	3.00E-76	[illegible]	[illegible]
comp16756_c0_seq1.p1				
comp16761_c0_seq1.p1	sp|P40191|PDXK_ECOLI_Pyridoxine_kinase_OS=Escherichia_coli_(strain_K12)_GN=pdxK_PE=1_SV=2	0	[illegible]	[illegible]
comp16761_c0_seq1.p2	sp|P69785|PTGA_SHIFL_Glucose-specific_phosphotransferase_enzyme_IIA_component_OS=Shigella_flexneri_GN=crr_PE=3_SV=2	5.00E-69	[illegible]	[illegible]
comp16765_c0_seq2.p1				
comp16768_c0_seq1.p1	sp|Q940M4|OCT7_ARATH_Organic_cation/carnitine_transporter_7_OS=Arabidopsis_thaliana_GN=OCT7_PE=2_SV=1	4.00E-22	[illegible]	[illegible]
comp16769_c0_seq1.p1	sp|Q3Z5I1|YAET_SHISS_Outer_membrane_protein_assembly_factor_yaeT_OS=Shigella_sonnei_(strain_Ss046)_GN=yaeT_PE=3_SV=1	9.00E-119	[illegible]	[illegible]
comp16771_c0_seq1.p1	sp|P0AFJ7|PITA_ECOLI_Low-affinity_inorganic_phosphate_transporter_1_OS=Escherichia_coli_(strain_K12)_GN=pitA_PE=1_SV=1	1.00E-40	[illegible]	[illegible]
comp16788_c0_seq1.p1				
comp16789_c0_seq1.p1	sp|Q0J4P2|HSP81_ORYSJ_Heat_shock_protein_81-1_OS=Oryza_sativa_subsp._japonica_GN=HSP81-1_PE=2_SV=2	7.00E-49	[illegible]	[illegible]
comp16795_c0_seq1.p1	sp|Q9FHN8|KCBP_ARATH_Kinesin-like_calmodulin-binding_protein_OS=Arabidopsis_thaliana_GN=KCBP_PE=1_SV=1	1.00E-29	[illegible]	[illegible]
comp16798_c0_seq1.p1				
comp16798_c1_seq1.p1				
comp16804_c0_seq1.p1				
comp16804_c0_seq2.p1				
comp16822_c0_seq1.p1	sp|P33355|YEHS_ECOLI_Uncharacterized_protein_yehS_OS=Escherichia_coli_(strain_K12)_GN=yehS_PE=4_SV=1	6.00E-89		
comp16823_c1_seq1.p1	sp|P00550|PTM3C_ECOLI_PTS_system_mannitol-specific_EIICBA_component_OS=Escherichia_coli_(strain_K12)_GN=mtlA_PE=1_SV=1	2.00E-84	[illegible]	[illegible]
comp16830_c0_seq2.p1				
comp16834_c0_seq1.p2				
comp16834_c0_seq2.p1				
comp16840_c0_seq1.p1				
comp16842_c0_seq1.p1	sp|P08839|PT1_ECOLI_Phosphoenolpyruvate-protein_phosphotransferase_OS=Escherichia_coli_(strain_K12)_GN=ptsI_PE=1_SV=1	2.00E-89	[illegible]	[illegible]
comp16842_c1_seq1.p2	sp|P08839|PT1_ECOLI_Phosphoenolpyruvate-protein_phosphotransferase_OS=Escherichia_coli_(strain_K12)_GN=ptsI_PE=1_SV=1	5.00E-116	[illegible]	[illegible]
comp16848_c0_seq1.p1	sp|P25998|RL8_TOBAC_60S_ribosomal_protein_L8_OS=Nicotiana_tabacum_GN=RPL8_PE=2_SV=1	2.00E-124	[illegible]	[illegible]
comp16855_c0_seq1.p1				
comp16856_c1_seq1.p1	sp|P0AG83|PSTS_SHIFL_Phosphate-binding_protein_pstS_OS=Shigella_flexneri_GN=pstS_PE=3_SV=1	5.00E-85	[illegible]	[illegible]
comp16862_c0_seq1.p1				
comp16862_c0_seq2.p1				
comp16899_c0_seq1.p1	sp|P0AAG5|MDLB_ECOLI_Multidrug_resistance-like_ATP-binding_protein_MdlB_OS=Escherichia_coli_(strain_K12)_GN=mdlB_PE=1_SV=1	3.00E-93	[illegible]	[illegible]
comp16899_c0_seq1.p4	sp|P0AC58|GLNK_SHIFL_Nitrogen_regulatory_protein_P-II_2_OS=Shigella_flexneri_GN=glnK_PE=3_SV=1	1.00E-71	[illegible]	[illegible]
comp16909_c0_seq1.p1	sp|Q62036|AZI1_MOUSE_5-azacytidine-induced_protein_1_OS=Mus_musculus_GN=Azi1_PE=1_SV=2	2.00E-16	[illegible]	[illegible]
comp16918_c0_seq1.p1				
comp16922_c0_seq2.p1				
comp16927_c0_seq1.p1	sp|P09053|AVTA_ECOLI_Valine--pyruvate_aminotransferase_OS=Escherichia_coli_(strain_K12)_GN=avtA_PE=1_SV=3	6.00E-93	[illegible]	[illegible]
comp16928_c0_seq1.p2				
comp16928_c0_seq2.p2				
comp16929_c0_seq1.p1	sp|P0A9U3|YBIT_ECOLI_Uncharacterized_ABC_transporter_ATP-binding_protein_YbiT_OS=Escherichia_coli_(strain_K12)_GN=ybiT_PE=3_SV=1	3.00E-148	[illegible]	[illegible]
comp16940_c0_seq1.p1	sp|P27848|YIGL_ECOLI_Uncharacterized_protein_YigL_OS=Escherichia_coli_(strain_K12)_GN=yigL_PE=3_SV=4	1.00E-87	[illegible]	[illegible]
comp16940_c1_seq1.p2	sp|P27848|YIGL_ECOLI_Uncharacterized_protein_YigL_OS=Escherichia_coli_(strain_K12)_GN=yigL_PE=3_SV=4	2.00E-68	[illegible]	[illegible]
comp16944_c0_seq1.p1	sp|Q1HPS0|MLR_BOMMO_Myosin_regulatory_light_chain_2_OS=Bombyx_mori_PE=1_SV=1	4.00E-49	[illegible]	[illegible]
comp16958_c0_seq2.p1	sp|Q7RTR2|NLRC3_HUMAN_Protein_NLRC3_OS=Homo_sapiens_GN=NLRC3_PE=2_SV=2	3.00E-20	[illegible]	[illegible]
comp16971_c0_seq1.p1				
comp16975_c1_seq1.p1				
comp16985_c0_seq1.p3				
comp17002_c1_seq1.p1	sp|Q3YUE7|RS6_SHISS_30S_ribosomal_protein_S6_OS=Shigella_sonnei_(strain_Ss046)_GN=rpsF_PE=3_SV=1	5.00E-77	[illegible]	[illegible]
comp17009_c0_seq1.p2				
comp17010_c0_seq1.p1	sp|Q31TY2|PEPE_SHIBS_Peptidase_E_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=pepE_PE=3_SV=1	6.00E-112	[illegible]	[illegible]
comp17025_c0_seq1.p1	sp|P00370|DHE4_ECOLI_NADP-specific_glutamate_dehydrogenase_OS=Escherichia_coli_(strain_K12)_GN=gdhA_PE=1_SV=1	2.00E-99	[illegible]	[illegible]
comp17031_c0_seq1.p1				
comp17033_c0_seq1.p1	sp|P0AAC3|USPE_SHIFL_Universal_stress_protein_E_OS=Shigella_flexneri_GN=uspE_PE=3_SV=2	4.00E-72	[illegible]	[illegible]
comp17037_c0_seq1.p1	sp|P25888|RHLE_ECOLI_ATP-dependent_RNA_helicase_rhlE_OS=Escherichia_coli_(strain_K12)_GN=rhlE_PE=1_SV=3	3.00E-104	[illegible]	[illegible]
comp17038_c0_seq1.p1	sp|P31679|YAAU_ECOLI_Putative_metabolite_transport_protein_yaaU_OS=Escherichia_coli_(strain_K12)_GN=yaaU_PE=3_SV=2	4.00E-91	[illegible]	[illegible]
comp17039_c0_seq1.p1	sp|P22729|LIVM_ECOLI_High-affinity_branched-chain_amino_acid_transport_system_permease_protein_livM_OS=Escherichia_coli_(strain_K12)_GN=livM_PE=3_SV=2	8.00E-52	[illegible]	[illegible]
comp17039_c1_seq1.p1	sp|P0A9S9|LIVG_SHIFL_High-affinity_branched-chain_amino_acid_transport_ATP-binding_protein_LivG_OS=Shigella_flexneri_GN=livG_PE=3_SV=1	4.00E-67	[illegible]	[illegible]
comp17040_c0_seq2.p1				
comp17041_c0_seq1.p3				
comp17054_c0_seq1.p1	sp|P30157|TBB6_ECTVR_Tubulin_beta-6_chain_OS=Ectocarpus_variabilis_GN=TUBB6_PE=2_SV=1	2.00E-156	[illegible]	[illegible]
comp17067_c0_seq1.p1	sp|P76551|EUTA_ECOLI_Ethanolamine_utilization_protein_eutA_OS=Escherichia_coli_(strain_K12)_GN=eutA_PE=3_SV=1	2.00E-63	[illegible]	[illegible]
comp17070_c0_seq1.p1	sp|P54654|CAP_DICDI_Adenylyl_cyclase-associated_protein_OS=Dictyostelium_discoideum_GN=cap_PE=1_SV=1	4.00E-67	[illegible]	[illegible]
comp17074_c0_seq1.p1	sp|P46118|HEXR_ECOLI_HTH-type_transcriptional_regulator_hexR_OS=Escherichia_coli_(strain_K12)_GN=hexR_PE=3_SV=2	8.00E-80	[illegible]	[illegible]
comp17075_c0_seq1.p1				
comp17078_c0_seq1.p1	sp|P32129|YIHG_ECOLI_Probable_acyltransferase_yihG_OS=Escherichia_coli_(strain_K12)_GN=yihG_PE=1_SV=1	0	[illegible]	[illegible]
comp17080_c0_seq1.p2				
comp17090_c0_seq1.p1				
comp17099_c0_seq1.p1				
comp17106_c0_seq1.p1	sp|Q3YVN9|ATPD_SHISS_ATP_synthase_subunit_delta_OS=Shigella_sonnei_(strain_Ss046)_GN=atpH_PE=3_SV=1	5.00E-81	[illegible]	[illegible]
comp17116_c0_seq1.p2				
comp17121_c1_seq1.p1	sp|B8J3V0|BIOF_DESDA_Putative_8-amino-7-oxononanoate_synthase_OS=Desulfovibrio_desulfuricans_(strain_ATCC_27774_/_DSM_6949)_GN=bioF_PE=3_SV=1	6.00E-60	[illegible]	[illegible]
comp17122_c0_seq2.p1	sp|Q58760|Y1365_METJA_Uncharacterized_protein_MJ1365_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ1365_PE=4_SV=1	6.00E-14	[illegible]	[illegible]
comp17126_c0_seq1.p1				
comp17130_c0_seq1.p1	sp|Q4P3X7|BRE1_USTMA_E3_ubiquitin-protein_ligase_BRE1_OS=Ustilago_maydis_(strain_521_/_FGSC_9021)_GN=BRE1_PE=3_SV=1	4.00E-28	[illegible]	[illegible]
comp17133_c0_seq1.p1				
comp17159_c0_seq1.p1				
comp17165_c0_seq1.p1				
comp17178_c0_seq2.p1	sp|Q8N5B7|CERS5_HUMAN_Ceramide_synthase_5_OS=Homo_sapiens_GN=CERS5_PE=1_SV=1	2.00E-31	[illegible]	[illegible]
comp17184_c0_seq1.p1	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	3.00E-66	[illegible]	[illegible]
comp17189_c0_seq1.p1				
comp17195_c0_seq1.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	1.00E-21	[illegible]	[illegible]
comp17207_c0_seq1.p1				
comp17207_c1_seq1.p1				
comp17210_c0_seq1.p1	sp|P32152|FRVR_ECOLI_Putative_frv_operon_regulatory_protein_OS=Escherichia_coli_(strain_K12)_GN=frvR_PE=3_SV=1	0	[illegible]	[illegible]
comp17212_c0_seq1.p1				
comp17212_c1_seq1.p1				
comp17217_c0_seq1.p1				
comp17229_c0_seq1.p1				
comp17254_c0_seq2.p1				
comp17262_c0_seq1.p1				
comp17262_c0_seq2.p1				
comp17262_c0_seq2.p4				
comp17274_c0_seq1.p1				
comp17283_c0_seq1.p1	sp|Q3YVC2|FADA_SHISS_3-ketoacyl-CoA_thiolase_OS=Shigella_sonnei_(strain_Ss046)_GN=fadA_PE=3_SV=1	6.00E-114	[illegible]	[illegible]
comp17286_c0_seq1.p1				
comp17288_c1_seq1.p1	sp|P77625|YFBT_ECOLI_Phosphatase_YfbT_OS=Escherichia_coli_(strain_K12)_GN=yfbT_PE=1_SV=2	2.00E-94	[illegible]	[illegible]
comp17293_c0_seq1.p1	sp|A5DB51|RISA_PICGU_Riboflavin_synthase_alpha_chain_OS=Meyerozyma_guilliermondii_(strain_ATCC_6260_/_CBS_566_/_DSM_6381_/_JCM_1539_/_NBRC_10279_/_NRRL_Y-324)_GN=RIB5_PE=2_SV=3	4.00E-28	[illegible]	[illegible]
comp17301_c0_seq1.p2				
comp17308_c0_seq1.p1	sp|P38134|ETK_ECOLI_Tyrosine-protein_kinase_etk_OS=Escherichia_coli_(strain_K12)_GN=etk_PE=1_SV=2	2.00E-47	[illegible]	[illegible]
comp17316_c0_seq1.p1				
comp17318_c0_seq1.p1	sp|Q54HL8|Y9381_DICDI_FNIP_repeat-containing_protein_DDB_G0289381_OS=Dictyostelium_discoideum_GN=DDB_G0289381_PE=4_SV=1	9.00E-14	[illegible]	[illegible]
comp17324_c0_seq1.p1				
comp17324_c0_seq2.p1				
comp17326_c0_seq1.p2				
comp17332_c0_seq1.p1				
comp17339_c1_seq1.p2				
comp17344_c1_seq1.p2				
comp17345_c0_seq1.p1	sp|Q3U3N6|CQ056_MOUSE_Uncharacterized_protein_C17orf56_homolog_OS=Mus_musculus_PE=1_SV=1	6.00E-21	[illegible]	[illegible]
comp17347_c0_seq1.p1				
comp17351_c0_seq1.p1				
comp17351_c0_seq1.p2				
comp17351_c0_seq2.p1				
comp17356_c0_seq1.p1				
comp17370_c0_seq1.p2	sp|P51427|RS52_ARATH_40S_ribosomal_protein_S5-2_OS=Arabidopsis_thaliana_GN=RPS5B_PE=1_SV=2	1.00E-48	[illegible]	[illegible]
comp17372_c0_seq1.p1				
comp17420_c0_seq1.p1				
comp17432_c0_seq1.p1				
comp17442_c0_seq1.p2	sp|P32672|PTFC2_ECOLI_Fructose-like_permease_IIC_component_2_OS=Escherichia_coli_(strain_K12)_GN=frwC_PE=3_SV=1	9.00E-86	[illegible]	[illegible]
comp17442_c0_seq2.p1	sp|P32154|PTFLB_ECOLI_Fructose-like_PTS_system_EIIBC_component_OS=Escherichia_coli_(strain_K12)_GN=frvB_PE=3_SV=2	5.00E-131	[illegible]	[illegible]
comp17452_c0_seq1.p1	sp|P32138|YIHQ_ECOLI_Alpha-glucosidase_yihQ_OS=Escherichia_coli_(strain_K12)_GN=yihQ_PE=3_SV=3	4.00E-134	[illegible]	[illegible]
comp17465_c0_seq1.p1	sp|Q9BW72|HIG2A_HUMAN_HIG1_domain_family_member_2A_OS=Homo_sapiens_GN=HIGD2A_PE=1_SV=1	5.00E-15	[illegible]	[illegible]
comp17483_c0_seq1.p1	sp|P0AAS4|YBBJ_SHIFL_Inner_membrane_protein_ybbJ_OS=Shigella_flexneri_GN=ybbJ_PE=3_SV=2	4.00E-73	[illegible]	[illegible]
comp17489_c0_seq1.p1	sp|P59302|ARGB_SHIFL_Acetylglutamate_kinase_OS=Shigella_flexneri_GN=argB_PE=3_SV=1	1.00E-113	[illegible]	[illegible]
comp17494_c0_seq1.p1	sp|P0A6A2|UBIB_SHIFL_Probable_ubiquinone_biosynthesis_protein_UbiB_OS=Shigella_flexneri_GN=ubiB_PE=3_SV=1	0	[illegible]	[illegible]
comp17498_c0_seq1.p1				
comp17502_c0_seq1.p2				
comp17517_c0_seq1.p1				
comp17520_c0_seq1.p1	sp|O88618|FTCD_RAT_Formimidoyltransferase-cyclodeaminase_OS=Rattus_norvegicus_GN=Ftcd_PE=1_SV=4	5.00E-13	[illegible]	[illegible]
comp17520_c0_seq2.p1				
comp17524_c0_seq1.p1				
comp17537_c0_seq1.p1				
comp17539_c0_seq1.p1	sp|B7M458|MDTB_ECO8A_Multidrug_resistance_protein_MdtB_OS=Escherichia_coli_O8_(strain_IAI1)_GN=mdtB_PE=2_SV=1	7.00E-169	[illegible]	[illegible]
comp17557_c0_seq1.p1	sp|P06959|ODP2_ECOLI_Dihydrolipoyllysine-residue_acetyltransferase_component_of_pyruvate_dehydrogenase_complex_OS=Escherichia_coli_(strain_K12)_GN=aceF_PE=1_SV=3	2.00E-77	[illegible]	[illegible]
comp17572_c0_seq1.p1	sp|B7NFY5|PLSB_ECOLU_Glycerol-3-phosphate_acyltransferase_OS=Escherichia_coli_O17:K52:H18_(strain_UMN026_/_ExPEC)_GN=plsB_PE=3_SV=1	9.00E-58	[illegible]	[illegible]
comp17572_c1_seq1.p1	sp|B2TX75|PLSB_SHIB3_Glycerol-3-phosphate_acyltransferase_OS=Shigella_boydii_serotype_18_(strain_CDC_3083-94_/_BS512)_GN=plsB_PE=3_SV=1	1.00E-125	[illegible]	[illegible]
comp17575_c0_seq1.p2	sp|Q3Z5Q6|COAE_SHISS_Dephospho-CoA_kinase_OS=Shigella_sonnei_(strain_Ss046)_GN=coaE_PE=3_SV=1	8.00E-90	[illegible]	[illegible]
comp17583_c0_seq1.p1				
comp17591_c0_seq1.p1	sp|Q9HLX5|SYH_THEAC_Histidine--tRNA_ligase_OS=Thermoplasma_acidophilum_(strain_ATCC_25905_/_DSM_1728_/_JCM_9062_/_NBRC_15155_/_AMRC-C165)_GN=hisS_PE=1_SV=1	7.00E-47	[illegible]	[illegible]
comp17595_c0_seq1.p1	sp|Q3YVX0|LLDD_SHISS_L-lactate_dehydrogenase_[cytochrome]_OS=Shigella_sonnei_(strain_Ss046)_GN=lldD_PE=3_SV=1	7.00E-76	[illegible]	[illegible]
comp17598_c0_seq2.p1	sp|Q9UI26|IPO11_HUMAN_Importin-11_OS=Homo_sapiens_GN=IPO11_PE=1_SV=1	5.00E-54	[illegible]	[illegible]
comp17609_c0_seq1.p1				
comp17616_c0_seq1.p1				
comp17621_c0_seq1.p2				
comp17621_c0_seq2.p2				
comp17625_c0_seq2.p2				
comp17631_c0_seq1.p1				
comp17646_c0_seq1.p1				
comp17646_c1_seq1.p1	sp|P08472|M130_STRPU_Mesenchyme-specific_cell_surface_glycoprotein_OS=Strongylocentrotus_purpuratus_PE=2_SV=2	2.00E-22	[illegible]	[illegible]
comp17654_c0_seq1.p2	sp|Q8IT98|RS18_AEQIR_40S_ribosomal_protein_S18_OS=Aequipecten_irradians_GN=RPS18_PE=2_SV=1	2.00E-46	[illegible]	[illegible]
comp17657_c0_seq1.p1				
comp17663_c0_seq1.p1				
comp17664_c0_seq1.p1	sp|B6I3P6|ADEC_ECOSE_Adenine_deaminase_OS=Escherichia_coli_(strain_SE11)_GN=ade_PE=3_SV=1	1.00E-60	[illegible]	[illegible]
comp17664_c1_seq1.p1	sp|Q7BZ90|ADEC_SHIFL_Adenine_deaminase_OS=Shigella_flexneri_GN=ade_PE=3_SV=1	5.00E-88	[illegible]	[illegible]
comp17669_c0_seq1.p1	sp|P0AEH5|ELAB_ECOLI_Protein_elaB_OS=Escherichia_coli_(strain_K12)_GN=elaB_PE=1_SV=1	8.00E-39	[illegible]	[illegible]
comp17669_c1_seq1.p2	sp|P0AEH4|ELAA_SHIFL_Protein_elaA_OS=Shigella_flexneri_GN=elaA_PE=3_SV=1	6.00E-74	GO:0008080,GO:0008152	[illegible]
comp17671_c0_seq1.p1				
comp17673_c0_seq1.p1	sp|P24193|HYPE_ECOLI_Hydrogenase_isoenzymes_formation_protein_hypE_OS=Escherichia_coli_(strain_K12)_GN=hypE_PE=1_SV=2	6.00E-132	[illegible]	[illegible]
comp17677_c0_seq2.p1	sp|Q92DM1|PHOT_LISIN_Blue-light_photoreceptor_OS=Listeria_innocua_GN=lin0792_PE=3_SV=1	4.00E-22	[illegible]	[illegible]
comp17678_c0_seq1.p1	sp|Q8BMS1|ECHA_MOUSE_Trifunctional_enzyme_subunit_alpha,_mitochondrial_OS=Mus_musculus_GN=Hadha_PE=1_SV=1	7.00E-97	[illegible]	[illegible]
comp17678_c1_seq1.p1	sp|Q5QXM1|FADJ_IDILO_Fatty_acid_oxidation_complex_subunit_alpha_OS=Idiomarina_loihiensis_(strain_ATCC_BAA-735_/_DSM_15497_/_L2-TR)_GN=fadJ_PE=3_SV=1	4.00E-46	[illegible]	[illegible]
comp17688_c0_seq1.p2				
comp17689_c0_seq1.p1	sp|Q46811|YGFK_ECOLI_Uncharacterized_protein_ygfK_OS=Escherichia_coli_(strain_K12)_GN=ygfK_PE=4_SV=1	3.00E-85	[illegible]	[illegible]
comp17690_c0_seq1.p1	sp|Q9LHA8|HSP7D_ARATH_Heat_shock_70_kDa_protein_4_OS=Arabidopsis_thaliana_GN=HSP70-4_PE=1_SV=1	2.00E-28	[illegible]	[illegible]
comp17696_c0_seq1.p1				
comp17698_c0_seq1.p2	sp|P11350|NARI_ECOLI_Respiratory_nitrate_reductase_1_gamma_chain_OS=Escherichia_coli_(strain_K12)_GN=narI_PE=1_SV=1	2.00E-78	[illegible]	[illegible]
comp17701_c0_seq1.p1				
comp17703_c0_seq1.p1				
comp17703_c0_seq1.p2				
comp17703_c0_seq2.p1				
comp17721_c0_seq1.p2	sp|P77510|DPIB_ECOLI_Sensor_histidine_kinase_DpiB_OS=Escherichia_coli_(strain_K12)_GN=dpiB_PE=1_SV=1	1.00E-64	[illegible]	[illegible]
comp17722_c0_seq1.p1	sp|P40525|RL34B_YEAST_60S_ribosomal_protein_L34-B_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=RPL34B_PE=1_SV=1	1.00E-24	[illegible]	[illegible]
comp17728_c0_seq1.p2				
comp17745_c0_seq1.p1				
comp17754_c0_seq1.p1	sp|Q3Z5V2|RAPA_SHISS_RNA_polymerase-associated_protein_RapA_OS=Shigella_sonnei_(strain_Ss046)_GN=rapA_PE=3_SV=1	9.00E-68	[illegible]	[illegible]
comp17760_c0_seq1.p1	sp|Q83PU5|UGPB_SHIFL_sn-glycerol-3-phosphate-binding_periplasmic_protein_ugpB_OS=Shigella_flexneri_GN=ugpB_PE=3_SV=1	1.00E-91	[illegible]	[illegible]
comp17760_c1_seq1.p1	sp|Q83PU6|UGPA_SHIFL_sn-glycerol-3-phosphate_transport_system_permease_protein_ugpA_OS=Shigella_flexneri_GN=ugpA_PE=3_SV=1	4.00E-100	[illegible]	[illegible]
comp17766_c0_seq1.p1	sp|Q94B38|GPT2_ARATH_Glucose-6-phosphate/phosphate_translocator_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=GPT2_PE=2_SV=2	6.00E-59	[illegible]	[illegible]
comp177673_c0_seq1.p1				
comp17768_c0_seq1.p2				
comp17780_c1_seq1.p1	sp|Q9MBF8|DYH1B_CHLRE_Dynein-1-beta_heavy_chain,_flagellar_inner_arm_I1_complex_OS=Chlamydomonas_reinhardtii_GN=DHC10_PE=1_SV=1	6.00E-14	[illegible]	[illegible]
comp17781_c0_seq1.p1	sp|P39285|YJEP_ECOLI_Uncharacterized_MscS_family_protein_YjeP_OS=Escherichia_coli_(strain_K12)_GN=yjeP_PE=3_SV=3	3.00E-113	[illegible]	[illegible]
comp17782_c0_seq1.p1				
comp17783_c0_seq1.p1	sp|Q0T0D4|LPOA_SHIF8_Penicillin-binding_protein_activator_LpoA_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=lpoA_PE=3_SV=2	4.00E-76	[illegible]	[illegible]
comp17783_c1_seq1.p1	sp|P45464|LPOA_ECOLI_Penicillin-binding_protein_activator_LpoA_OS=Escherichia_coli_(strain_K12)_GN=lpoA_PE=1_SV=1	4.00E-77	[illegible]	[illegible]
comp17783_c1_seq1.p2	sp|P67087|RSMI_ECOLI_Ribosomal_RNA_small_subunit_methyltransferase_I_OS=Escherichia_coli_(strain_K12)_GN=rsmI_PE=1_SV=1	1.00E-68	[illegible]	[illegible]
comp17785_c0_seq2.p1	sp|P92958|KIN11_ARATH_SNF1-related_protein_kinase_catalytic_subunit_alpha_KIN11_OS=Arabidopsis_thaliana_GN=KIN11_PE=1_SV=1	3.00E-146	[illegible]	[illegible]
comp17786_c0_seq1.p1				
comp17813_c0_seq1.p1				
comp17814_c1_seq1.p1				
comp17819_c0_seq1.p1				
comp17824_c0_seq1.p1				
comp17839_c0_seq1.p1				
comp17841_c0_seq1.p1				
comp17841_c0_seq2.p1				
comp17843_c0_seq1.p1				
comp17843_c1_seq1.p1				
comp17845_c0_seq1.p1	sp|Q9FVR6|Y1222_ARATH_Uncharacterized_protein_At1g32220,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g32220_PE=1_SV=1	2.00E-31	[illegible]	[illegible]
comp17849_c0_seq1.p1				
comp17868_c0_seq1.p1	sp|P17888|PRIA_ECOLI_Primosomal_protein_N'_OS=Escherichia_coli_(strain_K12)_GN=priA_PE=1_SV=2	9.00E-109	[illegible]	[illegible]
comp17881_c0_seq1.p1	sp|Q83RQ5|NHAB_SHIFL_Na(+)/H(+)_antiporter_nhaB_OS=Shigella_flexneri_GN=nhaB_PE=3_SV=4	1.00E-73	[illegible]	[illegible]
comp17885_c0_seq1.p1	sp|Q9XF98|CALR_PRUAR_Calreticulin_OS=Prunus_armeniaca_PE=2_SV=1	8.00E-131	[illegible]	[illegible]
comp17893_c0_seq1.p1	sp|B2U1Q2|CLCB_SHIB3_Voltage-gated_ClC-type_chloride_channel_ClcB_OS=Shigella_boydii_serotype_18_(strain_CDC_3083-94_/_BS512)_GN=clcB_PE=3_SV=1	9.00E-56	[illegible]	[illegible]
comp17894_c0_seq1.p2				
comp17895_c0_seq1.p3				
comp17900_c0_seq1.p1	sp|P0AEZ9|MOAB_ECOLI_Molybdenum_cofactor_biosynthesis_protein_B_OS=Escherichia_coli_(strain_K12)_GN=moaB_PE=1_SV=2	2.00E-73	[illegible]	[illegible]
comp17902_c0_seq2.p2				
comp17904_c0_seq1.p1				
comp17906_c0_seq1.p1				
comp17912_c0_seq1.p1	sp|P45537|YHFK_ECOLI_Uncharacterized_protein_yhfK_OS=Escherichia_coli_(strain_K12)_GN=yhfK_PE=3_SV=2	0	[illegible]	[illegible]
comp17914_c0_seq1.p1	sp|Q3TDN0|DISP1_MOUSE_Protein_dispatched_homolog_1_OS=Mus_musculus_GN=Disp1_PE=1_SV=2	7.00E-21	[illegible]	[illegible]
comp17915_c0_seq1.p1				
comp17919_c0_seq1.p1	sp|Q83P87|MDTP_SHIFL_Multidrug_resistance_outer_membrane_protein_MdtP_OS=Shigella_flexneri_GN=mdtP_PE=3_SV=1	6.00E-79	[illegible]	[illegible]
comp1795_c0_seq1.p1	sp|P33363|BGLX_ECOLI_Periplasmic_beta-glucosidase_OS=Escherichia_coli_(strain_K12)_GN=bglX_PE=1_SV=2	3.00E-105	[illegible]	[illegible]
comp17950_c0_seq1.p1				
comp17960_c0_seq1.p1				
comp17985_c0_seq1.p1				
comp17989_c0_seq1.p1	sp|Q80YX1|TENA_MOUSE_Tenascin_OS=Mus_musculus_GN=Tnc_PE=1_SV=1	2.00E-13	[illegible]	[illegible]
comp17995_c0_seq1.p2				
comp17995_c0_seq2.p1				
comp18005_c0_seq1.p1				
comp18006_c0_seq1.p1	sp|Q3YWA7|MNME_SHISS_tRNA_modification_GTPase_MnmE_OS=Shigella_sonnei_(strain_Ss046)_GN=mnmE_PE=3_SV=1	1.00E-83	[illegible]	[illegible]
comp18007_c0_seq1.p1	sp|Q9ZTN2|ERD2_PETHY_ER_lumen_protein_retaining_receptor_OS=Petunia_hybrida_GN=ERD2_PE=2_SV=1	1.00E-38	[illegible]	[illegible]
comp18007_c0_seq2.p1	sp|Q9ZTN2|ERD2_PETHY_ER_lumen_protein_retaining_receptor_OS=Petunia_hybrida_GN=ERD2_PE=2_SV=1	4.00E-39	[illegible]	[illegible]
comp18008_c0_seq1.p1				
comp18008_c0_seq1.p3	sp|P33331|NTF2_YEAST_Nuclear_transport_factor_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=NTF2_PE=1_SV=2	8.00E-17	[illegible]	[illegible]
comp18008_c0_seq2.p1				
comp18018_c0_seq1.p1				
comp18029_c0_seq1.p1	sp|Q5EA97|S38AB_BOVIN_Putative_sodium-coupled_neutral_amino_acid_transporter_11_OS=Bos_taurus_GN=SLC38A11_PE=2_SV=1	6.00E-43	[illegible]	[illegible]
comp18029_c0_seq2.p1	sp|Q3USY0|S38AB_MOUSE_Putative_sodium-coupled_neutral_amino_acid_transporter_11_OS=Mus_musculus_GN=Slc38a11_PE=2_SV=2	3.00E-19	[illegible]	[illegible]
comp18030_c0_seq1.p1				
comp18034_c0_seq1.p1				
comp1805_c0_seq1.p1	sp|P37330|MASZ_ECOLI_Malate_synthase_G_OS=Escherichia_coli_(strain_K12)_GN=glcB_PE=1_SV=3	7.00E-66	[illegible]	[illegible]
comp18058_c0_seq1.p2				
comp18064_c0_seq1.p1				
comp18098_c0_seq1.p1				
comp18104_c0_seq1.p1				
comp18104_c0_seq2.p2				
comp18107_c0_seq1.p1	sp|Q8VZB9|R10A1_ARATH_60S_ribosomal_protein_L10a-1_OS=Arabidopsis_thaliana_GN=RPL10AA_PE=2_SV=1	2.00E-79	[illegible]	[illegible]
comp18125_c0_seq1.p1				
comp18129_c0_seq1.p1	sp|Q11S94|BIOB_CYTH3_Biotin_synthase_OS=Cytophaga_hutchinsonii_(strain_ATCC_33406_/_NCIMB_9469)_GN=bioB_PE=3_SV=1	7.00E-82	[illegible]	[illegible]
comp18133_c0_seq1.p1				
comp18137_c0_seq1.p1	sp|P42825|DNAJ2_ARATH_Chaperone_protein_dnaJ_2_OS=Arabidopsis_thaliana_GN=ATJ2_PE=1_SV=2	2.00E-17	[illegible]	[illegible]
comp18158_c0_seq1.p1				
comp18159_c0_seq1.p1				
comp18160_c0_seq1.p1				
comp18160_c0_seq2.p1				
comp18162_c0_seq1.p4				
comp18162_c1_seq1.p1				
comp18163_c0_seq1.p1				
comp18174_c0_seq1.p1	sp|B5ENA2|DNAJ_ACIF5_Chaperone_protein_DnaJ_OS=Acidithiobacillus_ferrooxidans_(strain_ATCC_53993)_GN=dnaJ_PE=3_SV=1	6.00E-14	[illegible]	[illegible]
comp18184_c0_seq1.p1				
comp18199_c0_seq2.p1	sp|Q66HB3|IFT80_RAT_Intraflagellar_transport_protein_80_homolog_OS=Rattus_norvegicus_GN=Ift80_PE=2_SV=1	2.00E-16	[illegible]	[illegible]
comp18214_c0_seq1.p1				
comp18215_c0_seq1.p1				
comp18225_c0_seq1.p1				
comp18227_c0_seq1.p1	sp|Q9UHG3|PCYOX_HUMAN_Prenylcysteine_oxidase_1_OS=Homo_sapiens_GN=PCYOX1_PE=1_SV=3	9.00E-25	[illegible]	[illegible]
comp18232_c0_seq1.p1				
comp1824_c0_seq1.p2	sp|P45550|YHFX_ECOLI_Uncharacterized_protein_yhfX_OS=Escherichia_coli_(strain_K12)_GN=yhfX_PE=4_SV=1	3.00E-62		
comp18253_c0_seq1.p1				
comp18254_c0_seq1.p1	sp|P29495|PFP_PROFR_Pyrophosphate--fructose_6-phosphate_1-phosphotransferase_OS=Propionibacterium_freudenreichii_subsp._shermanii_GN=pfp_PE=1_SV=2	3.00E-27	[illegible]	[illegible]
comp18256_c0_seq1.p1	sp|P02924|ARAF_ECOLI_L-arabinose-binding_periplasmic_protein_OS=Escherichia_coli_(strain_K12)_GN=araF_PE=1_SV=2	0	[illegible]	[illegible]
comp18261_c0_seq1.p1	sp|Q7XSZ4|PAS2A_ORYSJ_3-hydroxyacyl-CoA_dehydratase_PASTICCINO_2A_OS=Oryza_sativa_subsp._japonica_GN=PAS2A_PE=2_SV=2	9.00E-35	[illegible]	[illegible]
comp18282_c0_seq1.p1				
comp18284_c0_seq1.p1	sp|P38981|RSSA_URECA_40S_ribosomal_protein_SA_OS=Urechis_caupo_PE=2_SV=1	1.00E-40	[illegible]	[illegible]
comp18289_c0_seq1.p1				
comp1830_c0_seq1.p1				
comp1830_c1_seq1.p1				
comp18318_c0_seq1.p1				
comp18324_c0_seq2.p1				
comp18331_c0_seq1.p1				
comp18333_c0_seq1.p1				
comp18343_c0_seq2.p2				
comp18345_c0_seq1.p1	sp|Q9Y7K2|TOR2_SCHPO_Phosphatidylinositol_3-kinase_tor2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=tor2_PE=1_SV=2	7.00E-23	[illegible]	[illegible]
comp18347_c0_seq1.p1	sp|P24169|DCOS_ECOLI_Ornithine_decarboxylase,_inducible_OS=Escherichia_coli_(strain_K12)_GN=speF_PE=2_SV=1	7.00E-104	[illegible]	[illegible]
comp18353_c0_seq1.p1				
comp18354_c0_seq1.p2				
comp18355_c0_seq1.p1				
comp18357_c0_seq1.p2				
comp18366_c0_seq1.p1				
comp18372_c1_seq1.p1				
comp18374_c0_seq1.p1				
comp18374_c0_seq2.p1				
comp18384_c0_seq1.p1				
comp18384_c0_seq2.p1				
comp18387_c0_seq1.p1	sp|Q9MBF8|DYH1B_CHLRE_Dynein-1-beta_heavy_chain,_flagellar_inner_arm_I1_complex_OS=Chlamydomonas_reinhardtii_GN=DHC10_PE=1_SV=1	4.00E-78	[illegible]	[illegible]
comp18396_c1_seq1.p1	sp|Q3YYH1|LUXS_SHISS_S-ribosylhomocysteine_lyase_OS=Shigella_sonnei_(strain_Ss046)_GN=luxS_PE=3_SV=1	1.00E-74	[illegible]	[illegible]
comp18399_c0_seq1.p1	sp|Q962Q7|RS23_SPOFR_40S_ribosomal_protein_S23_OS=Spodoptera_frugiperda_GN=RpS23_PE=2_SV=1	4.00E-56	[illegible]	[illegible]
comp18401_c1_seq1.p1	sp|P05041|PABB_ECOLI_Para-aminobenzoate_synthase_component_1_OS=Escherichia_coli_(strain_K12)_GN=pabB_PE=1_SV=1	1.00E-97	[illegible]	[illegible]
comp18402_c0_seq1.p1				
comp18404_c0_seq1.p1				
comp18407_c0_seq1.p1	sp|P63389|YHES_ECOLI_Uncharacterized_ABC_transporter_ATP-binding_protein_YheS_OS=Escherichia_coli_(strain_K12)_GN=yheS_PE=1_SV=1	0	[illegible]	[illegible]
comp18408_c0_seq1.p2				
comp18411_c0_seq1.p1				
comp18417_c0_seq1.p1				
comp18424_c0_seq1.p1				
comp1843_c0_seq1.p1	sp|P45508|YFAL_ECOLI_Uncharacterized_protein_YfaL_OS=Escherichia_coli_(strain_K12)_GN=yfaL_PE=4_SV=2	1.00E-76	GO:0019867,GO:0043708	[illegible]
comp18437_c0_seq1.p1	sp|P52645|YDBH_ECOLI_Uncharacterized_protein_ydbH_OS=Escherichia_coli_(strain_K12)_GN=ydbH_PE=4_SV=2	5.00E-91		
comp18454_c0_seq1.p1				
comp1846_c0_seq1.p1	sp|P77748|YDIJ_ECOLI_Uncharacterized_protein_ydiJ_OS=Escherichia_coli_(strain_K12)_GN=ydiJ_PE=4_SV=1	8.00E-76	[illegible]	[illegible]
comp18465_c1_seq1.p1	sp|P39277|YJEH_ECOLI_Inner_membrane_protein_yjeH_OS=Escherichia_coli_(strain_K12)_GN=yjeH_PE=1_SV=1	0	[illegible]	[illegible]
comp18475_c0_seq1.p2				
comp18478_c0_seq1.p1				
comp18480_c0_seq1.p1				
comp18481_c0_seq1.p1	sp|Q39604|IDLC_CHLRE_28_kDa_inner_dynein_arm_light_chain,_axonemal_OS=Chlamydomonas_reinhardtii_GN=IDA4_PE=1_SV=1	1.00E-35	[illegible]	[illegible]
comp18481_c0_seq2.p1	sp|Q39604|IDLC_CHLRE_28_kDa_inner_dynein_arm_light_chain,_axonemal_OS=Chlamydomonas_reinhardtii_GN=IDA4_PE=1_SV=1	1.00E-56	[illegible]	[illegible]

comp18487_c0_seq1.p2				
comp18488_c0_seq1.p1				
comp18489_c0_seq1.p1	sp|Q99L28|RLP24_MOUSE_Probable_ribosome_biogenesis_protein_RLP24_OS=Mus_musculus_GN=Rsl24d1_PE=2_SV=1	3.00E-53	GO:0003674,GO:0005575,GO:0005634,GO:0005730,GO:0008150,GO:0042254,GO:0042254	molecular_function,cellular_component,nucleus,nucleolus,biological_process,ribosome biogenesis,ribosome biogenesis
comp18504_c0_seq1.p1				
comp18505_c0_seq1.p1				
comp18508_c0_seq1.p1	sp|P39383|YJIL_ECOLI_Uncharacterized_protein_yjiL_OS=Escherichia_coli_(strain_K12)_GN=yjiL_PE=4_SV=2	5.00E-64	GO:0046872,GO:0051536,GO:0051539	metal ion binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp1851_c0_seq1.p2	sp|P10961|HSF_YEAST_Heat_shock_factor_protein_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=HSF1_PE=1_SV=1	3.00E-11	GO:0003677,GO:0003700,GO:0003700,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0006355,GO:0006357,GO:0009408,GO:0009408,GO:0009408,GO:0030474,GO:0032007,GO:0043565	DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,nucleus,nucleus,nucleus,nucleus,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription from RNA polymerase II promoter,response to heat,response to heat,response to heat,spindle pole body duplication,negative regulation of TOR signaling,sequence-specific DNA binding
comp18512_c0_seq1.p2	sp|P32670|PTFX2_ECOLI_Multiphosphoryl_transfer_protein_2_OS=Escherichia_coli_(strain_K12)_GN=ptsA_PE=3_SV=2	2.00E-59	GO:0003824,GO:0005215,GO:0005737,GO:0005737,GO:0006810,GO:0006810,GO:0008643,GO:0008965,GO:0009401,GO:0009401,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0046872	catalytic activity,transporter activity,cytoplasm,cytoplasm,transport,transport,carbohydrate transport,phosphoenolpyruvate-protein phosphotransferase activity,phosphoenolpyruvate-dependent sugar phosphotransferase system,phosphoenolpyruvate-dependent sugar phosphotransferase system,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,metal ion binding
comp185179_c0_seq1.p1	sp|Q05311|UVRD_SALTY_DNA_helicase_II_OS=Salmonella_typhimurium_GN=uvrD_PE=3_SV=2	4.00E-58	GO:0000166,GO:0003677,GO:0003677,GO:0004003,GO:0004386,GO:0005524,GO:0005524,GO:0005737,GO:0006260,GO:0006268,GO:0006281,GO:0006974,GO:0009432,GO:0016787,GO:0016787	nucleotide binding,DNA binding,DNA binding,ATP-dependent DNA helicase activity,helicase activity,ATP binding,ATP binding,cytoplasm,DNA replication,DNA unwinding involved in DNA replication,DNA repair,cellular response to DNA damage stimulus,SOS response,hydrolase activity,hydrolase activity
comp18534_c0_seq1.p1	sp|P33226|TORC_ECOLI_Cytochrome_c-type_protein_TorC_OS=Escherichia_coli_(strain_K12)_GN=torC_PE=1_SV=3	6.00E-90	GO:0005506,GO:0005506,GO:0005515,GO:0005515,GO:0005886,GO:0005886,GO:0005886,GO:0009055,GO:0009055,GO:0009060,GO:0009061,GO:0009276,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0020037,GO:0046872,GO:0055114	iron ion binding,iron ion binding,protein binding,protein binding,plasma membrane,plasma membrane,plasma membrane,electron carrier activity,electron carrier activity,aerobic respiration,anaerobic respiration,Gram-negative-bacterium-type cell wall,membrane,integral component of membrane,integral component of membrane,integral component of membrane,heme binding,metal ion binding,oxidation-reduction process
comp18541_c0_seq1.p1	sp|Q9QXL7|NDK7_RAT_Nucleoside_diphosphate_kinase_7_OS=Rattus_norvegicus_GN=Nme7_PE=1_SV=1	4.00E-20	GO:0000166,GO:0004550,GO:0004550,GO:0005524,GO:0005524,GO:0006165,GO:0006183,GO:0006228,GO:0006241,GO:0009117,GO:0016301,GO:0016310,GO:0016740,GO:0046872	nucleotide binding,nucleoside diphosphate kinase activity,nucleoside diphosphate kinase activity,ATP binding,ATP binding,nucleoside diphosphate phosphorylation,GTP biosynthetic process,UTP biosynthetic process,CTP biosynthetic process,nucleotide metabolic process,kinase activity,phosphorylation,transferase activity,metal ion binding
comp18542_c0_seq1.p1	sp|P79733|RIR2_DANRE_Ribonucleoside-diphosphate_reductase_subunit_M2_OS=Danio_rerio_GN=rrm2_PE=1_SV=1	2.00E-161	GO:0004748,GO:0005737,GO:0005737,GO:0006260,GO:0006260,GO:0009186,GO:0016491,GO:0016491,GO:0046872,GO:0055114,GO:0055114	ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor,cytoplasm,cytoplasm,DNA replication,DNA replication,deoxyribonucleoside diphosphate metabolic process,oxidoreductase activity,oxidoreductase activity,metal ion binding,oxidation-reduction process,oxidation-reduction process
comp18551_c0_seq2.p1				
comp18556_c0_seq1.p1	sp|O13739|CHMU_SCHPO_Probable_chorismate_mutase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC16E8.04c_PE=2_SV=1	5.00E-58	GO:0000162,GO:0003824,GO:0004106,GO:0004106,GO:0004106,GO:0005634,GO:0005634,GO:0005737,GO:0005829,GO:0006571,GO:0008152,GO:0008652,GO:0009073,GO:0009073,GO:0009094,GO:0016853,GO:0046417	tryptophan biosynthetic process,catalytic activity,chorismate mutase activity,chorismate mutase activity,chorismate mutase activity,nucleus,nucleus,cytoplasm,cytosol,tyrosine biosynthetic process,metabolic process,cellular amino acid biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,L-phenylalanine biosynthetic process,isomerase activity,chorismate metabolic process
comp18559_c0_seq1.p1				
comp18565_c0_seq1.p1				
comp18566_c0_seq1.p2				
comp18584_c0_seq1.p2	sp|O60488|ACSL4_HUMAN_Long-chain-fatty-acid--CoA_ligase_4_OS=Homo_sapiens_GN=ACSL4_PE=1_SV=2	4.00E-11	GO:0000166,GO:0001676,GO:0001676,GO:0001676,GO:0001676,GO:0003824,GO:0004467,GO:0004467,GO:0004467,GO:0004467,GO:0005524,GO:0005737,GO:0005739,GO:0005739,GO:0005741,GO:0005741,GO:0005777,GO:0005777,GO:0005778,GO:0005783,GO:0005783,GO:0005789,GO:0005789,GO:0005811,GO:0006629,GO:0006629,GO:0006631,GO:0006641,GO:0007584,GO:0008152,GO:0008610,GO:0015908,GO:0016020,GO:0016020,GO:0016021,GO:0016874,GO:0019432,GO:0030182,GO:0030307,GO:0031090,GO:0031957,GO:0031966,GO:0032307,GO:0035338,GO:0035338,GO:0043025,GO:0043231,GO:0044233,GO:0044255,GO:0044281,GO:0047676,GO:0047676,GO:0060136,GO:0060996,GO:0070062,GO:0070062,GO:0070062,GO:0070672	nucleotide binding,long-chain fatty acid metabolic process,long-chain fatty acid metabolic process,long-chain fatty acid metabolic process,long-chain fatty acid metabolic process,catalytic activity,long-chain fatty acid-CoA ligase activity,long-chain fatty acid-CoA ligase activity,long-chain fatty acid-CoA ligase activity,long-chain fatty acid-CoA ligase activity,ATP binding,cytoplasm,mitochondrion,mitochondrion,mitochondrial outer membrane,mitochondrial outer membrane,peroxisome,peroxisome,peroxisomal membrane,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,endoplasmic reticulum membrane,lipid particle,lipid metabolic process,lipid metabolic process,fatty acid metabolic process,triglyceride metabolic process,response to nutrient,metabolic process,lipid biosynthetic process,fatty acid transport,membrane,membrane,integral component of membrane,ligase activity,triglyceride biosynthetic process,neuron differentiation,positive regulation of cell growth,organelle membrane,very long-chain fatty acid-CoA ligase activity,mitochondrial membrane,negative regulation of prostaglandin secretion,long-chain fatty-acyl-CoA biosynthetic process,long-chain fatty-acyl-CoA biosynthetic process,neuronal cell body,intracellular membrane-bounded organelle,ER-mitochondrion membrane contact site,cellular lipid metabolic process,small molecule metabolic process,arachidonate-CoA ligase activity,arachidonate-CoA ligase activity,embryonic process involved in female pregnancy,dendritic spine development,extracellular vesicular exosome,extracellular vesicular exosome,extracellular vesicular exosome,response to interleukin-15
comp18587_c0_seq1.p1	sp|P11557|DAMX_ECOLI_Protein_damX_OS=Escherichia_coli_(strain_K12)_GN=damX_PE=1_SV=2	4.00E-26	GO:0005515,GO:0005886,GO:0005886,GO:0007049,GO:0016020,GO:0016021,GO:0030428,GO:0032153,GO:0042834,GO:0051301	protein binding,plasma membrane,plasma membrane,cell cycle,membrane,integral component of membrane,cell septum,cell division site,peptidoglycan binding,cell division
comp18604_c0_seq1.p1	sp|P21865|KDPD_ECOLI_Sensor_protein_KdpD_OS=Escherichia_coli_(strain_K12)_GN=kdpD_PE=1_SV=2	3.00E-135	GO:0000155,GO:0000155,GO:0000160,GO:0000160,GO:0000166,GO:0004072,GO:0004673,GO:0004673,GO:0004871,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0006950,GO:0007165,GO:0007234,GO:0009593,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0018106,GO:0023014,GO:0023014,GO:0031235,GO:0046777	phosphorelay sensor kinase activity,phosphorelay sensor kinase activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,aspartate kinase activity,protein histidine kinase activity,protein histidine kinase activity,signal transducer activity,protein binding,protein binding,protein binding,protein binding,ATP binding,plasma membrane,plasma membrane,plasma membrane,response to stress,signal transduction,osmosensory signaling via phosphorelay pathway,detection of chemical stimulus,membrane,membrane,integral component of membrane,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-histidine phosphorylation,signal transduction by phosphorylation,signal transduction by phosphorylation,intrinsic component of the cytoplasmic side of the plasma membrane,protein autophosphorylation
comp18614_c0_seq1.p1				
comp18619_c0_seq1.p1				
comp18620_c0_seq1.p1				
comp18620_c0_seq2.p1				
comp18640_c0_seq1.p1	sp|P56262|DLHH_ECOLI_Putative_carboxymethylenebutenolidase_OS=Escherichia_coli_(strain_K12)_GN=ysgA_PE=3_SV=3	3.00E-113	GO:0008152,GO:0008152,GO:0008152,GO:0008806,GO:0016787,GO:0016787	metabolic process,metabolic process,metabolic process,carboxymethylenebutenolidase activity,hydrolase activity,hydrolase activity
comp18653_c0_seq1.p1				
comp18657_c0_seq1.p1	sp|Q3YV20|CAPP_SHISS_Phosphoenolpyruvate_carboxylase_OS=Shigella_sonnei_(strain_Ss046)_GN=ppc_PE=3_SV=1	1.00E-62	GO:0000287,GO:0003824,GO:0006099,GO:0006107,GO:0008964,GO:0008964,GO:0008964,GO:0015977,GO:0015977,GO:0015977,GO:0016829	magnesium ion binding,catalytic activity,tricarboxylic acid cycle,oxaloacetate metabolic process,phosphoenolpyruvate carboxylase activity,phosphoenolpyruvate carboxylase activity,phosphoenolpyruvate carboxylase activity,carbon fixation,carbon fixation,carbon fixation,lyase activity
comp18658_c0_seq1.p2	sp|P77265|MDLA_ECOLI_Multidrug_resistance-like_ATP-binding_protein_MdlA_OS=Escherichia_coli_(strain_K12)_GN=mdlA_PE=3_SV=1	6.00E-62	GO:0000166,GO:0005524,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0006200,GO:0006810,GO:0006810,GO:0006855,GO:0008152,GO:0008559,GO:0016020,GO:0016021,GO:0016021,GO:0016787,GO:0016887,GO:0042626,GO:0042908,GO:0055085	nucleotide binding,ATP binding,ATP binding,plasma membrane,plasma membrane,plasma membrane,ATP catabolic process,transport,transport,drug transmembrane transport,metabolic process,xenobiotic-transporting ATPase activity,membrane,integral component of membrane,integral component of membrane,hydrolase activity,ATPase activity,ATPase activity, coupled to transmembrane movement of substances,xenobiotic transport,transmembrane transport
comp1866_c0_seq1.p2				
comp18667_c0_seq1.p1				
comp1867_c0_seq1.p1	sp|P0A9F1|MNTR_ECOLI_Transcriptional_regulator_MntR_OS=Escherichia_coli_(strain_K12)_GN=mntR_PE=1_SV=1	2.00E-63	GO:0003677,GO:0003677,GO:0003700,GO:0003700,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0006355,GO:0045892,GO:0046914,GO:0046983,GO:2000144	DNA binding,DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,protein binding,protein binding,protein binding,protein binding,protein binding,cytoplasm,cytoplasm,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,negative regulation of transcription, DNA-templated,transition metal ion binding,protein dimerization activity,positive regulation of DNA-templated transcription, initiation
comp18676_c0_seq1.p1				
comp18680_c0_seq1.p1	sp|Q5S1S6|PRXQ_WHEAT_Peroxiredoxin_Q,_chloroplastic_OS=Triticum_aestivum_GN=PRX1_PE=1_SV=1	6.00E-36	GO:0004601,GO:0009507,GO:0009534,GO:0009536,GO:0009579,GO:0016209,GO:0016209,GO:0016491,GO:0016491,GO:0051920,GO:0055114,GO:0055114	peroxidase activity,chloroplast,chloroplast thylakoid,plastid,thylakoid,antioxidant activity,antioxidant activity,oxidoreductase activity,oxidoreductase activity,peroxiredoxin activity,oxidation-reduction process,oxidation-reduction process
comp18683_c0_seq1.p1	sp|P54746|MNGB_ECOLI_Mannosylglycerate_hydrolase_OS=Escherichia_coli_(strain_K12)_GN=mngB_PE=1_SV=2	3.00E-162	GO:0003824,GO:0004553,GO:0004559,GO:0004559,GO:0005975,GO:0006013,GO:0008152,GO:0008270,GO:0015923,GO:0016787,GO:0016798,GO:0030246,GO:0046872	catalytic activity,hydrolase activity, hydrolyzing O-glycosyl compounds,alpha-mannosidase activity,alpha-mannosidase activity,carbohydrate metabolic process,mannose metabolic process,metabolic process,zinc ion binding,mannosidase activity,hydrolase activity,hydrolase activity, acting on glycosyl bonds,carbohydrate binding,metal ion binding
comp18684_c0_seq1.p1	sp|P32176|FDOG_ECOLI_Formate_dehydrogenase-O_major_subunit_OS=Escherichia_coli_(strain_K12)_GN=fdoG_PE=1_SV=5	1.00E-61	GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0006974,GO:0008863,GO:0008863,GO:0009055,GO:0009061,GO:0016020,GO:0016491,GO:0016491,GO:0016491,GO:0030151,GO:0042597,GO:0042597,GO:0043546,GO:0043546,GO:0045333,GO:0045333,GO:0046872,GO:0051536,GO:0051539,GO:0051539,GO:0055114,GO:0055114	protein binding,protein binding,protein binding,cytoplasm,cytoplasm,cellular response to DNA damage stimulus,formate dehydrogenase (NAD+) activity,formate dehydrogenase (NAD+) activity,electron carrier activity,anaerobic respiration,membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,molybdenum ion binding,periplasmic space,periplasmic space,molybdopterin cofactor binding,molybdopterin cofactor binding,cellular respiration,cellular respiration,metal ion binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,oxidation-reduction process,oxidation-reduction process
comp18684_c1_seq1.p1	sp|P32176|FDOG_ECOLI_Formate_dehydrogenase-O_major_subunit_OS=Escherichia_coli_(strain_K12)_GN=fdoG_PE=1_SV=5	7.00E-85	GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0006974,GO:0008863,GO:0008863,GO:0009055,GO:0009061,GO:0016020,GO:0016491,GO:0016491,GO:0016491,GO:0030151,GO:0042597,GO:0042597,GO:0043546,GO:0043546,GO:0045333,GO:0045333,GO:0046872,GO:0051536,GO:0051539,GO:0051539,GO:0055114,GO:0055114	protein binding,protein binding,protein binding,cytoplasm,cytoplasm,cellular response to DNA damage stimulus,formate dehydrogenase (NAD+) activity,formate dehydrogenase (NAD+) activity,electron carrier activity,anaerobic respiration,membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,molybdenum ion binding,periplasmic space,periplasmic space,molybdopterin cofactor binding,molybdopterin cofactor binding,cellular respiration,cellular respiration,metal ion binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,oxidation-reduction process,oxidation-reduction process
comp18704_c0_seq2.p1	sp|Q3SXM5|HSDL1_HUMAN_Inactive_hydroxysteroid_dehydrogenase-like_protein_1_OS=Homo_sapiens_GN=HSDL1_PE=1_SV=3	2.00E-23	GO:0005739,GO:0005739,GO:0005739,GO:0008152,GO:0016491,GO:0055114	mitochondrion,mitochondrion,mitochondrion,metabolic process,oxidoreductase activity,oxidation-reduction process

comp19582_c0_seq1.p1		
comp19583_c0_seq1.p1		
comp19585_c0_seq1.p1		
comp19586_c0_seq1.p1	sp|O04714|GCR1_ARATH_G-protein_coupled_receptor_1_OS=Arabidopsis_thaliana_GN=GCR1_PE=1_SV=1	6.00E-45
comp19586_c0_seq1.p2		
comp19588_c0_seq1.p1		
comp19590_c0_seq1.p1		
comp19592_c0_seq1.p1		
comp19593_c0_seq1.p1		
comp19593_c0_seq2.p1		
comp19594_c0_seq1.p1		
comp19598_c0_seq1.p1		
comp19599_c0_seq1.p1	sp|Q962X9|BUD31_BRABE_Protein_BUD31_homolog_OS=Branchiostoma_belcheri_PE=2_SV=1	6.00E-39
comp19599_c0_seq1.p4		
comp19600_c0_seq1.p1	sp|Q754N7|CBK1_ASHGO_Serine/threonine-protein_kinase_CBK1_OS=Ashbya_gossypii_(strain_ATCC_10895_/_CBS_109.51_/_FGSC_9923_/_NRRL_Y-1056)_GN=CBK1_PE=3_SV=1	2.00E-115
comp19602_c0_seq1.p2	sp|P46279|RPB7_SOYBN_DNA-directed_RNA_polymerase_II_subunit_RPB7_OS=Glycine_max_PE=2_SV=1	5.00E-36
comp19606_c0_seq2.p1	sp|O94235|MPH1_SCHPO_Serine/threonine-protein_kinase_mph1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=mph1_PE=2_SV=1	1.00E-66
comp19607_c0_seq2.p1	sp|Q1ZXF1|ECHM_DICDI_Probable_enoyl-CoA_hydratase,_mitochondrial_OS=Dictyostelium_discoideum_GN=echs1_PE=3_SV=1	1.00E-105
comp19608_c0_seq1.p1		
comp19608_c0_seq2.p1		
comp19609_c0_seq1.p1		
comp19612_c0_seq1.p1		
comp19613_c0_seq1.p1	sp|Q9NR64|KLHL1_HUMAN_Kelch-like_protein_1_OS=Homo_sapiens_GN=KLHL1_PE=2_SV=1	1.00E-20
comp19614_c0_seq1.p1		
comp19615_c0_seq2.p1	sp|Q8CFK2|TF3B_MOUSE_Transcription_factor_IIIB_90_kDa_subunit_OS=Mus_musculus_GN=Brf1_PE=1_SV=1	3.00E-64
comp19622_c0_seq1.p1	sp|Q54BI3|Y3610_DICDI_LIMR_family_protein_DDB_G0293610_OS=Dictyostelium_discoideum_GN=DDB_G0293610_PE=3_SV=1	4.00E-56
comp19624_c0_seq2.p1		
comp19624_c0_seq2.p3		
comp19624_c0_seq3.p1	sp|Q9FVX1|GRXC3_ARATH_Glutaredoxin-C3_OS=Arabidopsis_thaliana_GN=GRXC3_PE=2_SV=1	2.00E-13
comp19625_c0_seq1.p1		
comp19625_c0_seq2.p1		
comp19626_c0_seq1.p1	sp|Q8HXH0|LONF3_MACFA_LON_peptidase_N-terminal_domain_and_RING_finger_protein_3_OS=Macaca_fascicularis_GN=LONRF3_PE=2_SV=1	4.00E-22
comp19627_c0_seq2.p1	sp|Q8DM56|NDK_THEEB_Nucleoside_diphosphate_kinase_OS=Thermosynechococcus_elongatus_(strain_BP-1)_GN=ndk_PE=3_SV=1	2.00E-65
comp19627_c0_seq3.p1	sp|B0C4I0|NDK_ACAM1_Nucleoside_diphosphate_kinase_OS=Acaryochloris_marina_(strain_MBIC_11017)_GN=ndk_PE=3_SV=1	4.00E-36
comp19629_c0_seq1.p1		
comp19629_c0_seq2.p1		
comp19631_c0_seq3.p1		
comp19631_c0_seq4.p1		
comp19635_c0_seq1.p1		
comp19636_c0_seq1.p1		
comp19637_c0_seq1.p1		
comp19638_c0_seq1.p1		
comp19638_c0_seq2.p1		
comp19642_c0_seq1.p1		
comp19643_c0_seq1.p1	sp|P12337|EST1_RABIT_Liver_carboxylesterase_1_OS=Oryctolagus_cuniculus_PE=1_SV=3	4.00E-53
comp19645_c0_seq1.p1	sp|O13983|HRQ1_SCHPO_Putative_ATP-dependent_helicase_hrq1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=hrq1_PE=2_SV=4	7.00E-24
comp19646_c0_seq1.p1		
comp19647_c0_seq1.p1		
comp19654_c0_seq1.p1		
comp19659_c0_seq1.p1		
comp19660_c0_seq1.p1		
comp19661_c1_seq1.p1	sp|Q7XR06|P2C45_ORYSJ_Probable_protein_phosphatase_2C_45_OS=Oryza_sativa_subsp._japonica_GN=Os04g0659500_PE=2_SV=2	3.00E-23
comp19663_c0_seq1.p1		
comp19667_c0_seq1.p1		
comp19670_c0_seq1.p1		
comp19672_c1_seq1.p1	sp|Q6P1B1|XPP1_MOUSE_Xaa-Pro_aminopeptidase_1_OS=Mus_musculus_GN=Xpnpep1_PE=2_SV=1	1.00E-169
comp19674_c0_seq1.p1		
comp19675_c0_seq1.p1		
comp19675_c0_seq2.p1		
comp19676_c0_seq1.p1	sp|Q87AD3|Y1893_XYLFT_UPF0394_membrane_protein_PD_1893_OS=Xylella_fastidiosa_(strain_Temecula1_/_ATCC_700964)_GN=PD_1893_PE=3_SV=1	4.00E-16
comp19678_c0_seq1.p1		
comp19678_c0_seq2.p1		
comp19679_c0_seq1.p1	sp|P0ABX5|FLGG_ECOLI_Flagellar_basal-body_rod_protein_flgG_OS=Escherichia_coli_(strain_K12)_GN=flgG_PE=3_SV=1	4.00E-63
comp19679_c0_seq2.p1	sp|P0AGM0|YHHT_ECOLI_UPF0118_inner_membrane_protein_yhhT_OS=Escherichia_coli_(strain_K12)_GN=yhhT_PE=1_SV=1	1.00E-93
comp19680_c0_seq2.p1	sp|Q9UTA8|YL8A_SCHPO_Uncharacterized_methyltransferase-like_C25B8.10_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC25B8.10_PE=2_SV=1	5.00E-24
comp19681_c0_seq1.p1		
comp19682_c0_seq1.p1		
comp19685_c0_seq2.p1		
comp19686_c1_seq1.p2		
comp19686_c2_seq1.p1	sp|Q9ASX5|Y5520_ARATH_Uncharacterized_aarF_domain-containing_protein_kinase_At5g05200,_chloroplastic_OS=Arabidopsis_thaliana_GN=At5g05200_PE=1_SV=1	1.00E-132
comp19687_c1_seq1.p2		
comp19690_c0_seq1.p1		
comp19690_c0_seq4.p1		
comp19691_c0_seq2.p1		
comp19696_c0_seq1.p1	sp|P18445|RL27A_RAT_60S_ribosomal_protein_L27a_OS=Rattus_norvegicus_GN=Rpl27a_PE=1_SV=3	4.00E-61
comp19697_c0_seq1.p1		
comp19698_c0_seq1.p1		
comp19698_c0_seq2.p1		
comp19699_c0_seq1.p1		
comp19700_c0_seq2.p1		
comp19705_c0_seq2.p1	sp|Q9H0A0|NAT10_HUMAN_N-acetyltransferase_10_OS=Homo_sapiens_GN=NAT10_PE=1_SV=2	0
comp19706_c0_seq1.p1	sp|P0A9T5|TAS_SHIFL_Protein_tas_OS=Shigella_flexneri_GN=tas_PE=3_SV=1	2.00E-72
comp19707_c0_seq2.p2		
comp19708_c0_seq1.p1	sp|Q6CIY7|SYM1_KLULA_Protein_SYM1_OS=Kluyveromyces_lactis_(strain_ATCC_8585_/_CBS_2359_/_DSM_70799_/_NBRC_1267_/_NRRL_Y-1140_/_WM37)_GN=SYM1_PE=3_SV=1	2.00E-16
comp19713_c0_seq1.p1	sp|P0AEY5|MDAB_ECOLI_Modulator_of_drug_activity_B_OS=Escherichia_coli_(strain_K12)_GN=mdaB_PE=1_SV=1	6.00E-144
comp19714_c0_seq1.p1		
comp19715_c0_seq3.p1	sp|Q9U1M8|MYOI_DICDI_Myosin-I_heavy_chain_OS=Dictyostelium_discoideum_GN=myoI_PE=1_SV=1	2.00E-102
comp19716_c0_seq2.p1	sp|Q6P5M2|WDR61_DANRE_WD_repeat-containing_protein_61_OS=Danio_rerio_GN=wdr61_PE=2_SV=1	2.00E-83
comp19717_c0_seq1.p2		
comp19718_c0_seq1.p1	sp|Q981V0|ARLY2_RHILO_Argininosuccinate_lyase_2_OS=Rhizobium_loti_(strain_MAFF303099)_GN=argH2_PE=3_SV=1	2.00E-12
comp19718_c0_seq2.p1	sp|Q981V0|ARLY2_RHILO_Argininosuccinate_lyase_2_OS=Rhizobium_loti_(strain_MAFF303099)_GN=argH2_PE=3_SV=1	9.00E-14
comp19719_c0_seq1.p1		
comp19721_c0_seq1.p1		
comp19723_c0_seq1.p2		
comp19726_c0_seq1.p1		
comp19726_c0_seq1.p2	sp|Q59022|Y1628_METJA_Uncharacterized_protein_MJ1628_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ1628_PE=4_SV=1	6.00E-12
comp19731_c0_seq1.p1	sp|Q29RY8|AP4M1_BOVIN_AP-4_complex_subunit_mu-1_OS=Bos_taurus_GN=AP4M1_PE=2_SV=1	3.00E-93
comp19735_c0_seq1.p1		
comp19736_c0_seq1.p1		
comp19742_c0_seq1.p1	sp|Q9FY65|RS153_ARATH_40S_ribosomal_protein_S15-3_OS=Arabidopsis_thaliana_GN=RPS15C_PE=2_SV=1	8.00E-43
comp19743_c0_seq1.p1	sp|P40937|RFC5_HUMAN_Replication_factor_C_subunit_5_OS=Homo_sapiens_GN=RFC5_PE=1_SV=1	7.00E-125
comp19743_c0_seq2.p1	sp|P40937|RFC5_HUMAN_Replication_factor_C_subunit_5_OS=Homo_sapiens_GN=RFC5_PE=1_SV=1	6.00E-125
comp19747_c0_seq2.p1		
comp19749_c0_seq1.p1	sp|P72926|Y1024_SYNY3_UPF0187_protein_sll1024_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll1024_PE=3_SV=2	4.00E-34
comp1975_c1_seq1.p1	sp|Q3Z5V2|RAPA_SHISS_RNA_polymerase-associated_protein_RapA_OS=Shigella_sonnei_(strain_Ss046)_GN=rapA_PE=3_SV=1	2.00E-60
comp19750_c0_seq1.p1	sp|Q84W65|SUFE_ARATH_SufE-like_protein,_chloroplastic_OS=Arabidopsis_thaliana_GN=EMB1374_PE=1_SV=2	5.00E-31
comp19755_c0_seq1.p1	sp|B7V2K4|AGUA_PSEA8_Agmatine_deiminase_OS=Pseudomonas_aeruginosa_(strain_LESB58)_GN=aguA_PE=3_SV=1	5.00E-122
comp19758_c0_seq2.p1	sp|O14155|YE72_SCHPO_UPF0047_protein_C4A8.02c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC4A8.02c_PE=2_SV=1	5.00E-36
comp19760_c1_seq1.p1		
comp19760_c1_seq3.p1		
comp19765_c0_seq1.p1		
comp19765_c0_seq2.p1		
comp19769_c0_seq1.p1		
comp19769_c0_seq2.p1		
comp19771_c0_seq1.p1		
comp19773_c0_seq1.p1	sp|B7N602|DNLJ_ECOLU_DNA_ligase_OS=Escherichia_coli_O17:K52:H18_(strain_UMN026_/_ExPEC)_GN=ligA_PE=3_SV=1	2.00E-94
comp19773_c1_seq1.p2	sp|Q32DE2|DNLJ_SHIDS_DNA_ligase_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=ligA_PE=3_SV=1	2.00E-62
comp19775_c0_seq1.p1		
comp19776_c0_seq1.p1		
comp19780_c0_seq1.p1	sp|Q54U31|SHKD_DICDI_Dual_specificity_protein_kinase_shkD_OS=Dictyostelium_discoideum_GN=shkD_PE=3_SV=1	8.00E-26
comp19782_c0_seq1.p1		
comp19789_c0_seq1.p1		
comp19789_c0_seq2.p2		
comp19794_c0_seq1.p1	sp|P08451|FER2_SYNP6_Ferredoxin-2_OS=Synechococcus_sp._(strain_ATCC_27144_/_PCC_6301_/_SAUG_1402/1)_GN=petF2_PE=3_SV=2	2.00E-11
comp19796_c0_seq1.p1	sp|O61122|SVKA_DICDI_Serine/threonine-protein_kinase_svkA_OS=Dictyostelium_discoideum_GN=svkA_PE=1_SV=1	2.00E-85
comp19799_c0_seq1.p1	sp|Q39022|MPK2_ARATH_Mitogen-activated_protein_kinase_2_OS=Arabidopsis_thaliana_GN=MPK2_PE=1_SV=2	4.00E-49
comp19801_c0_seq1.p1	sp|Q5R6G2|JMJD6_PONAB_Bifunctional_arginine_demethylase_and_lysyl-hydroxylase_JMJD6_OS=Pongo_abelii_GN=JMJD6_PE=2_SV=1	5.00E-104
comp19802_c0_seq3.p1		
comp19803_c0_seq1.p4		
comp19803_c0_seq2.p3		
comp19804_c0_seq1.p1		
comp19804_c0_seq1.p5		
comp19808_c0_seq1.p2		
comp19809_c0_seq1.p1	sp|Q3ZBU2|CISD1_BOVIN_CDGSH_iron-sulfur_domain-containing_protein_1_OS=Bos_taurus_GN=CISD1_PE=1_SV=1	2.00E-20
comp19810_c0_seq1.p1	sp|C8VCL5|Y0929_EMENI_Uncharacterized_rhomboid_protein_AN10929_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=AN10929_PE=3_SV=1	3.00E-21
comp19813_c0_seq1.p1		
comp19814_c0_seq1.p1		
comp19814_c0_seq1.p3		
comp19816_c0_seq1.p1	sp|Q8LDP4|CP19D_ARATH_Peptidyl-prolyl_cis-trans_isomerase_CYP19-4_OS=Arabidopsis_thaliana_GN=CYP19-4_PE=1_SV=2	2.00E-69
comp19816_c0_seq1.p2		
comp19822_c0_seq1.p1		
comp19822_c0_seq1.p3		
comp19828_c0_seq2.p1	sp|A6YB01|TKT_PHYPO_Transketolase_OS=Physarum_polycephalum_GN=tkt_PE=2_SV=1	0
comp19828_c0_seq2.p2	sp|Q9ASU1|DGAT2_ARATH_Diacylglycerol_O-acyltransferase_2_OS=Arabidopsis_thaliana_GN=DGAT2_PE=2_SV=1	4.00E-27
comp19828_c0_seq2.p3		
comp19832_c0_seq2.p1		
comp19832_c0_seq3.p1	sp|Q28GD4|ELAV2_XENTR_ELAV-like_protein_2_OS=Xenopus_tropicalis_GN=elavl2_PE=2_SV=2	5.00E-39
comp19834_c0_seq1.p1		
comp19835_c0_seq1.p1		
comp19839_c0_seq1.p1		
comp19844_c0_seq2.p2		
comp19847_c0_seq1.p1	sp|P15710|PHO4_NEUCR_Phosphate-repressible_phosphate_permease_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=pho-4_PE=3_SV=1	3.00E-15
comp19851_c0_seq1.p1	sp|Q9SUS3|APBLB_ARATH_Beta-adaptin-like_protein_B_OS=Arabidopsis_thaliana_GN=BETAB-AD_PE=1_SV=1	0
comp19851_c0_seq1.p2	sp|Q9CQ37|UBE2T_MOUSE_Ubiquitin-conjugating_enzyme_E2_T_OS=Mus_musculus_GN=Ube2t_PE=2_SV=1	5.00E-57
comp19851_c0_seq2.p1	sp|Q9SUS3|APBLB_ARATH_Beta-adaptin-like_protein_B_OS=Arabidopsis_thaliana_GN=BETAB-AD_PE=1_SV=1	0
comp19851_c0_seq2.p2	sp|Q9CQ37|UBE2T_MOUSE_Ubiquitin-conjugating_enzyme_E2_T_OS=Mus_musculus_GN=Ube2t_PE=2_SV=1	5.00E-57
comp19852_c0_seq2.p1	sp|O23920|HPPD_DAUCA_4-hydroxyphenylpyruvate_dioxygenase_OS=Daucus_carota_PE=2_SV=1	4.00E-53
comp19853_c0_seq1.p1		
comp19853_c0_seq2.p2		
comp19857_c0_seq1.p1		
comp19857_c0_seq2.p1		
comp19858_c0_seq1.p1	sp|O74113|CDC45_SCHPO_Cell_division_control_protein_45_homolog_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=sna41_PE=1_SV=1	8.00E-89
comp19858_c0_seq1.p2		
comp19859_c0_seq1.p1		
comp19860_c0_seq1.p1		
comp19860_c1_seq1.p3		
comp19862_c0_seq1.p1	sp|P37662|YHJX_ECOLI_Inner_membrane_protein_yhjX_OS=Escherichia_coli_(strain_K12)_GN=yhjX_PE=1_SV=1	2.00E-11
comp19863_c0_seq1.p1	sp|Q6AZT7|NPHP3_XENLA_Nephrocystin-3_OS=Xenopus_laevis_GN=nphp3_PE=2_SV=1	9.00E-28
comp19868_c0_seq1.p1	sp|Q6GQT0|CC14A_MOUSE_Dual_specificity_protein_phosphatase_CDC14A_OS=Mus_musculus_GN=Cdc14a_PE=2_SV=2	3.00E-81
comp19868_c0_seq1.p2		
comp19869_c0_seq2.p1	sp|P14686|GRST_ANEMI_Gramicidin_S_biosynthesis_protein_GrsT_OS=Aneurinibacillus_migulanus_GN=grsT_PE=3_SV=1	6.00E-27
comp19874_c0_seq2.p1		
comp19875_c0_seq1.p1		
comp19880_c0_seq1.p1		
comp19880_c0_seq1.p4		
comp19881_c0_seq1.p1	sp|Q9U7D0|H4_MASBA_Histone_H4_OS=Mastigamoeba_balamuthi_PE=3_SV=3	1.00E-50
comp19883_c0_seq1.p1	sp|A7MGW9|PEPB_CROS8_Peptidase_B_OS=Cronobacter_sakazakii_(strain_ATCC_BAA-894)_GN=pepB_PE=3_SV=1	1.00E-62
comp19884_c0_seq1.p1	sp|Q9PTY0|ATPB_CYPCA_ATP_synthase_subunit_beta,_mitochondrial_OS=Cyprinus_carpio_GN=atp5b_PE=2_SV=1	0
comp19887_c0_seq1.p1	sp|Q54LV8|RL34_DICDI_60S_ribosomal_protein_L34_OS=Dictyostelium_discoideum_GN=rpl34_PE=3_SV=1	2.00E-36
comp19891_c0_seq1.p2		
comp19893_c0_seq2.p1		
comp19893_c0_seq3.p1		
comp19895_c0_seq1.p1		
comp19899_c0_seq2.p1		
comp19900_c0_seq1.p1		
comp19901_c0_seq2.p1	sp|P54703|DYIN_DICDI_Cytoplasmic_dynein_1_intermediate_chain_OS=Dictyostelium_discoideum_GN=dicA_PE=2_SV=2	2.00E-83
comp19905_c0_seq1.p1		
comp19905_c0_seq3.p1		
comp19906_c0_seq1.p1		
comp19910_c0_seq1.p1		
comp19912_c0_seq1.p1		
comp19913_c0_seq1.p1		
comp19914_c0_seq1.p1		
comp19918_c0_seq1.p1	sp|Q9Y2D2|S35A3_HUMAN_UDP-N-acetylglucosamine_transporter_OS=Homo_sapiens_GN=SLC35A3_PE=2_SV=1	2.00E-74
comp19919_c0_seq1.p1	sp|Q01578|GNL_ZYMMO_Gluconolactonase_OS=Zymomonas_mobilis_(strain_ATCC_31821_/_ZM4_/_CP4)_GN=gnl_PE=1_SV=2	4.00E-42
comp19921_c0_seq1.p1		
comp19923_c0_seq2.p2		
comp19927_c0_seq1.p1		
comp19929_c0_seq1.p1		
comp19934_c0_seq1.p1	sp|P61237|YPEL3_MOUSE_Protein_yippee-like_3_OS=Mus_musculus_GN=Ypel3_PE=1_SV=1	1.00E-31
comp19937_c0_seq1.p1		
comp19938_c0_seq2.p1		
comp19941_c0_seq1.p1		
comp19943_c0_seq1.p1		
comp19943_c0_seq2.p1		
comp19944_c0_seq1.p1	sp|Q9ST27|PHOT2_ORYSJ_Phototropin-2_OS=Oryza_sativa_subsp._japonica_GN=PHOT2_PE=1_SV=1	9.00E-28
comp19947_c0_seq2.p1		
comp19950_c0_seq1.p1	sp|Q5ZJF4|PRDX6_CHICK_Peroxiredoxin-6_OS=Gallus_gallus_GN=PRDX6_PE=2_SV=3	1.00E-80
comp19954_c0_seq1.p1		
comp19955_c0_seq1.p1		
comp19955_c0_seq1.p4		
comp19955_c0_seq2.p1		
comp19956_c0_seq1.p1		
comp19957_c0_seq2.p1		
comp19958_c0_seq1.p2	sp|P32024|JI23_HORVU_23_kDa_jasmonate-induced_protein_OS=Hordeum_vulgare_PE=2_SV=1	7.00E-24
comp19960_c1_seq1.p1	sp|Q9HCS2|CP4FC_HUMAN_Cytochrome_P450_4F12_OS=Homo_sapiens_GN=CYP4F12_PE=1_SV=2	2.00E-26
comp19963_c0_seq1.p1	sp|Q9V492|MPV17_DROME_Mpv17-like_protein_OS=Drosophila_melanogaster_GN=CG11077_PE=2_SV=1	6.00E-16
comp19966_c0_seq1.p1		
comp19968_c0_seq1.p1	sp|Q9LZ03|TOP6A_ARATH_DNA_topoisomerase_6_subunit_A_OS=Arabidopsis_thaliana_GN=TOP6A_PE=1_SV=1	2.00E-171
comp19969_c0_seq1.p1	sp|Q3ZBH0|TCPB_BOVIN_T-complex_protein_1_subunit_beta_OS=Bos_taurus_GN=CCT2_PE=1_SV=3	0
comp19970_c0_seq1.p1		
comp19971_c0_seq1.p1	sp|Q9SLK2|ALIS3_ARATH_ALA-interacting_subunit_3_OS=Arabidopsis_thaliana_GN=ALIS3_PE=1_SV=1	1.00E-62
comp19972_c0_seq2.p1		
comp19974_c0_seq1.p1	sp|Q9C512|MNS1_ARATH_Mannosyl-oligosaccharide_1,2-alpha-mannosidase_MNS1_OS=Arabidopsis_thaliana_GN=MNS1_PE=1_SV=1	1.00E-136
comp19975_c0_seq1.p1		
comp19976_c0_seq1.p1	sp|Q3A6L9|RL17_PELCD_50S_ribosomal_protein_L17_OS=Pelobacter_carbinolicus_(strain_DSM_2380_/_Gra_Bd_1)_GN=rplQ_PE=3_SV=1	2.00E-36
comp19978_c0_seq2.p1	sp|Q9FNN5|NDUV1_ARATH_NADH_dehydrogenase_[ubiquinone]_flavoprotein_1,_mitochondrial_OS=Arabidopsis_thaliana_GN=At5g08530_PE=2_SV=1	0
comp19979_c0_seq2.p1	sp|Q91348|F26L_CHICK_6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase_OS=Gallus_gallus_PE=2_SV=2	1.00E-112
comp1998_c0_seq1.p2	sp|Q46807|ARCL_ECOLI_Carbamate_kinase-like_protein_YqeA_OS=Escherichia_coli_(strain_K12)_GN=yqeA_PE=3_SV=1	4.00E-56
comp19982_c0_seq2.p1	sp|Q3HVN1|AGUB_SOLTU_N-carbamoylputrescine_amidase_OS=Solanum_tuberosum_GN=CPA_PE=2_SV=1	5.00E-118
comp19983_c0_seq1.p1	sp|Q8VCN5|CGL_MOUSE_Cystathionine_gamma-lyase_OS=Mus_musculus_GN=Cth_PE=1_SV=1	2.00E-109
comp19983_c1_seq1.p1	sp|Q58DW2|CGL_BOVIN_Cystathionine_gamma-lyase_OS=Bos_taurus_GN=CTH_PE=2_SV=1	6.00E-30
comp19986_c0_seq1.p1	sp|P46428|GST_ANOGA_Glutathione_S-transferase_OS=Anopheles_gambiae_GN=GstS1_PE=2_SV=4	1.00E-18
comp19989_c0_seq1.p3		
comp19990_c0_seq1.p1		
comp19991_c0_seq1.p1	sp|P90587|WD66_PHYPO_66_kDa_stress_protein_OS=Physarum_polycephalum_PE=2_SV=1	2.00E-115
comp19991_c1_seq1.p1	sp|Q9V3J8|WDS_DROME_Protein_will_die_slowly_OS=Drosophila_melanogaster_GN=wds_PE=2_SV=1	4.00E-104
comp19993_c0_seq1.p1	sp|Q54BV6|PTER_DICDI_Phosphotriesterase-related_protein_OS=Dictyostelium_discoideum_GN=pter_PE=3_SV=1	3.00E-12
comp19994_c0_seq1.p1		
comp19996_c0_seq1.p1		
comp19997_c0_seq1.p1		
comp19999_c0_seq1.p1	sp|Q9Y282|ERGI3_HUMAN_Endoplasmic_reticulum-Golgi_intermediate_compartment_protein_3_OS=Homo_sapiens_GN=ERGIC3_PE=1_SV=1	7.00E-71
comp19999_c0_seq2.p1		
comp20000_c0_seq1.p3		
comp20001_c0_seq1.p1	sp|Q39493|DSK1_CYLFU_Diatom_spindle_kinesin_1_OS=Cylindrotheca_fusiformis_GN=DSK1_PE=2_SV=1	4.00E-132
comp20006_c0_seq1.p1	sp|Q41365|PRS7_SPIOL_26S_protease_regulatory_subunit_7_OS=Spinacia_oleracea_GN=RPT1_PE=2_SV=1	0
comp20008_c0_seq1.p1		
comp2001_c0_seq1.p1		
comp20010_c0_seq3.p1		
comp20011_c0_seq1.p1	sp|Q9FRL8|DHAR2_ARATH_Glutathione_S-transferase_DHAR2_OS=Arabidopsis_thaliana_GN=DHAR2_PE=1_SV=1	2.00E-20
comp20011_c0_seq2.p1		
comp20014_c0_seq1.p1	sp|P43299|PROL_ARATH_Protein_PROLIFERA_OS=Arabidopsis_thaliana_GN=PRL_PE=1_SV=2	0
comp20015_c0_seq1.p1		
comp20018_c0_seq1.p1		
comp20020_c0_seq1.p1		
comp20023_c0_seq1.p1		
comp20024_c0_seq1.p1	sp|P28523|CSK2A_MAIZE_Casein_kinase_II_subunit_alpha_OS=Zea_mays_GN=ACK2_PE=1_SV=1	0
comp20025_c0_seq1.p1		
comp20027_c0_seq1.p1		
comp20028_c0_seq1.p1		
comp20030_c0_seq1.p1	sp|A5PN09|UBP20_DANRE_Ubiquitin_carboxyl-terminal_hydrolase_20_OS=Danio_rerio_GN=usp20_PE=3_SV=1	4.00E-15
comp20031_c0_seq1.p1		
comp20031_c0_seq1.p3		
comp20033_c0_seq1.p1	sp|Q9LDC0|FKB42_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP42_OS=Arabidopsis_thaliana_GN=FKBP42_PE=1_SV=1	7.00E-13
comp20035_c0_seq1.p1		
comp20038_c0_seq1.p1	sp|Q5R8J8|DNJB4_PONAB_DnaJ_homolog_subfamily_B_member_4_OS=Pongo_abelii_GN=DNAJB4_PE=2_SV=1	9.00E-21
comp20038_c0_seq2.p1	sp|Q869Z0|Y5025_DICDI_Putative_protein_disulfide-isomerase_DDB_G0275025_OS=Dictyostelium_discoideum_GN=DDB_G0275025_PE=1_SV=1	2.00E-19
comp20039_c0_seq1.p1	sp|Q86L04|TRAP1_DICDI_TNF_receptor-associated_protein_1_homolog,_mitochondrial_OS=Dictyostelium_discoideum_GN=trap1_PE=2_SV=1	0
comp20041_c0_seq1.p1	sp|Q6BPT6|AIM32_DEBHA_Altered_inheritance_of_mitochondria_protein_32_OS=Debaryomyces_hansenii_(strain_ATCC_36239_/_CBS_767_/_JCM_1990_/_NBRC_0083_/_IGC_2968)_GN=AIM32_PE=3_SV=2	3.00E-14
comp20045_c0_seq1.p1	sp|Q54DD3|GCST_DICDI_Aminomethyltransferase,_mitochondrial_OS=Dictyostelium_discoideum_GN=gcvT_PE=3_SV=1	7.00E-88
comp20047_c0_seq1.p1	sp|O33513|CBBY_RHOCA_Protein_CbbY_OS=Rhodobacter_capsulatus_GN=cbbY_PE=3_SV=1	8.00E-17
comp20051_c1_seq1.p1	sp|Q9LTV6|DECR2_ARATH_Peroxisomal_2,4-dienoyl-CoA_reductase_OS=Arabidopsis_thaliana_GN=At3g12800_PE=2_SV=1	8.00E-88
comp20053_c0_seq1.p1	sp|Q58542|ARSA_METJA_Putative_arsenical_pump-driving_ATPase_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ1142_PE=1_SV=1	4.00E-38
comp20054_c0_seq1.p1	sp|Q9SA27|RH36_ARATH_DEAD-box_ATP-dependent_RNA_helicase_36_OS=Arabidopsis_thaliana_GN=RH36_PE=2_SV=1	2.00E-115
comp20055_c0_seq1.p1	sp|Q4KM34|CDK20_RAT_Cyclin-dependent_kinase_20_OS=Rattus_norvegicus_GN=Cdk20_PE=2_SV=2	2.00E-71
comp20056_c0_seq2.p1	sp|O75347|TBCA_HUMAN_Tubulin-specific_chaperone_A_OS=Homo_sapiens_GN=TBCA_PE=1_SV=3	4.00E-24
comp20059_c0_seq2.p1		
comp20061_c0_seq1.p1		
comp20062_c0_seq1.p1	sp|Q9SHC8|VAP12_ARATH_Vesicle-associated_protein_1-2_OS=Arabidopsis_thaliana_GN=PVA12_PE=1_SV=1	8.00E-13
comp20062_c0_seq1.p2		
comp20064_c0_seq1.p1	sp|Q9QYI3|DNJC7_MOUSE_DnaJ_homolog_subfamily_C_member_7_OS=Mus_musculus_GN=Dnajc7_PE=1_SV=2	6.00E-11
comp20065_c0_seq1.p1		
comp20067_c0_seq1.p2	sp|Q6DGQ0|SPT4H_DANRE_Transcription_elongation_factor_SPT4_OS=Danio_rerio_GN=supt4h1_PE=3_SV=1	1.00E-28
comp20068_c0_seq1.p2	sp|Q7XA67|MTN2_ARATH_5'-methylthioadenosine/S-adenosylhomocysteine_nucleosidase_2_OS=Arabidopsis_thaliana_GN=MTN2_PE=1_SV=1	2.00E-43
comp20068_c0_seq1.p3		
comp20069_c0_seq1.p1		
comp20070_c0_seq1.p1	sp|P32899|IMP3_YEAST_U3_small_nucleolar_ribonucleoprotein_protein_IMP3_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=IMP3_PE=1_SV=1	4.00E-72
comp20073_c0_seq1.p1	sp|P16164|URIC_PIG_Uricase_OS=Sus_scrofa_GN=UOX_PE=2_SV=3	2.00E-46
comp20075_c0_seq1.p2		
comp20076_c0_seq1.p1	sp|P40796|LA_DROME_La_protein_homolog_OS=Drosophila_melanogaster_GN=La_PE=1_SV=2	9.00E-18
comp20077_c0_seq1.p1		
comp20078_c0_seq1.p1	sp|O48741|PORC_ARATH_Protochlorophyllide_reductase_C,_chloroplastic_OS=Arabidopsis_thaliana_GN=PORC_PE=1_SV=1	3.00E-46
comp20081_c0_seq2.p1		
comp20082_c0_seq2.p1	sp|P62752|RL23A_RAT_60S_ribosomal_protein_L23a_OS=Rattus_norvegicus_GN=Rpl23a_PE=2_SV=1	8.00E-52
comp20083_c0_seq3.p1	sp|Q80Z32|ORC1_RAT_Origin_recognition_complex_subunit_1_OS=Rattus_norvegicus_GN=Orc1_PE=2_SV=1	1.00E-66
comp20084_c0_seq1.p1		
comp20084_c0_seq1.p4		
comp20086_c0_seq1.p1		
comp20087_c0_seq1.p1	sp|A0AK43|UBIE_LISW6_Demethylmenaquinone_methyltransferase_OS=Listeria_welshimeri_serovar_6b_(strain_ATCC_35897_/_DSM_20650_/_SLCC5334)_GN=ubiE_PE=3_SV=1	4.00E-13
comp20087_c0_seq2.p1		
comp20088_c0_seq1.p1		
comp20089_c0_seq2.p1		
comp20089_c0_seq3.p1		
comp20091_c0_seq1.p1		
comp20092_c0_seq1.p1		
comp20094_c0_seq1.p2		
comp20095_c0_seq1.p1		
comp20096_c0_seq1.p1	sp|Q6P5F9|XPO1_MOUSE_Exportin-1_OS=Mus_musculus_GN=Xpo1_PE=1_SV=1	0
comp20097_c0_seq1.p1	sp|Q8WVM8|SCFD1_HUMAN_Sec1_family_domain-containing_protein_1_OS=Homo_sapiens_GN=SCFD1_PE=1_SV=4	1.00E-102
comp20098_c0_seq1.p1		
comp20099_c0_seq1.p1	sp|Q12118|SGT2_YEAST_Small_glutamine-rich_tetratricopeptide_repeat-containing_protein_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=SGT2_PE=1_SV=1	1.00E-24
comp20103_c0_seq1.p1		
comp20105_c0_seq1.p1	sp|P0C0L1|APX6_ORYSJ_Probable_L-ascorbate_peroxidase_6,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=APX6_PE=2_SV=1	2.00E-94
comp20106_c0_seq1.p1	sp|Q9LVM5|TTHL_ARATH_Uric_acid_degradation_bifunctional_protein_TTL_OS=Arabidopsis_thaliana_GN=TTL_PE=1_SV=1	9.00E-16
comp20109_c0_seq1.p1	sp|Q6P0F0|TMM93_DANRE_Transmembrane_protein_93_OS=Danio_rerio_GN=tmem93_PE=2_SV=1	2.00E-11
comp20109_c0_seq1.p2		
comp20109_c0_seq2.p1		
comp20110_c0_seq1.p1		
comp20111_c0_seq1.p2		
comp20111_c0_seq2.p1		
comp20114_c0_seq1.p1	sp|P63155|CRNL1_RAT_Crooked_neck-like_protein_1_OS=Rattus_norvegicus_GN=Crnkl1_PE=2_SV=1	0
comp20115_c0_seq1.p1	sp|Q9SLX0|IMA1B_ORYSJ_Importin_subunit_alpha-1b_OS=Oryza_sativa_subsp._japonica_GN=Os05g0155500_PE=1_SV=2	3.00E-50
comp20116_c0_seq1.p1		
comp20122_c0_seq1.p1		
comp20124_c0_seq1.p1		
comp20126_c0_seq1.p1		
comp20127_c0_seq1.p1	sp|Q84RR2|ARI2_ARATH_Probable_E3_ubiquitin-protein_ligase_ARI2_OS=Arabidopsis_thaliana_GN=ARI2_PE=2_SV=1	7.00E-18
comp20128_c1_seq1.p1	sp|Q9CZE3|RAB32_MOUSE_Ras-related_protein_Rab-32_OS=Mus_musculus_GN=Rab32_PE=2_SV=3	3.00E-26
comp20131_c0_seq1.p1	sp|Q9FPJ8|RB45A_ARATH_Polyadenylate-binding_protein_RBP45A_OS=Arabidopsis_thaliana_GN=RBP45A_PE=2_SV=1	9.00E-71

comp20131_c0_seq1.p7				
comp20132_c0_seq1.p1	sp|P80313|TCPH_MOUSE_T-complex_protein_1_subunit_eta_OS=Mus_musculus_GN=Cct7_PE=1_SV=1	0	[illegible]	[illegible]
comp20133_c0_seq1.p1				
comp20137_c1_seq1.p1	sp|P02385|RL4B_XENLA_60S_ribosomal_protein_L4-B_OS=Xenopus_laevis_GN=rpl4-b_PE=2_SV=2	2.00E-64	[illegible]	[illegible]
comp20138_c0_seq1.p1	sp|Q8L7A9|AP4E_ARATH_AP-4_complex_subunit_epsilon_OS=Arabidopsis_thaliana_GN=At1g31730_PE=1_SV=1	1.00E-174	[illegible]	[illegible]
comp20141_c0_seq1.p1	sp|Q9ZPH2|GRS17_ARATH_Monothiol_glutaredoxin-S17_OS=Arabidopsis_thaliana_GN=GRXS17_PE=2_SV=1	1.00E-126	[illegible]	[illegible]
comp20141_c0_seq1.p3				
comp20142_c0_seq2.p1	sp|P21577|6PGD_SYNE7_6-phosphogluconate_dehydrogenase,_decarboxylating_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=gnd_PE=1_SV=4	2.00E-169	[illegible]	[illegible]
comp20143_c0_seq1.p1	sp|P51152|RAB12_CANFA_Ras-related_protein_Rab-12_(Fragment)_OS=Canis_familiaris_GN=RAB12_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp20146_c0_seq1.p1				
comp20147_c0_seq2.p1	sp|Q9CI80|TRUA_LACLA_tRNA_pseudouridine_synthase_A_OS=Lactococcus_lactis_subsp._lactis_(strain_IL1403)_GN=truA_PE=3_SV=1	4.00E-36	[illegible]	[illegible]
comp20148_c0_seq1.p1				
comp20150_c0_seq1.p1	sp|Q39584|DYL3_CHLRE_Dynein_18_kDa_light_chain,_flagellar_outer_arm_OS=Chlamydomonas_reinhardtii_PE=1_SV=1	3.00E-34	[illegible]	[illegible]
comp20151_c0_seq2.p1	sp|P53042|PPP5_RAT_Serine/threonine-protein_phosphatase_5_OS=Rattus_norvegicus_GN=Ppp5c_PE=2_SV=1	1.00E-162	[illegible]	[illegible]
comp20153_c0_seq2.p1	sp|Q6PC14|RL23_DANRE_60S_ribosomal_protein_L23_OS=Danio_rerio_GN=rpl23_PE=2_SV=1	4.00E-83	[illegible]	[illegible]
comp20155_c0_seq3.p1	sp|O65440|BAME3_ARATH_Leucine-rich_repeat_receptor-like_serine/threonine-protein_kinase_BAM3_OS=Arabidopsis_thaliana_GN=BAM3_PE=2_SV=3	1.00E-17	[illegible]	[illegible]
comp20155_c0_seq4.p1	sp|O65440|BAME3_ARATH_Leucine-rich_repeat_receptor-like_serine/threonine-protein_kinase_BAM3_OS=Arabidopsis_thaliana_GN=BAM3_PE=2_SV=3	1.00E-17	[illegible]	[illegible]
comp20156_c0_seq2.p1				
comp20157_c0_seq1.p1	sp|O89017|LGMN_MOUSE_Legumain_OS=Mus_musculus_GN=Lgmn_PE=1_SV=1	2.00E-84	[illegible]	[illegible]
comp20158_c0_seq2.p1	sp|O22160|TL15A_ARATH_Thylakoid_lumenal_15_kDa_protein_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g44920_PE=1_SV=2	1.00E-27	[illegible]	[illegible]
comp20158_c0_seq3.p1				
comp20158_c0_seq3.p2				
comp20159_c0_seq1.p1	sp|Q54QQ0|IMDH_DICDI_Inosine-5'-monophosphate_dehydrogenase_OS=Dictyostelium_discoideum_GN=impdh_PE=1_SV=1	4.00E-153	[illegible]	[illegible]
comp20162_c0_seq1.p1	sp|Q55D90|CDSA_DICDI_Probable_phosphatidate_cytidylyltransferase_OS=Dictyostelium_discoideum_GN=cdsA_PE=3_SV=1	4.00E-99	[illegible]	[illegible]
comp20163_c0_seq1.p1	sp|Q09225|NRF6_CAEEL_Nose_resistant_to_fluoxetine_protein_6_OS=Caenorhabditis_elegans_GN=nrf-6_PE=1_SV=3	8.00E-24	[illegible]	[illegible]
comp20163_c0_seq1.p3				
comp20165_c0_seq1.p1				
comp20165_c0_seq2.p1				
comp20166_c0_seq1.p1				
comp20167_c0_seq2.p1				
comp20168_c0_seq1.p1	sp|Q9LR78|BSU1_ARATH_Serine/threonine-protein_phosphatase_BSU1_OS=Arabidopsis_thaliana_GN=BSU1_PE=2_SV=2	5.00E-43	[illegible]	[illegible]
comp20172_c0_seq2.p1				
comp20175_c0_seq1.p1	sp|Q7SYD9|INT6_DANRE_Integrator_complex_subunit_6_OS=Danio_rerio_GN=ints6_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp20176_c0_seq1.p2				
comp20177_c0_seq2.p1				
comp20179_c0_seq1.p1				
comp20180_c0_seq1.p1				
comp20181_c0_seq1.p1	sp|Q5REG4|DTX3_PONAB_Protein_deltex-3_OS=Pongo_abelii_GN=DTX3_PE=2_SV=1	1.00E-52	[illegible]	[illegible]
comp20182_c0_seq1.p1	sp|P09195|F16P1_WHEAT_Fructose-1,6-bisphosphatase,_chloroplastic_OS=Triticum_aestivum_GN=FBP_PE=2_SV=1	6.00E-139	[illegible]	[illegible]
comp20182_c0_seq1.p2	sp|Q9BV79|MECR_HUMAN_Trans-2-enoyl-CoA_reductase,_mitochondrial_OS=Homo_sapiens_GN=MECR_PE=1_SV=2	1.00E-15	[illegible]	[illegible]
comp20184_c0_seq1.p1				
comp20187_c0_seq1.p1				
comp20188_c0_seq2.p1	sp|P33333|PLSC_YEAST_Probable_1-acyl-sn-glycerol-3-phosphate_acyltransferase_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=SLC1_PE=1_SV=1	2.00E-17	[illegible]	[illegible]
comp20189_c0_seq1.p1				
comp20190_c0_seq1.p1	sp|Q8LBP4|ALB3_ARATH_Inner_membrane_protein_ALBINO3,_chloroplastic_OS=Arabidopsis_thaliana_GN=ALB3_PE=1_SV=2	7.00E-69	[illegible]	[illegible]
comp20191_c0_seq1.p1	sp|Q9LE82|RAGP1_ARATH_RAN_GTPase-activating_protein_1_OS=Arabidopsis_thaliana_GN=RANGAP1_PE=1_SV=1	2.00E-61	[illegible]	[illegible]
comp20191_c1_seq1.p2				
comp20192_c0_seq1.p1	sp|Q2KIP8|HACD2_BOVIN_3-hydroxyacyl-CoA_dehydratase_2_OS=Bos_taurus_GN=PTPLB_PE=2_SV=2	7.00E-32	[illegible]	[illegible]
comp20192_c0_seq2.p1	sp|Q2KIP8|HACD2_BOVIN_3-hydroxyacyl-CoA_dehydratase_2_OS=Bos_taurus_GN=PTPLB_PE=2_SV=2	1.00E-25	[illegible]	[illegible]
comp20193_c0_seq1.p1				
comp20195_c0_seq1.p1	sp|A8WMY3|HKE41_CAEBR_Histidine-rich_membrane_protein_KE4_homolog_1_OS=Caenorhabditis_briggsae_GN=hke-4.1_PE=3_SV=2	5.00E-23	[illegible]	[illegible]
comp20196_c0_seq1.p1				
comp20197_c0_seq1.p1				
comp20198_c0_seq1.p1				
comp20198_c1_seq1.p1				
comp20198_c1_seq3.p1				
comp20199_c0_seq2.p2	sp|P48588|RS25_DROME_40S_ribosomal_protein_S25_OS=Drosophila_melanogaster_GN=RpS25_PE=1_SV=3	1.00E-31	[illegible]	[illegible]
comp20200_c0_seq1.p1	sp|O60573|IF4E2_HUMAN_Eukaryotic_translation_initiation_factor_4E_type_2_OS=Homo_sapiens_GN=EIF4E2_PE=1_SV=1	4.00E-54	[illegible]	[illegible]
comp20202_c0_seq1.p1				
comp20204_c0_seq2.p1				
comp20205_c0_seq1.p1				
comp20205_c1_seq1.p1				
comp20206_c0_seq1.p1				
comp20207_c0_seq2.p1				
comp20208_c0_seq1.p1	sp|Q17N71|K0664_AEDAE_Protein_KIAA0664_homolog_OS=Aedes_aegypti_GN=AAEL000794_PE=3_SV=1	2.00E-39	[illegible]	[illegible]
comp20209_c0_seq1.p1	sp|A7SLC8|NAT9_NEMVE_N-acetyltransferase_9-like_protein_OS=Nematostella_vectensis_GN=nat9_PE=3_SV=1	2.00E-51	[illegible]	[illegible]
comp20209_c0_seq2.p1	sp|Q9BTE0|NAT9_HUMAN_N-acetyltransferase_9_OS=Homo_sapiens_GN=NAT9_PE=2_SV=1	7.00E-35	[illegible]	[illegible]
comp20209_c0_seq3.p1	sp|Q9BTE0|NAT9_HUMAN_N-acetyltransferase_9_OS=Homo_sapiens_GN=NAT9_PE=2_SV=1	6.00E-38	[illegible]	[illegible]
comp20212_c0_seq1.p1				
comp20212_c0_seq2.p1				
comp20214_c0_seq1.p1				
comp20218_c0_seq1.p1				
comp20219_c1_seq1.p1				
comp20220_c0_seq1.p1				
comp20221_c0_seq1.p1				
comp20222_c0_seq1.p1	sp|Q1D7Y2|FOLD2_MYXXD_Bifunctional_protein_FolD_2_OS=Myxococcus_xanthus_(strain_DK_1622)_GN=folD2_PE=3_SV=1	7.00E-72	[illegible]	[illegible]
comp20223_c0_seq1.p1				
comp20225_c0_seq3.p1				
comp20228_c0_seq1.p1	sp|Q9V730|EXT1_DROME_Exostosin-1_OS=Drosophila_melanogaster_GN=ttv_PE=1_SV=1	1.00E-23	[illegible]	[illegible]
comp2023_c0_seq1.p1	sp|P09980|REP_ECOLI_ATP-dependent_DNA_helicase_rep_OS=Escherichia_coli_(strain_K12)_GN=rep_PE=1_SV=3	2.00E-73	[illegible]	[illegible]
comp20232_c0_seq1.p1	sp|Q9SAB1|HSP7Q_ARATH_Heat_shock_70_kDa_protein_16_OS=Arabidopsis_thaliana_GN=HSP70-16_PE=2_SV=1	1.00E-49	[illegible]	[illegible]
comp20235_c0_seq1.p2	sp|Q8AWF2|NACA_ORENI_Nascent_polypeptide-associated_complex_subunit_alpha_OS=Oreochromis_niloticus_GN=naca_PE=2_SV=1	4.00E-17	[illegible]	[illegible]
comp20236_c0_seq1.p1	sp|Q7ZZ25|ATD1A_DANRE_ATPase_family_AAA_domain-containing_protein_1-A_OS=Danio_rerio_GN=atad1a_PE=2_SV=2	2.00E-59	[illegible]	[illegible]
comp20236_c0_seq1.p2	sp|Q9DB26|PHYD1_MOUSE_Phytanoyl-CoA_dioxygenase_domain-containing_protein_1_OS=Mus_musculus_GN=Phyhd1_PE=2_SV=2	3.00E-66	[illegible]	[illegible]
comp20236_c0_seq2.p1	sp|Q7ZZ25|ATD1A_DANRE_ATPase_family_AAA_domain-containing_protein_1-A_OS=Danio_rerio_GN=atad1a_PE=2_SV=2	2.00E-59	[illegible]	[illegible]
comp20236_c0_seq2.p2	sp|Q0IIB1|PHYD1_BOVIN_Phytanoyl-CoA_dioxygenase_domain-containing_protein_1_OS=Bos_taurus_GN=PHYHD1_PE=2_SV=1	1.00E-56	[illegible]	[illegible]
comp20237_c0_seq1.p1				
comp20239_c0_seq2.p1				
comp2024_c0_seq1.p1	sp|Q83JV7|AAS_SHIFL_Bifunctional_protein_aas_OS=Shigella_flexneri_GN=aas_PE=3_SV=1	1.00E-94	[illegible]	[illegible]
comp20240_c0_seq1.p1				
comp20240_c0_seq2.p1				
comp20243_c0_seq1.p1	sp|Q55GV3|PAKC_DICDI_Serine/threonine-protein_kinase_pakC_OS=Dictyostelium_discoideum_GN=pakC_PE=1_SV=2	3.00E-78	[illegible]	[illegible]
comp20244_c0_seq2.p1				
comp20245_c0_seq1.p2	sp|Q9NE83|RS6_LEIMA_40S_ribosomal_protein_S6_OS=Leishmania_major_GN=RPS6_PE=3_SV=1	2.00E-58	[illegible]	[illegible]
comp20248_c0_seq2.p1	sp|Q8H124|Y2446_ARATH_Uncharacterized_protein_At2g34460,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g34460_PE=1_SV=1	8.00E-14	[illegible]	[illegible]
comp20251_c1_seq1.p1				
comp20253_c0_seq1.p1				
comp20255_c0_seq1.p2				
comp20255_c0_seq2.p1				
comp20256_c0_seq1.p1	sp|Q8GYC7|PGL1B_ARATH_PGR5-like_protein_1B,_chloroplastic_OS=Arabidopsis_thaliana_GN=PGRL1B_PE=1_SV=1	1.00E-35	[illegible]	[illegible]
comp20258_c0_seq1.p1	sp|A8CEP3|CALM_SACJA_Calmodulin_OS=Saccharina_japonica_GN=cam_PE=2_SV=1	6.00E-102	[illegible]	[illegible]
comp20259_c0_seq2.p1				
comp20260_c0_seq1.p1	sp|Q9C5Z2|EIF3H_ARATH_Eukaryotic_translation_initiation_factor_3_subunit_H_OS=Arabidopsis_thaliana_GN=TIF3H1_PE=2_SV=2	8.00E-87	[illegible]	[illegible]
comp20261_c0_seq2.p1				
comp20261_c0_seq2.p2	sp|B3ETC6|ERA_AMOA5_GTPase_Era_OS=Amoebophilus_asiaticus_(strain_5a2)_GN=era_PE=3_SV=1	8.00E-85	[illegible]	[illegible]
comp20262_c1_seq1.p1	sp|Q8LFY8|ATL54_ARATH_RING-H2_finger_protein_ATL54_OS=Arabidopsis_thaliana_GN=ATL54_PE=2_SV=2	1.00E-11	[illegible]	[illegible]
comp20264_c0_seq3.p1				
comp20264_c0_seq4.p1				
comp20266_c0_seq2.p1				
comp20270_c0_seq1.p1				
comp20271_c0_seq1.p1				
comp20272_c0_seq1.p1				
comp20272_c0_seq1.p3				
comp20272_c0_seq2.p1				
comp20273_c0_seq1.p1	sp|Q2TGJ1|ZDH18_RAT_Palmitoyltransferase_ZDHHC18_OS=Rattus_norvegicus_GN=Zdhhc18_PE=2_SV=1	8.00E-17	[illegible]	[illegible]
comp20276_c0_seq1.p1	sp|P0AER5|GLTK_ECOLI_Glutamate/aspartate_transport_system_permease_protein_gltK_OS=Escherichia_coli_(strain_K12)_GN=gltK_PE=1_SV=1	1.00E-72	[illegible]	[illegible]
comp20278_c0_seq1.p1				
comp20279_c0_seq1.p2				
comp20280_c0_seq1.p1				
comp20280_c0_seq2.p1				
comp20281_c0_seq1.p2				
comp20282_c0_seq1.p1				
comp20283_c0_seq1.p1	sp|Q119S8|RL10_TRIEI_50S_ribosomal_protein_L10_OS=Trichodesmium_erythraeum_(strain_IMS101)_GN=rplJ_PE=3_SV=1	6.00E-17	[illegible]	[illegible]
comp20286_c0_seq1.p1	sp|P49469|CHLI_ODOSI_Magnesium-chelatase_subunit_chlI_OS=Odontella_sinensis_GN=chlI_PE=3_SV=1	4.00E-172	[illegible]	[illegible]
comp20287_c0_seq1.p1				
comp20290_c0_seq1.p1	sp|P40215|NDH1_YEAST_External_NADH-ubiquinone_oxidoreductase_1,_mitochondrial_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=NDE1_PE=1_SV=1	8.00E-77	[illegible]	[illegible]
comp20291_c0_seq1.p1				
comp20292_c0_seq1.p1				
comp20292_c0_seq3.p1	sp|Q7YZH1|RNO_DROME_PHD_finger_protein_rhinoceros_OS=Drosophila_melanogaster_GN=rno_PE=1_SV=1	2.00E-28	[illegible]	[illegible]
comp20294_c0_seq1.p1	sp|Q9P7G4|OMA1_SCHPO_Mitochondrial_metalloendopeptidase_OMA1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=oma1_PE=2_SV=1	4.00E-46	[illegible]	[illegible]
comp20295_c0_seq1.p1				
comp20296_c0_seq2.p2				
comp20296_c0_seq3.p1				
comp20299_c0_seq1.p1	sp|Q3UGF1|WDR19_MOUSE_WD_repeat-containing_protein_19_OS=Mus_musculus_GN=Wdr19_PE=1_SV=1	4.00E-12	[illegible]	[illegible]
comp20300_c0_seq1.p1				
comp20302_c0_seq1.p1	sp|Q1RJT3|ODP2_RICBR_Dihydrolipoyllysine-residue_acetyltransferase_component_of_pyruvate_dehydrogenase_complex_OS=Rickettsia_bellii_(strain_RML369-C)_GN=pdhC_PE=3_SV=1	7.00E-61	[illegible]	[illegible]
comp20303_c0_seq1.p1				
comp20303_c0_seq3.p2	sp|P29763|RLA1_CHLRE_60S_acidic_ribosomal_protein_P1_OS=Chlamydomonas_reinhardtii_PE=3_SV=1	4.00E-11	[illegible]	[illegible]
comp20304_c0_seq1.p1				
comp20305_c0_seq1.p1				
comp20305_c0_seq2.p1				
comp20309_c0_seq1.p1	sp|Q9BVG8|KIFC3_HUMAN_Kinesin-like_protein_KIFC3_OS=Homo_sapiens_GN=KIFC3_PE=1_SV=4	1.00E-91	[illegible]	[illegible]
comp20310_c0_seq1.p1	sp|B0BNA9|CB029_RAT_UPF0760_protein_C2orf29_homolog_OS=Rattus_norvegicus_PE=2_SV=1	5.00E-116	[illegible]	[illegible]
comp20312_c0_seq1.p1				
comp20313_c0_seq1.p1	sp|P94170|CAH_NOSS1_Carbonic_anhydrase_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=ecaA_PE=3_SV=1	2.00E-24	[illegible]	[illegible]
comp20313_c0_seq2.p1				
comp20314_c0_seq1.p1	sp|Q55669|CTPA_SYNY3_Carboxyl-terminal-processing_protease_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=ctpA_PE=3_SV=1	7.00E-66	[illegible]	[illegible]
comp20319_c0_seq1.p1	sp|Q9SP37|SAHH_LUPLU_Adenosylhomocysteinase_OS=Lupinus_luteus_GN=SAHH_PE=1_SV=1	0	[illegible]	[illegible]
comp20321_c1_seq1.p1				
comp20321_c1_seq2.p1				
comp20323_c0_seq1.p1	sp|Q9P1Q0|VPS54_HUMAN_Vacuolar_protein_sorting-associated_protein_54_OS=Homo_sapiens_GN=VPS54_PE=1_SV=2	9.00E-33	[illegible]	[illegible]
comp20324_c0_seq1.p1				
comp20326_c0_seq2.p1				
comp20327_c0_seq2.p1				
comp20330_c0_seq1.p1	sp|Q6AYJ1|RECQ1_RAT_ATP-dependent_DNA_helicase_Q1_OS=Rattus_norvegicus_GN=Recql_PE=2_SV=1	2.00E-129	[illegible]	[illegible]
comp20330_c0_seq1.p4				
comp20333_c0_seq1.p1	sp|O43093|KINH_SYNRA_Kinesin_heavy_chain_OS=Syncephalastrum_racemosum_PE=2_SV=1	8.00E-54	[illegible]	[illegible]
comp20334_c0_seq1.p2				
comp20336_c0_seq1.p1				
comp20337_c0_seq2.p1				
comp20337_c0_seq3.p1				
comp20338_c0_seq1.p1	sp|P54641|VA0D_DICDI_V-type_proton_ATPase_subunit_d_OS=Dictyostelium_discoideum_GN=vatD-1_PE=1_SV=2	8.00E-109	[illegible]	[illegible]
comp20339_c0_seq1.p1				
comp20341_c0_seq1.p1				
comp20342_c0_seq1.p1				
comp20342_c0_seq2.p1	sp|Q07G10|ALKB8_XENTR_Alkylated_DNA_repair_protein_alkB_homolog_8_OS=Xenopus_tropicalis_GN=alkbh8_PE=2_SV=2	5.00E-25	[illegible]	[illegible]
comp20343_c0_seq1.p1	sp|Q7Y0D4|TR164_ORYSJ_Thioredoxin-like_protein_HCF164,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=Os03g0767500_PE=2_SV=1	2.00E-28	[illegible]	[illegible]
comp20346_c0_seq1.p1				
comp20348_c0_seq2.p1	sp|Q91WM3|U3IP2_MOUSE_U3_small_nucleolar_RNA-interacting_protein_2_OS=Mus_musculus_GN=Rrp9_PE=1_SV=1	1.00E-103	[illegible]	[illegible]
comp20348_c0_seq2.p2	sp|Q0P5A1|DCTN3_BOVIN_Dynactin_subunit_3_OS=Bos_taurus_GN=DCTN3_PE=2_SV=1	2.00E-11	[illegible]	[illegible]
comp20349_c0_seq1.p1	sp|Q6UVJ0|SAS6_HUMAN_Spindle_assembly_abnormal_protein_6_homolog_OS=Homo_sapiens_GN=SASS6_PE=1_SV=1	4.00E-35	[illegible]	[illegible]
comp2035_c0_seq1.p1	sp|Q31Z24|CCMA_SHIBS_Cytochrome_c_biogenesis_ATP-binding_export_protein_CcmA_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=ccmA_PE=3_SV=2	1.00E-120	[illegible]	[illegible]
comp20351_c0_seq1.p1				
comp20352_c0_seq1.p1				
comp20353_c0_seq2.p1	sp|Q39054|CNX1_ARATH_Molybdopterin_biosynthesis_protein_CNX1_OS=Arabidopsis_thaliana_GN=CNX1_PE=1_SV=2	3.00E-105	[illegible]	[illegible]
comp20354_c0_seq1.p1	sp|O49078|UCRIA_FRIAG_Cytochrome_b6-f_complex_iron-sulfur_subunit,_chloroplastic_OS=Fritillaria_agrestis_GN=petC_PE=2_SV=1	3.00E-41	[illegible]	[illegible]
comp20356_c0_seq1.p1	sp|Q0EEE2|PTHD3_MOUSE_Patched_domain-containing_protein_3_OS=Mus_musculus_GN=Ptchd3_PE=1_SV=1	2.00E-17	[illegible]	[illegible]
comp20356_c0_seq2.p1	sp|Q0EEE2|PTHD3_MOUSE_Patched_domain-containing_protein_3_OS=Mus_musculus_GN=Ptchd3_PE=1_SV=1	2.00E-17	[illegible]	[illegible]
comp20357_c0_seq2.p1				
comp20360_c0_seq2.p1	sp|Q6DRG1|RBM42_DANRE_RNA-binding_protein_42_OS=Danio_rerio_GN=rbm42_PE=2_SV=2	2.00E-33	[illegible]	[illegible]
comp20361_c1_seq1.p1				
comp20363_c0_seq1.p1	sp|Q6K548|VDAC1_ORYSJ_Mitochondrial_outer_membrane_protein_porin_1_OS=Oryza_sativa_subsp._japonica_GN=VDAC1_PE=1_SV=3	7.00E-14	[illegible]	[illegible]
comp20365_c0_seq1.p1	sp|Q6CVH3|NHP6_KLULA_Non-histone_chromosomal_protein_6_OS=Kluyveromyces_lactis_(strain_ATCC_8585_/_CBS_2359_/_DSM_70799_/_NBRC_1267_/_NRRL_Y-1140_/_WM37)_GN=NHP6_PE=3_SV=1	3.00E-11	[illegible]	[illegible]
comp20366_c0_seq1.p1				
comp20366_c0_seq2.p1				
comp20367_c0_seq1.p1	sp|P76403|YEGQ_ECOLI_Uncharacterized_protease_yegQ_OS=Escherichia_coli_(strain_K12)_GN=yegQ_PE=3_SV=1	3.00E-72	[illegible]	[illegible]
comp20369_c0_seq2.p1	sp|Q9P0U3|SENP1_HUMAN_Sentrin-specific_protease_1_OS=Homo_sapiens_GN=SENP1_PE=1_SV=2	1.00E-41	[illegible]	[illegible]
comp20370_c0_seq1.p1				
comp20374_c0_seq1.p1	sp|Q9FHN8|KCBP_ARATH_Kinesin-like_calmodulin-binding_protein_OS=Arabidopsis_thaliana_GN=KCBP_PE=1_SV=1	1.00E-48	[illegible]	[illegible]
comp20378_c0_seq1.p1				
comp20378_c0_seq2.p1				
comp20379_c0_seq1.p1				
comp20380_c0_seq1.p1				
comp20383_c0_seq1.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	9.00E-23	[illegible]	[illegible]
comp20383_c0_seq2.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	8.00E-23	[illegible]	[illegible]
comp20384_c0_seq1.p1				
comp20385_c0_seq1.p1	sp|P91622|PDK_DROME_[Pyruvate_dehydrogenase_[lipoamide]]_kinase,_mitochondrial_OS=Drosophila_melanogaster_GN=Pdk_PE=2_SV=2	3.00E-49	[illegible]	[illegible]
comp20386_c0_seq1.p1	sp|Q9HDY1|ASE1_SCHPO_Anaphase_spindle_elongation_protein_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ase1_PE=1_SV=1	1.00E-26	[illegible]	[illegible]
comp20387_c0_seq1.p1				
comp20389_c0_seq1.p1				
comp20391_c0_seq1.p1				
comp20391_c0_seq2.p1				
comp20393_c0_seq2.p1				
comp20397_c0_seq1.p1				
comp20398_c0_seq1.p1	sp|Q8N3A8|PARP8_HUMAN_Poly_[ADP-ribose]_polymerase_8_OS=Homo_sapiens_GN=PARP8_PE=1_SV=1	4.00E-16	[illegible]	[illegible]
comp20399_c0_seq1.p1				
comp20401_c0_seq1.p1				
comp20401_c0_seq2.p1				
comp20402_c0_seq2.p1				
comp20404_c0_seq2.p1	sp|Q7TSV9|CP048_MOUSE_Uncharacterized_protein_C16orf48_homolog_OS=Mus_musculus_PE=2_SV=1	1.00E-12	[illegible]	[illegible]
comp20406_c0_seq1.p1	sp|Q8N6V9|TEX9_HUMAN_Testis-expressed_sequence_9_protein_OS=Homo_sapiens_GN=TEX9_PE=2_SV=1	1.00E-34		
comp20407_c0_seq2.p1	sp|Q1LZ95|IDI1_BOVIN_Isopentenyl-diphosphate_Delta-isomerase_1_OS=Bos_taurus_GN=IDI1_PE=2_SV=2	6.00E-58	[illegible]	[illegible]
comp20409_c0_seq1.p1				
comp20411_c0_seq1.p2	sp|O23310|NFYB3_ARATH_Nuclear_transcription_factor_Y_subunit_B-3_OS=Arabidopsis_thaliana_GN=NFYB3_PE=2_SV=1	1.00E-51	[illegible]	[illegible]
comp20412_c0_seq1.p1	sp|Q8WUQ7|CS029_HUMAN_Uncharacterized_protein_C19orf29_OS=Homo_sapiens_GN=C19orf29_PE=1_SV=3	1.00E-61	[illegible]	[illegible]
comp20413_c0_seq1.p1	sp|Q29RZ2|PPWD1_BOVIN_Peptidylprolyl_isomerase_domain_and_WD_repeat-containing_protein_1_OS=Bos_taurus_GN=PPWD1_PE=2_SV=1	0	[illegible]	[illegible]
comp20413_c0_seq1.p2				
comp20414_c0_seq1.p1	sp|Q71VM4|IMA1A_ORYSJ_Importin_subunit_alpha-1a_OS=Oryza_sativa_subsp._japonica_GN=Os01g0253300_PE=1_SV=2	4.00E-80	[illegible]	[illegible]
comp20418_c0_seq1.p1	sp|P33025|PSUG_ECOLI_Pseudouridine-5'-phosphate_glycosidase_OS=Escherichia_coli_(strain_K12)_GN=psuG_PE=1_SV=1	4.00E-101	[illegible]	[illegible]
comp20419_c0_seq2.p1	sp|P52643|LDHD_ECOLI_D-lactate_dehydrogenase_OS=Escherichia_coli_(strain_K12)_GN=ldhA_PE=1_SV=1	2.00E-80	[illegible]	[illegible]
comp20421_c0_seq1.p1	sp|Q9CQ33|LZTR1_MOUSE_Leucine-zipper-like_transcriptional_regulator_1_OS=Mus_musculus_GN=Lztr1_PE=2_SV=2	2.00E-45	[illegible]	[illegible]
comp20423_c0_seq1.p1				
comp20427_c0_seq1.p1				
comp20430_c1_seq1.p1				
comp20431_c0_seq1.p1	sp|Q42404|RU17_ARATH_U1_small_nuclear_ribonucleoprotein_70_kDa_OS=Arabidopsis_thaliana_GN=RNU1_PE=1_SV=1	1.00E-39	[illegible]	[illegible]
comp20433_c0_seq1.p1				
comp20434_c0_seq4.p1				
comp20440_c0_seq2.p1				
comp20441_c0_seq1.p1	sp|Q9CYW4|HDHD3_MOUSE_Haloacid_dehalogenase-like_hydrolase_domain-containing_protein_3_OS=Mus_musculus_GN=Hdhd3_PE=2_SV=1	1.00E-15	[illegible]	[illegible]
comp20445_c0_seq1.p1				
comp20446_c0_seq1.p1	sp|Q5U8Z7|PPID_AMAMU_Peptidyl-prolyl_cis-trans_isomerase_D_OS=Amanita_muscaria_GN=Cyp40_PE=2_SV=1	3.00E-46	[illegible]	[illegible]
comp20447_c0_seq1.p1				
comp20451_c0_seq1.p2	sp|Q55FN7|ODBB_DICDI_2-oxoisovalerate_dehydrogenase_subunit_beta,_mitochondrial_OS=Dictyostelium_discoideum_GN=bkdB_PE=3_SV=1	2.00E-167	[illegible]	[illegible]
comp20452_c0_seq1.p1				
comp20452_c0_seq2.p1				
comp20454_c0_seq1.p1	sp|Q9STR4|1A17_ARATH_1-aminocyclopropane-1-carboxylate_synthase_7_OS=Arabidopsis_thaliana_GN=ACS7_PE=1_SV=1	8.00E-55	[illegible]	[illegible]
comp20455_c0_seq1.p1				
comp20456_c0_seq1.p1	sp|P73555|Y875_SYNY3_Uncharacterized_membrane_protein_sll0875_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll0875_PE=3_SV=1	4.00E-12	[illegible]	[illegible]
comp20456_c0_seq2.p1	sp|P73555|Y875_SYNY3_Uncharacterized_membrane_protein_sll0875_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll0875_PE=3_SV=1	2.00E-50	[illegible]	[illegible]
comp20457_c0_seq1.p1	sp|Q32PZ3|UN45A_RAT_Protein_unc-45_homolog_A_OS=Rattus_norvegicus_GN=Unc45a_PE=2_SV=1	3.00E-16	[illegible]	[illegible]
comp20458_c0_seq1.p1	sp|Q44879|CTPA_BARBK_Carboxy-terminal-processing_protease_OS=Bartonella_bacilliformis_(strain_ATCC_35685_/_KC583)_GN=ctpA_PE=3_SV=1	8.00E-37	[illegible]	[illegible]
comp20458_c0_seq3.p1	sp|Q44879|CTPA_BARBK_Carboxy-terminal-processing_protease_OS=Bartonella_bacilliformis_(strain_ATCC_35685_/_KC583)_GN=ctpA_PE=3_SV=1	6.00E-37	[illegible]	[illegible]
comp20459_c0_seq1.p1	sp|P15454|KGUA_YEAST_Guanylate_kinase_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=GUK1_PE=1_SV=2	3.00E-12	[illegible]	[illegible]
comp20460_c0_seq1.p1				
comp20464_c0_seq2.p1	sp|Q08062|MDHC_MAIZE_Malate_dehydrogenase,_cytoplasmic_OS=Zea_mays_PE=2_SV=2	1.00E-94	[illegible]	[illegible]
comp20465_c0_seq1.p1	sp|Q9LMX4|PPA1_ARATH_Probable_inactive_purple_acid_phosphatase_1_OS=Arabidopsis_thaliana_GN=PAP1_PE=1_SV=1	2.00E-79	[illegible]	[illegible]
comp20466_c0_seq1.p1				
comp20466_c0_seq2.p2				
comp20466_c0_seq2.p3				
comp20468_c0_seq1.p1	sp|P30268|Y2045_BACPE_Uncharacterized_aminotransferase_BpOF4_10225_OS=Bacillus_pseudofirmus_(strain_OF4)_GN=BpOF4_10225_PE=3_SV=2	6.00E-82	[illegible]	[illegible]
comp20469_c0_seq1.p1				
comp20470_c0_seq1.p1				
comp20472_c0_seq1.p1				
comp20474_c0_seq2.p1	sp|Q8VYP6|NOL9_ARATH_Polynucleotide_5'-hydroxyl-kinase_NOL9_OS=Arabidopsis_thaliana_GN=At5g11010_PE=2_SV=1	7.00E-36	[illegible]	[illegible]
comp20475_c0_seq2.p1	sp|P23398|UBIQP_STRPU_Polyubiquitin_(Fragment)_OS=Strongylocentrotus_purpuratus_PE=2_SV=2	9.00E-34	[illegible]	[illegible]
comp20477_c0_seq1.p1	sp|Q9H8M5|CNNM2_HUMAN_Metal_transporter_CNNM2_OS=Homo_sapiens_GN=CNNM2_PE=1_SV=2	1.00E-57	[illegible]	[illegible]
comp20478_c0_seq1.p1				
comp20478_c0_seq2.p1				
comp20481_c0_seq1.p1	sp|Q7XHN8|P2C61_ORYSJ_Probable_protein_phosphatase_2C_61_OS=Oryza_sativa_subsp._japonica_GN=Os07g0114000_PE=2_SV=1	5.00E-14	[illegible]	[illegible]
comp20482_c0_seq1.p1				
comp20484_c0_seq1.p1				
comp20485_c0_seq1.p1				
comp20486_c0_seq1.p1	sp|Q9AKH1|FER2_RICRI_2Fe-2S_ferredoxin_OS=Rickettsia_rickettsii_GN=fdxB_PE=3_SV=1	1.00E-15	[illegible]	[illegible]
comp20487_c0_seq3.p2				
comp20489_c0_seq1.p1	sp|Q3SZK1|AAMP_BOVIN_Angio-associated_migratory_cell_protein_OS=Bos_taurus_GN=AAMP_PE=2_SV=1	7.00E-64	[illegible]	[illegible]
comp20489_c0_seq2.p1				
comp20490_c0_seq2.p1	sp|P29677|MPPA_SOLTU_Mitochondrial-processing_peptidase_subunit_alpha_OS=Solanum_tuberosum_GN=MPP_PE=1_SV=1	2.00E-26	[illegible]	[illegible]
comp20491_c0_seq1.p1	sp|Q54JC0|CMBB_DICDI_Calmodulin-binding_protein_CmbB_OS=Dictyostelium_discoideum_GN=cmbB_PE=1_SV=1	3.00E-23	[illegible]	[illegible]
comp20492_c0_seq1.p1	sp|P0A9D7|CYSE_SHIFL_Serine_acetyltransferase_OS=Shigella_flexneri_GN=cysE_PE=3_SV=1	6.00E-151	[illegible]	[illegible]
comp20493_c0_seq2.p1				
comp20494_c0_seq1.p2				
comp20496_c0_seq1.p1	sp|Q5T280|CI114_HUMAN_Uncharacterized_protein_C9orf114_OS=Homo_sapiens_GN=C9orf114_PE=1_SV=3	4.00E-96	[illegible]	[illegible]
comp20497_c0_seq1.p1	sp|Q9ZUC1|QORL_ARATH_Quinone_oxidoreductase-like_protein_At1g23740,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g23740_PE=1_SV=2	3.00E-16	[illegible]	[illegible]
comp20498_c0_seq1.p2	sp|P85515|ACTZ_RAT_Alpha-centractin_OS=Rattus_norvegicus_GN=Actr1a_PE=1_SV=1	5.00E-166	[illegible]	[illegible]
comp20499_c0_seq1.p1	sp|Q38931|FKB62_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP62_OS=Arabidopsis_thaliana_GN=FKBP62_PE=1_SV=2	3.00E-31	[illegible]	[illegible]
comp20499_c1_seq1.p1	sp|Q43207|FKB70_WHEAT_70_kDa_peptidyl-prolyl_isomerase_OS=Triticum_aestivum_GN=FKBP70_PE=1_SV=1	8.00E-28	[illegible]	[illegible]
comp20501_c0_seq1.p1				
comp20502_c0_seq1.p1				
comp20502_c0_seq2.p1	sp|Q9LK65|Y3307_ARATH_Putative_DUF21_domain-containing_protein_At3g13070,_chloroplastic_OS=Arabidopsis_thaliana_GN=CBSDUFCH1_PE=4_SV=1	4.00E-73	[illegible]	[illegible]
comp20503_c0_seq2.p1				
comp20503_c0_seq2.p3				
comp20504_c0_seq1.p1				
comp20505_c0_seq1.p1				
comp20507_c0_seq2.p2				
comp20510_c0_seq1.p1	sp|Q6H6D2|HEM3_ORYSJ_Porphobilinogen_deaminase,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=HEMC_PE=2_SV=1	2.00E-126	[illegible]	[illegible]
comp20512_c0_seq2.p1				
comp20515_c0_seq2.p1	sp|Q53P54|PHT46_ORYSJ_Probable_anion_transporter_6_OS=Oryza_sativa_subsp._japonica_GN=PHT4;6_PE=2_SV=1	7.00E-86	[illegible]	[illegible]
comp20518_c0_seq1.p1				
comp20520_c0_seq1.p1				
comp20524_c0_seq1.p1				
comp20527_c0_seq1.p1				
comp20527_c0_seq1.p2				
comp20531_c1_seq1.p1	sp|Q6DCZ9|UBC12_XENLA_NEDD8-conjugating_enzyme_Ubc12_OS=Xenopus_laevis_GN=ube2m_PE=2_SV=1	3.00E-20	[illegible]	[illegible]
comp20531_c1_seq2.p1	sp|Q54TI6|UBC12_DICDI_NEDD8-conjugating_enzyme_Ubc12_OS=Dictyostelium_discoideum_GN=ube2m_PE=3_SV=1	3.00E-21	[illegible]	[illegible]
comp20532_c0_seq1.p1				
comp20532_c0_seq3.p1				
comp20533_c0_seq1.p1				
comp20533_c0_seq1.p2				
comp20533_c0_seq2.p1				
comp20533_c0_seq2.p2				
comp20533_c0_seq2.p6				
comp20534_c0_seq1.p1				
comp20536_c0_seq2.p1	sp|P46226|TPIS_SECCE_Triosephosphate_isomerase,_cytosolic_OS=Secale_cereale_PE=2_SV=3	4.00E-90	[illegible]	[illegible]
comp20538_c0_seq2.p1	sp|B5XB24|TMM85_SALSA_Transmembrane_protein_85_OS=Salmo_salar_GN=tmem85_PE=2_SV=1	4.00E-21	[illegible]	[illegible]
comp20540_c0_seq1.p1				
comp20541_c0_seq1.p1				
comp20542_c0_seq1.p1	sp|Q8GSD9|PHT12_ORYSJ_Inorganic_phosphate_transporter_1-2_OS=Oryza_sativa_subsp._japonica_GN=PTH1-2_PE=2_SV=1	6.00E-22	[illegible]	[illegible]
comp20544_c0_seq1.p1				
comp20552_c0_seq1.p1	sp|Q9ULJ7|ANR50_HUMAN_Ankyrin_repeat_domain-containing_protein_50_OS=Homo_sapiens_GN=ANKRD50_PE=1_SV=4	2.00E-70	GO:0005515	[illegible]
comp20552_c0_seq2.p1				
comp20554_c0_seq1.p1	sp|Q7TNH6|NPHP3_MOUSE_Nephrocystin-3_OS=Mus_musculus_GN=Nphp3_PE=1_SV=2	4.00E-45	[illegible]	[illegible]
comp20554_c0_seq2.p1	sp|Q7TNH6|NPHP3_MOUSE_Nephrocystin-3_OS=Mus_musculus_GN=Nphp3_PE=1_SV=2	3.00E-45	[illegible]	[illegible]
comp20555_c0_seq1.p1	sp|Q9SIC9|PP178_ARATH_Pentatricopeptide_repeat-containing_protein_At2g31400,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g31400_PE=2_SV=1	6.00E-30	[illegible]	[illegible]
comp20557_c0_seq1.p1	sp|P0A9D1|GLPX_SHIFL_Fructose-1,6-bisphosphatase_class_2_OS=Shigella_flexneri_GN=glpX_PE=3_SV=1	9.00E-88	[illegible]	[illegible]
comp20558_c0_seq1.p1				
comp20558_c0_seq2.p1				
comp20560_c0_seq1.p1				
comp20561_c0_seq1.p1				
comp20561_c0_seq2.p1				
comp20562_c0_seq1.p1				
comp20563_c0_seq1.p1				
comp20568_c0_seq1.p1				
comp20569_c0_seq2.p1	sp|Q7ZW86|CWC27_DANRE_Peptidyl-prolyl_cis-trans_isomerase_CWC27_homolog_OS=Danio_rerio_GN=cwc27_PE=2_SV=1	9.00E-67	[illegible]	[illegible]
comp20570_c0_seq1.p1	sp|Q56YP2|PI5K1_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_1_OS=Arabidopsis_thaliana_GN=PIP5K1_PE=1_SV=1	3.00E-22	[illegible]	[illegible]
comp20572_c0_seq1.p1				
comp20572_c1_seq1.p1	sp|Q55C77|FCL_DICDI_GDP-L-fucose_synthase_OS=Dictyostelium_discoideum_GN=ger_PE=3_SV=1	1.00E-144	[illegible]	[illegible]
comp20573_c0_seq1.p1				
comp20574_c0_seq1.p1	sp|Q6DG32|S2536_DANRE_Solute_carrier_family_25_member_36-A_OS=Danio_rerio_GN=slc25a36a_PE=2_SV=1	4.00E-63	[illegible]	[illegible]
comp20575_c0_seq1.p1	sp|Q9CQM0|NICN1_MOUSE_Nicolin-1_OS=Mus_musculus_GN=Nicn1_PE=1_SV=1	3.00E-11	[illegible]	[illegible]
comp20575_c0_seq2.p1	sp|Q9CQM0|NICN1_MOUSE_Nicolin-1_OS=Mus_musculus_GN=Nicn1_PE=1_SV=1	3.00E-11	[illegible]	[illegible]
comp20580_c0_seq2.p1	sp|Q94502|GANAB_DICDI_Neutral_alpha-glucosidase_AB_OS=Dictyostelium_discoideum_GN=modA_PE=3_SV=1	0	[illegible]	[illegible]
comp20582_c0_seq2.p1				
comp20583_c0_seq2.p1	sp|Q8QFR4|MD2L2_XENLA_Mitotic_spindle_assembly_checkpoint_protein_MAD2B_OS=Xenopus_laevis_GN=mad2l2_PE=1_SV=1	4.00E-20	[illegible]	[illegible]
comp20583_c0_seq2.p2				
comp20588_c0_seq1.p1	sp|Q8W0E4|SAT1_ORYSJ_Probable_serine_acetyltransferase_1_OS=Oryza_sativa_subsp._japonica_GN=SAT1_PE=2_SV=1	7.00E-82	[illegible]	[illegible]
comp20592_c0_seq1.p1				
comp20593_c0_seq1.p1				
comp20594_c0_seq2.p1	sp|Q72EK2|MSRB_DESVH_Peptide_methionine_sulfoxide_reductase_MsrB_OS=Desulfovibrio_vulgaris_(strain_Hildenborough_/_ATCC_29579_/_NCIMB_8303)_GN=msrB_PE=3_SV=1	2.00E-34	[illegible]	[illegible]

comp20595_c0_seq1.p1	sp|Q5ZI13|DNJC3_CHICK_DnaJ_homolog_subfamily_C_member_3_OS=Gallus_gallus_GN=DNAJC3_PE=2_SV=1	4.00E-44	GO:0005737,GO:0005783,GO:0005783,GO:0005788,GO:0006986,GO:0016020,GO:0031205,GO:0051087,GO:0051603,GO:0051787,GO:0070062	[illegible]
comp20596_c0_seq1.p1				
comp20598_c0_seq1.p1	sp|Q2VZV0|IF2_MAGSA_Translation_initiation_factor_IF-2_OS=Magnetospirillum_magneticum_(strain_AMB-1_/_ATCC_700264)_GN=infB_PE=3_SV=1	0	GO:0000166,GO:0003743,GO:0003743,GO:0003743,GO:0003924,GO:0003924,GO:0005525,GO:0005525,GO:0005622,GO:0005737,GO:0005737,GO:0005737,GO:0006184,GO:0006184,GO:0006412,GO:0006413,GO:0006413,GO:0006413	[illegible]
comp20599_c0_seq1.p1				
comp20608_c0_seq1.p1	sp|P66777|EPHD_MYCTU_Probable_oxidoreductase_ephD_OS=Mycobacterium_tuberculosis_GN=ephD_PE=3_SV=1	2.00E-12		
comp20609_c0_seq1.p1				
comp20610_c0_seq1.p1				
comp20611_c0_seq1.p1				
comp20616_c0_seq1.p1	sp|P77234|YBEQ_ECOLI_Uncharacterized_protein_ybeQ_OS=Escherichia_coli_(strain_K12)_GN=ybeQ_PE=4_SV=2	3.00E-21	GO:0006979	response to oxidative stress
comp20616_c0_seq2.p1	sp|Q9ZG88|PODJ_CAUCR_Localization_factor_podJL_OS=Caulobacter_crescentus_(strain_ATCC_19089_/_CB15)_GN=podJ_PE=1_SV=2	2.00E-15	GO:0007049,GO:0016020,GO:0016020,GO:0016021,GO:0030154,GO:0051301	cell cycle,membrane,membrane,integral component of membrane,cell differentiation,cell division
comp20616_c0_seq2.p3				
comp20617_c0_seq1.p1	sp|P19234|NDUV2_RAT_NADH_dehydrogenase_[ubiquinone]_flavoprotein_2,_mitochondrial_OS=Rattus_norvegicus_GN=Ndufv2_PE=1_SV=2	6.00E-81	GO:0003674,GO:0003954,GO:0005575,GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005747,GO:0005747,GO:0006120,GO:0006120,GO:0007399,GO:0008137,GO:0008137,GO:0008137,GO:0008150,GO:0009055,GO:0016020,GO:0016491,GO:0016491,GO:0046872,GO:0048738,GO:0051536,GO:0051537,GO:0055114,GO:0055114,GO:0055114,GO:0070469,GO:0045272	[illegible]
comp20617_c0_seq2.p1	sp|Q54F10|NDUV2_DICDI_NADH_dehydrogenase_[ubiquinone]_flavoprotein_2,_mitochondrial_OS=Dictyostelium_discoideum_GN=ndufv2_PE=3_SV=1	3.00E-47	GO:0003954,GO:0005739,GO:0005743,GO:0005743,GO:0005747,GO:0006120,GO:0008137,GO:0008137,GO:0009055,GO:0016020,GO:0016491,GO:0016491,GO:0044351,GO:0046872,GO:0051536,GO:0051537,GO:0055114,GO:0055114,GO:0055114,GO:0070469,GO:0045272	[illegible]
comp20619_c0_seq1.p1	sp|P49609|ACON_GRAGA_Aconitate_hydratase,_mitochondrial_OS=Gracilaria_gracilis_PE=3_SV=1	0	GO:0003994,GO:0003994,GO:0005739,GO:0005739,GO:0006099,GO:0006099,GO:0006099,GO:0008152,GO:0016829,GO:0046872,GO:0051536,GO:0051539,GO:0051539	[illegible]
comp20620_c0_seq2.p1				
comp20621_c0_seq1.p1	sp|P35381|ATPA_DROME_ATP_synthase_subunit_alpha,_mitochondrial_OS=Drosophila_melanogaster_GN=blw_PE=1_SV=2	0	GO:0000166,GO:0005524,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005811,GO:0005811,GO:0005875,GO:0006754,GO:0006810,GO:0006811,GO:0006909,GO:0007286,GO:0015986,GO:0015991,GO:0015992,GO:0015992,GO:0016020,GO:0016820,GO:0019915,GO:0022900,GO:0033178,GO:0040007,GO:0045261,GO:0045261,GO:0046034,GO:0046933,GO:0046961,GO:1902769	[illegible]
comp20622_c0_seq1.p1	sp|P09317|G3P_USTMA_Glyceraldehyde-3-phosphate_dehydrogenase_OS=Ustilago_maydis_(strain_521_/_FGSC_9021)_GN=GAPD_PE=3_SV=2	2.00E-84	GO:0004365,GO:0005737,GO:0005737,GO:0006006,GO:0006096,GO:0006096,GO:0016491,GO:0016620,GO:0050661,GO:0051287,GO:0055114,GO:0055114	[illegible]
comp20622_c1_seq1.p1	sp|P19089|G3P_CRYPA_Glyceraldehyde-3-phosphate_dehydrogenase_OS=Cryphonectria_parasitica_PE=3_SV=1	2.00E-60	GO:0004365,GO:0005737,GO:0005737,GO:0006006,GO:0006096,GO:0006096,GO:0016491,GO:0016620,GO:0050661,GO:0051287,GO:0055114,GO:0055114	[illegible]
comp20623_c0_seq1.p1	sp|Q9ZRZ8|RH28_ARATH_DEAD-box_ATP-dependent_RNA_helicase_28_OS=Arabidopsis_thaliana_GN=RH28_PE=2_SV=1	3.00E-166	GO:0000166,GO:0003676,GO:0003723,GO:0004386,GO:0005524,GO:0005524,GO:0006200,GO:0008026,GO:0008152,GO:0008152,GO:0016787	nucleotide binding,nucleic acid binding,RNA binding,helicase activity,ATP binding,ATP binding,ATP catabolic process,ATP-dependent helicase activity,metabolic process,metabolic process,hydrolase activity
comp20623_c0_seq2.p1	sp|Q0INC5|RH28_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_28_OS=Oryza_sativa_subsp._japonica_GN=Os12g0481100_PE=2_SV=2	2.00E-90	GO:0000166,GO:0000166,GO:0003676,GO:0003676,GO:0003723,GO:0003723,GO:0004386,GO:0004386,GO:0005524,GO:0005524,GO:0005524,GO:0006200,GO:0006200,GO:0008026,GO:0008026,GO:0008152,GO:0008152,GO:0008152,GO:0016787,GO:0016787	[illegible]
comp20623_c0_seq2.p2	sp|Q0INC5|RH28_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_28_OS=Oryza_sativa_subsp._japonica_GN=Os12g0481100_PE=2_SV=2	6.00E-45	GO:0000166,GO:0000166,GO:0003676,GO:0003676,GO:0003723,GO:0003723,GO:0004386,GO:0004386,GO:0005524,GO:0005524,GO:0005524,GO:0006200,GO:0006200,GO:0008026,GO:0008026,GO:0008152,GO:0008152,GO:0008152,GO:0016787,GO:0016787	[illegible]
comp20624_c0_seq1.p1				
comp20624_c0_seq2.p1	sp|Q9JIC3|DCR1A_MOUSE_DNA_cross-link_repair_1A_protein_OS=Mus_musculus_GN=Dclre1a_PE=1_SV=2	3.00E-21	GO:0005634,GO:0005634,GO:0005634,GO:0006281,GO:0006289,GO:0006974,GO:0007049,GO:0007067,GO:0051301	nucleus,nucleus,nucleus,DNA repair,nucleotide-excision repair,cellular response to DNA damage stimulus,cell cycle,mitotic nuclear division,cell division
comp20624_c0_seq2.p2				
comp20625_c0_seq1.p1	sp|Q9CAP8|LACS9_ARATH_Long_chain_acyl-CoA_synthetase_9,_chloroplastic_OS=Arabidopsis_thaliana_GN=LACS9_PE=2_SV=1	2.00E-52	GO:0000166,GO:0001676,GO:0001676,GO:0003824,GO:0004467,GO:0004467,GO:0005524,GO:0006629,GO:0006631,GO:0006631,GO:0006631,GO:0008152,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009536,GO:0009941,GO:0009941,GO:0009941,GO:0009941,GO:0016020,GO:0016874	[illegible]
comp20627_c0_seq1.p1				
comp20628_c0_seq1.p2				
comp20630_c0_seq1.p1	sp|Q54TS4|YIPF1_DICDI_Protein_YIPF1_homolog_OS=Dictyostelium_discoideum_GN=yipf1_PE=3_SV=1	4.00E-29	GO:0003674,GO:0008150,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0044351	molecular_function,biological_process,membrane,membrane,membrane,integral component of membrane,macropinocytosis
comp20631_c0_seq1.p1				
comp20632_c0_seq1.p1	sp|Q54GE3|VPS45_DICDI_Vacuolar_protein_sorting-associated_protein_45_OS=Dictyostelium_discoideum_GN=vps45_PE=1_SV=1	5.00E-146	GO:0000139,GO:0000139,GO:0005768,GO:0005794,GO:0006810,GO:0006896,GO:0006904,GO:0010008,GO:0015031,GO:0016020,GO:0016192,GO:0044351,GO:0045335,GO:0045335,GO:0051082	[illegible]
comp20635_c0_seq1.p1	sp|Q5F4K8|PAT_PINPS_Aspartate_aminotransferase_OS=Pinus_pinaster_GN=AAT_PE=1_SV=1	3.00E-111	GO:0003824,GO:0004069,GO:0008483,GO:0009058,GO:0009507,GO:0009507,GO:0009536,GO:0016740,GO:0030170,GO:0080130	catalytic activity,L-aspartate:2-oxoglutarate aminotransferase activity,transaminase activity,biosynthetic process,chloroplast,chloroplast,plastid,transferase activity,pyridoxal phosphate binding,L-phenylalanine:2-oxoglutarate aminotransferase activity
comp20640_c0_seq1.p1				
comp20641_c0_seq1.p1	sp|Q8S8S1|PEX16_ARATH_Peroxisome_biogenesis_protein_16_OS=Arabidopsis_thaliana_GN=PEX16_PE=1_SV=1	1.00E-11	GO:0005777,GO:0005777,GO:0005777,GO:0005778,GO:0005783,GO:0005789,GO:0005789,GO:0006633,GO:0006635,GO:0007031,GO:0007031,GO:0007031,GO:0007031,GO:0007031,GO:0016020,GO:0016021	[illegible]
comp20644_c0_seq1.p1				
comp20644_c0_seq3.p1				
comp20645_c0_seq1.p1				
comp20648_c0_seq1.p1				
comp20649_c0_seq1.p1				
comp20651_c0_seq1.p1				
comp20651_c0_seq1.p2	sp|Q5R4G6|CUL1_PONAB_Cullin-1_OS=Pongo_abelii_GN=CUL1_PE=2_SV=1	1.00E-32	GO:0006511,GO:0006513,GO:0006915,GO:0008283,GO:0009887,GO:0016567,GO:0016567,GO:0019005,GO:0019005,GO:0019005,GO:0031146,GO:0031146,GO:0031461,GO:0031625	[illegible]
comp20651_c0_seq2.p1				
comp20652_c0_seq1.p1	sp|A7HSH6|HSLV_PARL1_ATP-dependent_protease_subunit_HslV_OS=Parvibaculum_lavamentivorans_(strain_DS-1_/_DSM_13023_/_NCIMB_13966)_GN=hslV_PE=3_SV=1	4.00E-65	GO:0003824,GO:0004298,GO:0004298,GO:0005737,GO:0005737,GO:0005737,GO:0005839,GO:0006508,GO:0006508,GO:0008152,GO:0008233,GO:0008233,GO:0009376,GO:0009376,GO:0016787,GO:0030163,GO:0046872,GO:0051603	[illegible]
comp20653_c0_seq1.p2				
comp20653_c1_seq1.p1	sp|Q9P6P3|PPK15_SCHPO_Serine/threonine-protein_kinase_ppk15_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ppk15_PE=1_SV=1	7.00E-111	[illegible]	[illegible]
comp20654_c0_seq1.p1				
comp20657_c0_seq1.p1				
comp20658_c0_seq1.p2	sp|Q8NDF8|PAPD5_HUMAN_PAP-associated_domain-containing_protein_5_OS=Homo_sapiens_GN=PAPD5_PE=1_SV=2	1.00E-13	[illegible]	[illegible]
comp20660_c0_seq2.p1				
comp20667_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	4.00E-28		
comp20669_c0_seq1.p1	sp|P48612|PELO_DROME_Protein_pelota_OS=Drosophila_melanogaster_GN=pelo_PE=2_SV=2	9.00E-148	[illegible]	[illegible]
comp20670_c0_seq2.p1	sp|B7FUM7|PURA_PHATC_Adenylosuccinate_synthetase_OS=Phaeodactylum_tricornutum_(strain_CCAP_1055/1)_GN=PHATRDRAFT_26256_PE=3_SV=1	0	[illegible]	[illegible]
comp20671_c0_seq1.p1	sp|Q49117|Y182_METEA_Uncharacterized_oxidoreductase_MexAM1_META1p0182_OS=Methylobacterium_extorquens_(strain_ATCC_14718_/_DSM_1338_/_AM1)_GN=MexAM1_META1p0182_PE=3_SV=2	1.00E-21	[illegible]	[illegible]
comp20676_c0_seq1.p1				
comp20679_c0_seq1.p1	sp|Q9CRB3|HIUH_MOUSE_5-hydroxyisourate_hydrolase_OS=Mus_musculus_GN=Urah_PE=1_SV=1	3.00E-31	[illegible]	[illegible]
comp20681_c0_seq1.p1	sp|Q9LZ57|RL363_ARATH_60S_ribosomal_protein_L36-3_OS=Arabidopsis_thaliana_GN=RPL36C_PE=2_SV=1	3.00E-21	[illegible]	[illegible]
comp20683_c1_seq1.p1	sp|Q5ZM91|KAP0_CHICK_cAMP-dependent_protein_kinase_type_I-alpha_regulatory_subunit_OS=Gallus_gallus_GN=PRKAR1A_PE=2_SV=1	2.00E-55	[illegible]	[illegible]
comp20683_c1_seq1.p2				
comp20683_c1_seq2.p1	sp|P07802|KAP0_PIG_cAMP-dependent_protein_kinase_type_I-alpha_regulatory_subunit_OS=Sus_scrofa_GN=PRKAR1A_PE=1_SV=2	5.00E-68	[illegible]	[illegible]
comp20683_c1_seq2.p2				
comp20686_c0_seq1.p1	sp|Q9LUW6|RH9_ARATH_DEAD-box_ATP-dependent_RNA_helicase_9_OS=Arabidopsis_thaliana_GN=RH9_PE=2_SV=1	2.00E-102	[illegible]	[illegible]
comp20688_c0_seq1.p1	sp|P42925|PXMP2_MOUSE_Peroxisomal_membrane_protein_2_OS=Mus_musculus_GN=Pxmp2_PE=2_SV=2	5.00E-24	[illegible]	[illegible]
comp20690_c0_seq1.p1	sp|P93099|RL13A_CYAPA_60S_ribosomal_protein_L13a_OS=Cyanophora_paradoxa_PE=2_SV=1	4.00E-85	[illegible]	[illegible]
comp20692_c0_seq1.p2				
comp20692_c0_seq2.p1	sp|Q8MKN0|COQ9_DROME_Ubiquinone_biosynthesis_protein_COQ9,_mitochondrial_OS=Drosophila_melanogaster_GN=Coq9_PE=1_SV=1	3.00E-27	[illegible]	[illegible]
comp20693_c0_seq1.p1				
comp20696_c0_seq1.p1	sp|P74476|RF2_SYNY3_Peptide_chain_release_factor_2_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=prfB_PE=3_SV=2	1.00E-130	[illegible]	[illegible]
comp20699_c0_seq1.p2				
comp20703_c0_seq2.p1				
comp20704_c0_seq1.p2				
comp20704_c0_seq2.p1	sp|Q8GWB7|GUX6_ARATH_Putative_glucuronosyltransferase_PGSIP6_OS=Arabidopsis_thaliana_GN=PGSIP6_PE=2_SV=1	2.00E-35	[illegible]	[illegible]
comp20705_c0_seq1.p1				
comp20706_c0_seq1.p1	sp|Q07356|PDS_ARATH_15-cis-phytoene_desaturase,_chloroplastic/chromoplastic_OS=Arabidopsis_thaliana_GN=PDS_PE=1_SV=1	0	[illegible]	[illegible]
comp20707_c0_seq3.p1				
comp20707_c0_seq4.p1				
comp20708_c0_seq1.p2				
comp20708_c0_seq3.p1				
comp20711_c0_seq3.p1				
comp20712_c0_seq1.p1	sp|O94289|LUB1_SCHPO_Ubiquitin_homeostasis_protein_lub1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=lub1_PE=1_SV=1	9.00E-20	[illegible]	[illegible]
comp20714_c1_seq2.p1				
comp20715_c0_seq1.p1	sp|P80196|RNLX_SOLLC_Intracellular_ribonuclease_LX_OS=Solanum_lycopersicum_GN=RNALX_PE=1_SV=2	2.00E-24	[illegible]	[illegible]
comp20717_c0_seq1.p1				
comp20720_c0_seq1.p1	sp|Q945F0|EDS5_ARATH_Enhanced_disease_susceptibility_5_OS=Arabidopsis_thaliana_GN=EDS5_PE=2_SV=1	1.00E-43	[illegible]	[illegible]
comp20722_c0_seq3.p1				
comp20723_c0_seq1.p1				
comp20726_c0_seq1.p1	sp|Q8WUA2|PPIL4_HUMAN_Peptidyl-prolyl_cis-trans_isomerase-like_4_OS=Homo_sapiens_GN=PPIL4_PE=1_SV=1	2.00E-115	[illegible]	[illegible]
comp20727_c0_seq2.p2				
comp20728_c0_seq1.p1	sp|O61585|KTNB1_STRPU_Katanin_p80_WD40-containing_subunit_B1_OS=Strongylocentrotus_purpuratus_GN=KATNB1_PE=1_SV=1	8.00E-59	[illegible]	[illegible]
comp20730_c0_seq1.p1				
comp20732_c0_seq1.p1				
comp20732_c0_seq2.p1				
comp20737_c0_seq1.p1	sp|P73577|Y889_SYNY3_Uncharacterized_protein_slr0889_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0889_PE=3_SV=1	3.00E-29	[illegible]	[illegible]
comp20737_c0_seq1.p2	sp|Q54BC8|PSB5_DICDI_Proteasome_subunit_beta_type-5_OS=Dictyostelium_discoideum_GN=psmB5_PE=1_SV=1	8.00E-103	[illegible]	[illegible]
comp20739_c0_seq1.p1				
comp20739_c0_seq1.p2				
comp20741_c0_seq1.p1				
comp20743_c0_seq3.p1				
comp20744_c0_seq1.p1	sp|Q9LHE5|TO401_ARATH_Mitochondrial_import_receptor_subunit_TOM40_homolog_1_OS=Arabidopsis_thaliana_GN=TOM40-1_PE=1_SV=3	1.00E-13	[illegible]	[illegible]
comp20745_c0_seq1.p1	sp|A4R606|CCPR2_MAGO7_Putative_heme-binding_peroxidase_OS=Magnaporthe_oryzae_(strain_70-15_/_ATCC_MYA-4617_/_FGSC_8958)_GN=MGG_10368_PE=3_SV=1	8.00E-77	[illegible]	[illegible]
comp20749_c0_seq1.p1				
comp20753_c0_seq1.p1				
comp20756_c0_seq1.p1	sp|Q9HFU4|MPI_CRYNJ_Mannose-6-phosphate_isomerase_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=MAN1_PE=3_SV=2	4.00E-15	[illegible]	[illegible]
comp20759_c0_seq1.p1	sp|P77717|YBAY_ECOLI_Uncharacterized_lipoprotein_ybaY_OS=Escherichia_coli_(strain_K12)_GN=ybaY_PE=4_SV=1	4.00E-43	[illegible]	[illegible]
comp20759_c0_seq1.p2	sp|P0AFP3|YBAZ_SHIFL_Uncharacterized_protein_ybaZ_OS=Shigella_flexneri_GN=ybaZ_PE=3_SV=1	5.00E-71	[illegible]	[illegible]
comp20760_c0_seq1.p1	sp|Q7TPQ3|SHPRH_MOUSE_E3_ubiquitin-protein_ligase_SHPRH_OS=Mus_musculus_GN=Shprh_PE=1_SV=1	4.00E-39	[illegible]	[illegible]
comp20760_c0_seq2.p1				
comp20761_c0_seq1.p1	sp|Q3MHR0|LYPA1_BOVIN_Acyl-protein_thioesterase_1_OS=Bos_taurus_GN=LYPLA1_PE=2_SV=1	6.00E-47	[illegible]	[illegible]
comp20762_c0_seq2.p1				
comp20762_c0_seq3.p1				
comp20763_c0_seq1.p1	sp|F8W2M1|HACE1_DANRE_E3_ubiquitin-protein_ligase_HACE1_OS=Danio_rerio_GN=hace1_PE=3_SV=2	2.00E-25	[illegible]	[illegible]
comp20764_c0_seq1.p1				
comp20766_c0_seq2.p1				
comp20767_c0_seq1.p1				
comp20768_c0_seq1.p1				
comp20771_c0_seq1.p1				
comp20772_c0_seq1.p1				
comp20773_c0_seq1.p1				
comp20775_c0_seq2.p1	sp|Q5R8Q7|GTPB1_PONAB_GTP-binding_protein_1_(Fragment)_OS=Pongo_abelii_GN=GTPBP1_PE=2_SV=2	7.00E-122	[illegible]	[illegible]
comp20779_c0_seq1.p1				
comp20782_c0_seq2.p1	sp|Q5M823|NUDC2_RAT_NudC_domain-containing_protein_2_OS=Rattus_norvegicus_GN=Nudcd2_PE=2_SV=1	2.00E-20	[illegible]	[illegible]
comp20783_c0_seq1.p1	sp|Q9SLX0|IMA1B_ORYSJ_Importin_subunit_alpha-1b_OS=Oryza_sativa_subsp._japonica_GN=Os05g0155500_PE=1_SV=2	6.00E-45	[illegible]	[illegible]
comp20784_c0_seq2.p1	sp|Q6NZ09|ADRM1_DANRE_Proteasomal_ubiquitin_receptor_ADRM1_OS=Danio_rerio_GN=adrm1b_PE=1_SV=1	9.00E-26	[illegible]	[illegible]
comp20784_c0_seq3.p1	sp|Q6NZ09|ADRM1_DANRE_Proteasomal_ubiquitin_receptor_ADRM1_OS=Danio_rerio_GN=adrm1b_PE=1_SV=1	4.00E-26	[illegible]	[illegible]
comp20787_c0_seq1.p1	sp|Q6INS3|TC35A_XENLA_Tetratricopeptide_repeat_protein_35-A_OS=Xenopus_laevis_GN=ttc35-a_PE=2_SV=1	1.00E-56	[illegible]	[illegible]
comp20787_c0_seq2.p1	sp|Q6INS3|TC35A_XENLA_Tetratricopeptide_repeat_protein_35-A_OS=Xenopus_laevis_GN=ttc35-a_PE=2_SV=1	1.00E-56	[illegible]	[illegible]
comp20788_c0_seq1.p1				
comp20789_c0_seq2.p1	sp|O64885|BCCIP_ARATH_Protein_BCCIP_homolog_OS=Arabidopsis_thaliana_GN=At2g44510_PE=1_SV=2	2.00E-21	[illegible]	[illegible]
comp20790_c0_seq3.p1				
comp20790_c0_seq4.p1				
comp20791_c0_seq1.p3	sp|P93554|NDK1_SACOF_Nucleoside_diphosphate_kinase_1_OS=Saccharum_officinarum_GN=NDPK1_PE=1_SV=1	1.00E-61	[illegible]	[illegible]
comp20792_c0_seq1.p1				
comp20800_c0_seq1.p1				
comp20801_c0_seq1.p1				
comp20802_c0_seq1.p1				
comp20802_c1_seq1.p1	sp|P39788|END3_BACSU_Probable_endonuclease_III_OS=Bacillus_subtilis_GN=nth_PE=3_SV=1	4.00E-44	[illegible]	[illegible]
comp20804_c0_seq1.p1	sp|A2C5R7|TIG_PROM3_Trigger_factor_OS=Prochlorococcus_marinus_(strain_MIT_9303)_GN=tig_PE=3_SV=1	5.00E-54	[illegible]	[illegible]
comp20806_c0_seq1.p1				
comp20807_c0_seq1.p1	sp|Q8BNU0|ARMC6_MOUSE_Armadillo_repeat-containing_protein_6_OS=Mus_musculus_GN=Armc6_PE=2_SV=1	4.00E-48	[illegible]	[illegible]
comp20809_c0_seq1.p1	sp|Q2LZZ7|TRC_DROPS_Serine/threonine-protein_kinase_tricorner_OS=Drosophila_pseudoobscura_pseudoobscura_GN=trc_PE=3_SV=1	1.00E-84	[illegible]	[illegible]
comp20809_c0_seq2.p1	sp|Q2LZZ7|TRC_DROPS_Serine/threonine-protein_kinase_tricorner_OS=Drosophila_pseudoobscura_pseudoobscura_GN=trc_PE=3_SV=1	2.00E-101	[illegible]	[illegible]
comp20810_c0_seq1.p1	sp|Q9SGW3|RP12A_ARATH_26S_proteasome_non-ATPase_regulatory_subunit_RPN12A_OS=Arabidopsis_thaliana_GN=RPN12A_PE=1_SV=1	5.00E-64	[illegible]	[illegible]
comp20813_c0_seq1.p1	sp|P0C8M8|CCR1_MAIZE_Probable_serine/threonine-protein_kinase_CCRP1_OS=Zea_mays_GN=CCRP1_PE=1_SV=1	1.00E-16	[illegible]	[illegible]
comp20814_c0_seq1.p1				
comp20815_c0_seq1.p1	sp|O75832|PSD10_HUMAN_26S_proteasome_non-ATPase_regulatory_subunit_10_OS=Homo_sapiens_GN=PSMD10_PE=1_SV=1	2.00E-25	[illegible]	[illegible]
comp20816_c0_seq1.p1				
comp20817_c0_seq1.p1				
comp20818_c0_seq1.p1	sp|Q96FC9|DDX11_HUMAN_Probable_ATP-dependent_RNA_helicase_DDX11_OS=Homo_sapiens_GN=DDX11_PE=1_SV=1	1.00E-39	[illegible]	[illegible]
comp20819_c0_seq1.p1	sp|Q54HR6|PSF1_DICDI_Probable_DNA_replication_complex_GINS_protein_PSF1_OS=Dictyostelium_discoideum_GN=gins1_PE=3_SV=1	7.00E-40	[illegible]	[illegible]
comp20821_c0_seq1.p1				
comp20822_c0_seq2.p1	sp|P92958|KIN11_ARATH_SNF1-related_protein_kinase_catalytic_subunit_alpha_KIN11_OS=Arabidopsis_thaliana_GN=KIN11_PE=1_SV=1	3.00E-127	[illegible]	[illegible]
comp20823_c0_seq1.p1				
comp20825_c0_seq2.p1	sp|P34117|CDK5_DICDI_Cyclin-dependent_kinase_5_homolog_OS=Dictyostelium_discoideum_GN=cdk5_PE=2_SV=2	2.00E-150	[illegible]	[illegible]
comp20828_c0_seq1.p1				
comp20829_c0_seq1.p1				
comp20834_c0_seq2.p1	sp|Q8T126|FNKC_DICDI_Probable_inactive_serine/threonine-protein_kinase_fnkC_OS=Dictyostelium_discoideum_GN=fnkC_PE=3_SV=1	2.00E-13	[illegible]	[illegible]
comp20836_c0_seq1.p1	sp|A1CHL6|ATG1_ASPCL_Serine/threonine-protein_kinase_atg1_OS=Aspergillus_clavatus_(strain_ATCC_1007_/_CBS_513.65_/_DSM_816_/_NCTC_3887_/_NRRL_1)_GN=atg1_PE=3_SV=1	1.00E-61	[illegible]	[illegible]
comp20837_c0_seq1.p1	sp|Q12797|ASPH_HUMAN_Aspartyl/asparaginyl_beta-hydroxylase_OS=Homo_sapiens_GN=ASPH_PE=1_SV=3	1.00E-25	[illegible]	[illegible]
comp20839_c0_seq1.p1	sp|Q93W20|NIFU2_ARATH_NifU-like_protein_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=NIFU2_PE=1_SV=1	3.00E-42	[illegible]	[illegible]
comp20840_c0_seq1.p1	sp|A7RWD2|CIAO1_NEMVE_Probable_cytosolic_iron-sulfur_protein_assembly_protein_OS=Nematostella_vectensis_GN=v1g226592_PE=3_SV=1	2.00E-75	[illegible]	[illegible]
comp20840_c0_seq3.p1	sp|A7RWD2|CIAO1_NEMVE_Probable_cytosolic_iron-sulfur_protein_assembly_protein_OS=Nematostella_vectensis_GN=v1g226592_PE=3_SV=1	1.00E-75	[illegible]	[illegible]
comp20841_c0_seq2.p1	sp|Q9XF62|DIP13_CHLRE_13_kDa_deflagellation-inducible_protein_OS=Chlamydomonas_reinhardtii_GN=DIP13_PE=3_SV=1	2.00E-47	[illegible]	[illegible]
comp20842_c0_seq2.p1				
comp20843_c0_seq1.p1	sp|Q15003|CND2_HUMAN_Condensin_complex_subunit_2_OS=Homo_sapiens_GN=NCAPH_PE=1_SV=3	3.00E-20	[illegible]	[illegible]
comp20845_c0_seq1.p1	sp|P49105|G6PI_MAIZE_Glucose-6-phosphate_isomerase,_cytosolic_OS=Zea_mays_GN=PHI1_PE=2_SV=1	0	[illegible]	[illegible]
comp20846_c0_seq1.p1				
comp20850_c0_seq1.p1				
comp20850_c0_seq2.p1				
comp20850_c0_seq4.p2				
comp20853_c0_seq2.p1	sp|Q5ZKU8|PK1IP_CHICK_p21-activated_protein_kinase-interacting_protein_1-like_OS=Gallus_gallus_GN=PAK1IP1_PE=2_SV=1	4.00E-53	[illegible]	[illegible]
comp20854_c0_seq2.p1	sp|Q00808|HETE1_PODAS_Vegetative_incompatibility_protein_HET-E-1_OS=Podospora_anserina_GN=HET-E1_PE=4_SV=1	2.00E-40	[illegible]	[illegible]
comp20856_c0_seq1.p1				
comp20856_c0_seq2.p1				
comp20857_c0_seq1.p1				
comp20858_c0_seq1.p1				
comp20861_c0_seq1.p1	sp|Q8SR83|CDC72_ENCCU_Probable_cell_division_control_protein_7_homolog_2_OS=Encephalitozoon_cuniculi_(strain_GB-M1)_GN=CDC7-2_PE=3_SV=1	4.00E-51	[illegible]	[illegible]
comp20862_c0_seq1.p1				
comp20866_c0_seq1.p1				
comp20867_c0_seq2.p1				
comp20867_c0_seq4.p1				
comp20868_c0_seq1.p1	sp|Q2PFZ3|PRDX2_MACFA_Peroxiredoxin-2_OS=Macaca_fascicularis_GN=PRDX2_PE=2_SV=3	2.00E-76	[illegible]	[illegible]
comp20868_c0_seq1.p2				
comp20869_c0_seq1.p2	sp|Q29048|VATA_PIG_V-type_proton_ATPase_catalytic_subunit_A_OS=Sus_scrofa_GN=ATP6V1A_PE=2_SV=2	1.00E-44	[illegible]	[illegible]
comp20870_c0_seq2.p2	sp|Q8VZ19|RL302_ARATH_60S_ribosomal_protein_L30-2_OS=Arabidopsis_thaliana_GN=RPL30B_PE=2_SV=1	6.00E-48	[illegible]	[illegible]
comp20871_c0_seq1.p1	sp|P15567|PUR6_SCHPO_Phosphoribosylaminoimidazole_carboxylase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ade6_PE=2_SV=1	3.00E-174	[illegible]	[illegible]
comp20872_c0_seq1.p1	sp|Q9USN3|UTP13_SCHPO_Probable_U3_small_nucleolar_RNA-associated_protein_13_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=utp13_PE=2_SV=3	3.00E-13	[illegible]	[illegible]
comp20872_c0_seq1.p3				
comp20872_c0_seq1.p5				
comp20873_c0_seq3.p1				
comp20874_c0_seq1.p1	sp|P37198|NUP62_HUMAN_Nuclear_pore_glycoprotein_p62_OS=Homo_sapiens_GN=NUP62_PE=1_SV=3	2.00E-18	[illegible]	[illegible]
comp20877_c0_seq2.p1	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	4.00E-23	[illegible]	[illegible]
comp20879_c0_seq1.p1				
comp20881_c0_seq2.p1				
comp20882_c0_seq2.p1				
comp20884_c0_seq1.p1	sp|Q1AU89|TRPD_RUBXD_Anthranilate_phosphoribosyltransferase_OS=Rubrobacter_xylanophilus_(strain_DSM_9941_/_NBRC_16129)_GN=trpD_PE=3_SV=1	3.00E-83	[illegible]	[illegible]
comp20885_c0_seq1.p1				
comp20886_c0_seq2.p1				
comp20886_c0_seq3.p1				
comp20887_c0_seq1.p1	sp|O93257|XRCC6_CHICK_X-ray_repair_cross-complementing_protein_5_OS=Gallus_gallus_GN=XRCC6_PE=2_SV=1	9.00E-71	[illegible]	[illegible]
comp20889_c0_seq2.p1	sp|Q9ESL4|MLTK_MOUSE_Mitogen-activated_protein_kinase_kinase_kinase_MLT_OS=Mus_musculus_GN=Mltk_PE=1_SV=1	2.00E-22	[illegible]	[illegible]
comp20890_c0_seq1.p1	sp|Q8N0N3|BGBP_PENMO_Beta-1,3-glucan-binding_protein_OS=Penaeus_monodon_PE=2_SV=1	1.00E-97	[illegible]	[illegible]
comp20891_c0_seq1.p1				
comp20892_c0_seq1.p2				
comp20893_c0_seq2.p1				
comp20894_c0_seq1.p1				
comp20895_c0_seq1.p1	sp|Q94KJ7|VPS33_ARATH_Vacuolar_protein_sorting-associated_protein_33_homolog_OS=Arabidopsis_thaliana_GN=VPS33_PE=2_SV=1	1.00E-114	[illegible]	[illegible]
comp20896_c0_seq2.p1	sp|Q29RM3|REEP5_BOVIN_Receptor_expression-enhancing_protein_5_OS=Bos_taurus_GN=REEP5_PE=2_SV=1	8.00E-23	[illegible]	[illegible]
comp20900_c0_seq1.p1				
comp20903_c0_seq2.p1	sp|Q12907|LMAN2_HUMAN_Vesicular_integral-membrane_protein_VIP36_OS=Homo_sapiens_GN=LMAN2_PE=1_SV=1	1.00E-11	[illegible]	[illegible]
comp20904_c0_seq1.p1	sp|P56848|ISPE_MENPI_4-diphosphocytidyl-2-C-methyl-D-erythritol_kinase,_chloroplastic_OS=Mentha_piperita_GN=ISPE_PE=1_SV=1	2.00E-65	[illegible]	[illegible]
comp20905_c0_seq2.p1	sp|Q9LYA9|Y3314_ARATH_Uncharacterized_protein_At3g63140,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g63140_PE=1_SV=1	8.00E-57	[illegible]	[illegible]
comp20906_c0_seq2.p1				
comp20907_c0_seq1.p2	sp|Q55E35|SPCS2_DICDI_Signal_peptidase_complex_subunit_2_OS=Dictyostelium_discoideum_GN=spcs2_PE=3_SV=2	9.00E-20	[illegible]	[illegible]
comp20907_c0_seq3.p2	sp|Q55E35|SPCS2_DICDI_Signal_peptidase_complex_subunit_2_OS=Dictyostelium_discoideum_GN=spcs2_PE=3_SV=2	1.00E-19	[illegible]	[illegible]
comp20909_c0_seq1.p2	sp|Q06952|GM4D1_VIBCH_Probable_GDP-mannose_4,6-dehydratase_OS=Vibrio_cholerae_GN=rfbD_PE=3_SV=1	1.00E-55	[illegible]	[illegible]
comp20909_c1_seq1.p1	sp|Q9VMW9|GMDS_DROME_GDP-mannose_4,6_dehydratase_OS=Drosophila_melanogaster_GN=Gmd_PE=1_SV=2	9.00E-36	[illegible]	[illegible]
comp20912_c0_seq1.p1				
comp20915_c0_seq1.p1	sp|O95544|NADK_HUMAN_NAD_kinase_OS=Homo_sapiens_GN=NADK_PE=1_SV=1	1.00E-59	[illegible]	[illegible]
comp20916_c0_seq1.p1				
comp20916_c0_seq1.p2				
comp20916_c0_seq2.p1				
comp20917_c0_seq1.p1				
comp20917_c0_seq2.p1				
comp20918_c0_seq1.p1	sp|Q9C5Z1|EIF3B_ARATH_Eukaryotic_translation_initiation_factor_3_subunit_B_OS=Arabidopsis_thaliana_GN=TIF3B1_PE=1_SV=1	4.00E-150	[illegible]	[illegible]
comp20919_c0_seq1.p1	sp|O64886|COX10_ARATH_Protoheme_IX_farnesyltransferase,_mitochondrial_OS=Arabidopsis_thaliana_GN=COX10_PE=2_SV=4	4.00E-53	[illegible]	[illegible]
comp20919_c0_seq1.p2	sp|Q6ERE5|VIT12_ORYSJ_Vacuolar_iron_transporter_1.2_OS=Oryza_sativa_subsp._japonica_GN=VIT1.2_PE=3_SV=2	2.00E-26	[illegible]	[illegible]
comp20920_c0_seq1.p1				
comp20920_c0_seq1.p3				
comp20923_c0_seq1.p1				
comp20924_c0_seq1.p1	sp|Q0VD51|RNF13_BOVIN_E3_ubiquitin-protein_ligase_RNF13_OS=Bos_taurus_GN=RNF13_PE=2_SV=1	1.00E-17	[illegible]	[illegible]
comp20924_c0_seq2.p1				
comp20924_c0_seq2.p4	sp|Q0VD51|RNF13_BOVIN_E3_ubiquitin-protein_ligase_RNF13_OS=Bos_taurus_GN=RNF13_PE=2_SV=1	4.00E-13	[illegible]	[illegible]
comp20925_c0_seq1.p1				
comp20926_c0_seq2.p1	sp|Q90Z10|RL13_DANRE_60S_ribosomal_protein_L13_OS=Danio_rerio_GN=rpl13_PE=2_SV=3	6.00E-68	[illegible]	[illegible]
comp20927_c0_seq1.p1	sp|A0JP85|CNOT1_XENTR_CCR4-NOT_transcription_complex_subunit_1_OS=Xenopus_tropicalis_GN=cnot1_PE=2_SV=1	5.00E-151	[illegible]	[illegible]
comp20930_c0_seq2.p2				
comp20931_c0_seq2.p1	sp|Q8L3X9|KASM_ARATH_3-oxoacyl-[acyl-carrier-protein]_synthase,_mitochondrial_OS=Arabidopsis_thaliana_GN=KAS_PE=1_SV=1	1.00E-137	[illegible]	[illegible]
comp20933_c0_seq2.p1	sp|Q552W5|CCHL_DICDI_Probable_cytochrome_c-type_heme_lyase_OS=Dictyostelium_discoideum_GN=cchl_PE=3_SV=1	8.00E-40	[illegible]	[illegible]
comp20934_c0_seq1.p1	sp|Q9S7G7|MB3R1_ARATH_Myb-related_protein_3R-1_OS=Arabidopsis_thaliana_GN=MYB3R-1_PE=2_SV=1	8.00E-27	[illegible]	[illegible]
comp20936_c0_seq1.p1				
comp20938_c0_seq1.p1				
comp20938_c0_seq1.p3				
comp20939_c0_seq1.p1	sp|Q7Z406|MYH14_HUMAN_Myosin-14_OS=Homo_sapiens_GN=MYH14_PE=1_SV=2	1.00E-12	[illegible]	[illegible]
comp20939_c0_seq2.p2				
comp20940_c0_seq2.p1				
comp20941_c0_seq3.p1	sp|O06986|YVDD_BACSU_LOG_family_protein_yvdD_OS=Bacillus_subtilis_GN=yvdD_PE=1_SV=1	6.00E-20		
comp20942_c0_seq1.p1	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	3.00E-33	[illegible]	[illegible]
comp20943_c0_seq1.p1				
comp20944_c0_seq1.p1	sp|P51784|UBP11_HUMAN_Ubiquitin_carboxyl-terminal_hydrolase_11_OS=Homo_sapiens_GN=USP11_PE=1_SV=3	1.00E-39	[illegible]	[illegible]
comp20945_c0_seq1.p1				
comp20946_c0_seq1.p1	sp|P0CO78|GEM1_CRYNJ_Mitochondrial_Rho_GTPase_1_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=GEM1_PE=3_SV=1	3.00E-55	[illegible]	[illegible]
comp20948_c0_seq1.p1	sp|Q54DU9|TP4AA_DICDI_Probable_protein_tyrosine_phosphatase_type_IVA_A_OS=Dictyostelium_discoideum_GN=DDB_G0292024_PE=3_SV=1	7.00E-46	[illegible]	[illegible]
comp20949_c0_seq2.p1	sp|O13755|FRDS_SCHPO_Putative_fumarate_reductase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC17A2.05_PE=2_SV=1	2.00E-92	[illegible]	[illegible]
comp20951_c0_seq1.p2				
comp20954_c0_seq2.p1	sp|Q9M643|CCI1_ARATH_Cycloeucalenol_cycloisomerase_OS=Arabidopsis_thaliana_GN=CPI1_PE=2_SV=1	3.00E-61	[illegible]	[illegible]
comp20957_c0_seq1.p2	sp|Q9FWT2|UBC16_ARATH_Probable_ubiquitin-conjugating_enzyme_E2_16_OS=Arabidopsis_thaliana_GN=UBC16_PE=2_SV=1	5.00E-47	[illegible]	[illegible]
comp20959_c0_seq1.p1	sp|Q9P6V8|SPB1_NEUCR_AdoMet-dependent_rRNA_methyltransferase_spb-1_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=spb-1_PE=3_SV=2	3.00E-93	[illegible]	[illegible]
comp20960_c0_seq1.p1	sp|B7FA90|HPT1_ORYSJ_Probable_homogentisate_phytyltransferase_1,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=HPT1_PE=2_SV=1	2.00E-53	[illegible]	[illegible]
comp20964_c0_seq2.p1	sp|Q51371|ALGG_PSEAE_Poly(beta-D-mannuronate)_C5_epimerase_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=algG_PE=1_SV=1	4.00E-11	[illegible]	[illegible]
comp20964_c0_seq3.p2				
comp20965_c0_seq1.p1	sp|Q0IHQ9|ACPL2_XENTR_Acid_phosphatase-like_protein_2_OS=Xenopus_tropicalis_GN=acpl2_PE=2_SV=1	3.00E-24	[illegible]	[illegible]
comp20967_c0_seq1.p1				
comp20968_c0_seq1.p1				
comp20968_c0_seq2.p1				
comp20969_c0_seq1.p1	sp|O95340|PAPS2_HUMAN_Bifunctional_3'-phosphoadenosine_5'-phosphosulfate_synthase_2_OS=Homo_sapiens_GN=PAPSS2_PE=1_SV=2	4.00E-168	[illegible]	[illegible]
comp20971_c0_seq1.p1				
comp20976_c0_seq1.p1	sp|Q8GXU8|LPAT1_ARATH_1-acyl-sn-glycerol-3-phosphate_acyltransferase_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=LPAT1_PE=1_SV=1	2.00E-20	[illegible]	[illegible]
comp20978_c0_seq2.p1				
comp20979_c0_seq1.p1				
comp20980_c0_seq1.p1	sp|Q58EM4|CF211_DANRE_UPF0364_protein_C6orf211_homolog_OS=Danio_rerio_GN=zgc:110816_PE=2_SV=1	2.00E-43	[illegible]	[illegible]
comp20982_c0_seq1.p1				
comp20984_c0_seq2.p1	sp|Q9FL33|MCM3_ARATH_DNA_replication_licensing_factor_MCM3_homolog_OS=Arabidopsis_thaliana_GN=MCM3_PE=2_SV=1	0	[illegible]	[illegible]
comp20985_c0_seq1.p1	sp|Q8S0J7|IM30_ORYSJ_Probable_membrane-associated_30_kDa_protein,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=Os01g0895100_PE=1_SV=1	5.00E-27	[illegible]	[illegible]
comp20985_c0_seq2.p1	sp|Q8S0J7|IM30_ORYSJ_Probable_membrane-associated_30_kDa_protein,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=Os01g0895100_PE=1_SV=1	2.00E-54	[illegible]	[illegible]
comp20986_c1_seq2.p1				
comp20986_c1_seq3.p1	sp|Q7SX99|FUMH_DANRE_Fumarate_hydratase,_mitochondrial_OS=Danio_rerio_GN=fh_PE=2_SV=1	0	[illegible]	[illegible]
comp20986_c1_seq3.p2				
comp20986_c1_seq3.p6				
comp20987_c0_seq1.p1	sp|Q8VCX2|S35C2_MOUSE_Solute_carrier_family_35_member_C2_OS=Mus_musculus_GN=Slc35c2_PE=1_SV=1	8.00E-43	[illegible]	[illegible]
comp20990_c0_seq1.p1				
comp20990_c0_seq2.p1				
comp20991_c0_seq2.p1	sp|Q5ZHT1|ACD11_CHICK_Acyl-CoA_dehydrogenase_family_member_11_OS=Gallus_gallus_GN=ACAD11_PE=2_SV=1	1.00E-124	[illegible]	[illegible]
comp20994_c0_seq1.p2	sp|O43940|RLA2_LEIDO_60S_acidic_ribosomal_protein_P2_OS=Leishmania_donovani_GN=ARP-1_PE=3_SV=1	2.00E-14	[illegible]	[illegible]
comp20998_c0_seq1.p1	sp|P73689|SPPA_SYNY3_Protease_4_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sppA_PE=3_SV=1	7.00E-50	[illegible]	[illegible]
comp20998_c0_seq1.p4				
comp20999_c0_seq1.p1	sp|Q8GVC7|PKZ1_PHYIN_Serine/threonine-protein_kinase_PKZ1_OS=Phytophthora_infestans_GN=PKZ1_PE=1_SV=1	4.00E-32	[illegible]	[illegible]
comp21000_c0_seq1.p1				
comp21000_c0_seq2.p1				
comp21002_c0_seq1.p1	sp|Q54IK1|RRAGA_DICDI_Ras-related_GTP-binding_protein_A_OS=Dictyostelium_discoideum_GN=ragA_PE=2_SV=1	7.00E-133	[illegible]	[illegible]
comp21004_c0_seq1.p1	sp|P73689|SPPA_SYNY3_Protease_4_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sppA_PE=3_SV=1	8.00E-38	[illegible]	[illegible]
comp21005_c0_seq1.p1	sp|A7ETJ6|ATP23_SCLS1_Mitochondrial_inner_membrane_protease_atp23_OS=Sclerotinia_sclerotiorum_(strain_ATCC_18683_/_1980_/_Ss-1)_GN=atp23_PE=3_SV=1	7.00E-11	[illegible]	[illegible]
comp21007_c0_seq1.p1				
comp21009_c0_seq1.p1				
comp21010_c0_seq1.p1				

comp21011_c0_seq1.p1	sp|Q8RWV3|CCL11_ARATH_Cyclin-L1-1_OS=Arabidopsis_thaliana_GN=CYCL1-1_PE=2_SV=2	3.00E-63	[illegible]	[illegible]
comp21011_c0_seq2.p1	sp|Q8RWV3|CCL11_ARATH_Cyclin-L1-1_OS=Arabidopsis_thaliana_GN=CYCL1-1_PE=2_SV=2	3.00E-63	[illegible]	[illegible]
comp21016_c0_seq1.p1				
comp21016_c0_seq1.p3				
comp21016_c0_seq2.p1				
comp21017_c0_seq1.p1				
comp21017_c0_seq1.p2				
comp21017_c0_seq1.p5				
comp21018_c0_seq1.p1	sp|Q01V13|GLPK_SOLUE_Glycerol_kinase_OS=Solibacter_usitatus_(strain_Ellin6076)_GN=glpK_PE=3_SV=1	9.00E-91	[illegible]	[illegible]
comp21018_c0_seq3.p1				
comp21019_c0_seq1.p1				
comp21021_c0_seq1.p1				
comp21022_c0_seq1.p1	sp|Q55E13|ZPR1_DICDI_Zinc_finger_protein_ZPR1_homolog_OS=Dictyostelium_discoideum_GN=zpr1_PE=3_SV=1	2.00E-94	GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0008270,GO:0046872	[illegible]
comp21027_c0_seq1.p1	sp|Q9LY87|RGLG2_ARATH_E3_ubiquitin-protein_ligase_RGLG2_OS=Arabidopsis_thaliana_GN=RGLG2_PE=1_SV=1	6.00E-67	[illegible]	[illegible]
comp21028_c0_seq1.p1	sp|Q90YB1|DNLI4_CHICK_DNA_ligase_4_OS=Gallus_gallus_GN=LIG4_PE=2_SV=2	2.00E-16	[illegible]	[illegible]
comp21031_c0_seq2.p1				
comp21033_c0_seq1.p1				
comp21034_c0_seq2.p1	sp|Q59536|PTRB_MORLA_Protease_2_OS=Moraxella_lacunata_GN=ptrB_PE=3_SV=1	1.00E-150	[illegible]	[illegible]
comp21037_c0_seq2.p1				
comp21037_c0_seq3.p1				
comp21039_c0_seq1.p1				
comp21041_c0_seq1.p1				
comp21042_c0_seq1.p1	sp|Q94B38|GPT2_ARATH_Glucose-6-phosphate/phosphate_translocator_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=GPT2_PE=2_SV=2	2.00E-68	[illegible]	[illegible]
comp21042_c0_seq2.p1	sp|Q94B38|GPT2_ARATH_Glucose-6-phosphate/phosphate_translocator_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=GPT2_PE=2_SV=2	1.00E-55	[illegible]	[illegible]
comp21043_c0_seq1.p1				
comp21044_c0_seq1.p1	sp|O74468|SUMT_SCHPO_Probable_uroporphyrinogen-III_C-methyltransferase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC1739.06c_PE=2_SV=1	2.00E-54	[illegible]	[illegible]
comp21046_c0_seq1.p1				
comp21046_c1_seq2.p1				
comp21048_c0_seq1.p1	sp|Q24562|U2AF2_DROME_Splicing_factor_U2AF_50_kDa_subunit_OS=Drosophila_melanogaster_GN=U2af50_PE=2_SV=1	1.00E-36	[illegible]	[illegible]
comp21048_c0_seq1.p2	sp|P66777|EPHD_MYCTU_Probable_oxidoreductase_ephD_OS=Mycobacterium_tuberculosis_GN=ephD_PE=3_SV=1	2.00E-13		
comp21049_c0_seq1.p1	sp|P54276|MSH6_MOUSE_DNA_mismatch_repair_protein_Msh6_OS=Mus_musculus_GN=Msh6_PE=1_SV=3	0	[illegible]	[illegible]
comp21050_c0_seq1.p1				
comp21051_c0_seq1.p1				
comp21051_c0_seq2.p1	sp|Q53GS9|SNUT2_HUMAN_U4/U6.U5_tri-snRNP-associated_protein_2_OS=Homo_sapiens_GN=USP39_PE=1_SV=2	4.00E-147	[illegible]	[illegible]
comp21053_c0_seq1.p1				
comp21056_c0_seq1.p1	sp|Q6WKZ8|UBR2_MOUSE_E3_ubiquitin-protein_ligase_UBR2_OS=Mus_musculus_GN=Ubr2_PE=1_SV=2	6.00E-24	[illegible]	[illegible]
comp21059_c0_seq1.p1				
comp21061_c0_seq1.p1	sp|P32684|RLUF_ECOLI_Ribosomal_large_subunit_pseudouridine_synthase_F_OS=Escherichia_coli_(strain_K12)_GN=rluF_PE=1_SV=1	2.00E-116	[illegible]	[illegible]
comp21062_c0_seq1.p1				
comp21062_c0_seq2.p1				
comp21063_c0_seq2.p1				
comp21064_c0_seq3.p1				
comp21066_c0_seq1.p1	sp|Q3TZM9|ALG11_MOUSE_GDP-Man:Man(3)GlcNAc(2)-PP-Dol_alpha-1,2-mannosyltransferase_OS=Mus_musculus_GN=Alg11_PE=2_SV=1	9.00E-122	[illegible]	[illegible]
comp21075_c0_seq1.p1				
comp21075_c0_seq2.p1				
comp21077_c0_seq1.p1				
comp21077_c1_seq1.p1				
comp21078_c0_seq1.p3				
comp21080_c0_seq1.p1				
comp21082_c0_seq1.p1	sp|Q9H1X1|RSPH9_HUMAN_Radial_spoke_head_protein_9_homolog_OS=Homo_sapiens_GN=RSPH9_PE=1_SV=1	2.00E-40	[illegible]	[illegible]
comp21083_c0_seq1.p1				
comp21085_c0_seq2.p1				
comp21089_c0_seq1.p1				
comp21090_c0_seq1.p1	sp|Q39758|ACT_FUCVE_Actin_OS=Fucus_vesiculosus_PE=2_SV=1	0	[illegible]	[illegible]
comp21091_c0_seq2.p2				
comp21091_c0_seq2.p4				
comp21092_c0_seq1.p1				
comp21092_c0_seq1.p2	sp|P42795|RL111_ARATH_60S_ribosomal_protein_L11-1_OS=Arabidopsis_thaliana_GN=RPL11A_PE=1_SV=2	2.00E-94	[illegible]	[illegible]
comp21092_c0_seq2.p1				
comp21095_c0_seq1.p1	sp|O23365|C97B3_ARATH_Cytochrome_P450_97B3,_chloroplastic_OS=Arabidopsis_thaliana_GN=CYP97B3_PE=1_SV=2	0	[illegible]	[illegible]
comp21101_c0_seq1.p1				
comp21103_c0_seq1.p1	sp|Q9ZVH3|ORC6_ARATH_Origin_recognition_complex_subunit_6_OS=Arabidopsis_thaliana_GN=ORC6_PE=1_SV=2	5.00E-26	[illegible]	[illegible]
comp21103_c0_seq2.p1	sp|Q8VBZ3|CLPT1_MOUSE_Cleft_lip_and_palate_transmembrane_protein_1_homolog_OS=Mus_musculus_GN=Clptm1_PE=1_SV=1	2.00E-123	[illegible]	[illegible]
comp21105_c0_seq1.p1	sp|Q9VCA8|ANKHM_DROME_Ankyrin_repeat_and_KH_domain-containing_protein_mask_OS=Drosophila_melanogaster_GN=mask_PE=1_SV=2	6.00E-14	[illegible]	[illegible]
comp21107_c0_seq2.p3				
comp21109_c0_seq1.p1	sp|B2TYQ6|LPLT_SHIB3_Lysophospholipid_transporter_lplT_OS=Shigella_boydii_serotype_18_(strain_CDC_3083-94_/_BS512)_GN=lplT_PE=3_SV=1	8.00E-108	[illegible]	[illegible]
comp21110_c0_seq1.p1	sp|Q9DE26|RUVB1_XENLA_RuvB-like_1_OS=Xenopus_laevis_GN=ruvbl1_PE=2_SV=1	0	[illegible]	[illegible]
comp21110_c0_seq2.p1	sp|Q9DE26|RUVB1_XENLA_RuvB-like_1_OS=Xenopus_laevis_GN=ruvbl1_PE=2_SV=1	6.00E-140	[illegible]	[illegible]
comp21111_c0_seq1.p1				
comp21114_c0_seq1.p1				
comp21114_c0_seq3.p1				
comp21115_c0_seq1.p1	sp|Q91ZA3|PCCA_MOUSE_Propionyl-CoA_carboxylase_alpha_chain,_mitochondrial_OS=Mus_musculus_GN=Pcca_PE=2_SV=2	0	[illegible]	[illegible]
comp21116_c0_seq1.p1	sp|Q52JK6|VIP2_NICBE_Probable_NOT_transcription_complex_subunit_VIP2_(Fragment)_OS=Nicotiana_benthamiana_GN=VIP2_PE=1_SV=1	2.00E-43	[illegible]	[illegible]
comp21118_c0_seq1.p1				
comp21119_c0_seq1.p1	sp|P37662|YHJX_ECOLI_Inner_membrane_protein_yhjX_OS=Escherichia_coli_(strain_K12)_GN=yhjX_PE=1_SV=1	7.00E-18	[illegible]	[illegible]
comp21123_c0_seq1.p1				
comp21124_c0_seq2.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	4.00E-45		
comp21125_c0_seq2.p1	sp|B0G180|SPCS3_DICDI_Signal_peptidase_complex_subunit_3_OS=Dictyostelium_discoideum_GN=spcs3_PE=3_SV=1	1.00E-26	[illegible]	[illegible]
comp21125_c0_seq3.p1	sp|A8KBL5|S38AB_DANRE_Putative_sodium-coupled_neutral_amino_acid_transporter_11_OS=Danio_rerio_GN=slc38a11_PE=2_SV=2	1.00E-20	[illegible]	[illegible]
comp21126_c0_seq1.p2				
comp21128_c0_seq1.p1	sp|Q55AI5|SUCB1_DICDI_Succinyl-CoA_ligase_[ADP-forming]_subunit_beta,_mitochondrial_OS=Dictyostelium_discoideum_GN=scsC_PE=3_SV=1	3.00E-139	[illegible]	[illegible]
comp21130_c0_seq2.p1				
comp21130_c0_seq2.p2				
comp21130_c0_seq3.p1				
comp21131_c0_seq1.p2	sp|P61220|EIF1B_PIG_Eukaryotic_translation_initiation_factor_1b_OS=Sus_scrofa_GN=EIF1B_PE=3_SV=1	1.00E-33	[illegible]	[illegible]
comp21133_c0_seq2.p1				
comp21134_c0_seq1.p1				
comp21135_c0_seq1.p1				
comp21135_c0_seq4.p1				
comp21136_c0_seq1.p1	sp|Q60710|SAMH1_MOUSE_SAM_domain_and_HD_domain-containing_protein_1_OS=Mus_musculus_GN=Samhd1_PE=1_SV=2	2.00E-82	[illegible]	[illegible]
comp21138_c0_seq1.p1	sp|P0DI13|SA1B2_ARATH_SUMO-activating_enzyme_subunit_1B-2_OS=Arabidopsis_thaliana_GN=SAE1B-2_PE=2_SV=1	2.00E-42	[illegible]	[illegible]
comp21139_c0_seq1.p1	sp|Q95V39|RL8_SPOFR_60S_ribosomal_protein_L8_OS=Spodoptera_frugiperda_GN=RpL8_PE=2_SV=1	4.00E-43	[illegible]	[illegible]
comp21139_c0_seq2.p1	sp|P29766|RL8_SOLLC_60S_ribosomal_protein_L8_OS=Solanum_lycopersicum_GN=RPL8_PE=2_SV=1	1.00E-133	[illegible]	[illegible]
comp21140_c0_seq1.p1	sp|Q69XJ4|HMOX1_ORYSJ_Heme_oxygenase_1,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=HO1_PE=2_SV=1	2.00E-53	[illegible]	[illegible]
comp21141_c0_seq1.p2				
comp21141_c0_seq1.p3	sp|O14155|YE72_SCHPO_UPF0047_protein_C4A8.02c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC4A8.02c_PE=2_SV=1	5.00E-40	[illegible]	[illegible]
comp21145_c1_seq1.p1	sp|P00490|PHSM_ECOLI_Maltodextrin_phosphorylase_OS=Escherichia_coli_(strain_K12)_GN=malP_PE=1_SV=7	2.00E-94	[illegible]	[illegible]
comp21145_c2_seq1.p1	sp|P75874|YCCU_ECOLI_Uncharacterized_protein_yccU_OS=Escherichia_coli_(strain_K12)_GN=yccU_PE=1_SV=2	3.00E-78	GO:0048037	[illegible]
comp21148_c0_seq3.p1	sp|Q9Y3A2|UTP11_HUMAN_Probable_U3_small_nucleolar_RNA-associated_protein_11_OS=Homo_sapiens_GN=UTP11L_PE=1_SV=2	1.00E-55	[illegible]	[illegible]
comp21149_c0_seq1.p1				
comp21150_c0_seq1.p1	sp|Q3Z3F7|YCCT_SHISS_UPF0319_protein_YccT_OS=Shigella_sonnei_(strain_Ss046)_GN=yccT_PE=3_SV=1	2.00E-70		
comp21151_c1_seq1.p1				
comp21151_c1_seq2.p1				
comp21152_c0_seq1.p1				
comp21153_c0_seq1.p1				
comp21154_c0_seq1.p1				
comp21156_c0_seq1.p1	sp|Q9LH76|RHM3_ARATH_Probable_rhamnose_biosynthetic_enzyme_3_OS=Arabidopsis_thaliana_GN=RHM3_PE=1_SV=1	9.00E-92	[illegible]	[illegible]
comp21156_c0_seq2.p1	sp|Q9LPG6|RHM2_ARATH_Probable_rhamnose_biosynthetic_enzyme_2_OS=Arabidopsis_thaliana_GN=RHM2_PE=1_SV=1	2.00E-134	[illegible]	[illegible]
comp21157_c0_seq1.p1				
comp21159_c0_seq1.p1	sp|Q9LKI7|TCPG_THAWE_T-complex_protein_1_subunit_gamma_OS=Thalassiosira_weissflogii_PE=2_SV=1	0	[illegible]	[illegible]
comp21161_c0_seq1.p1	sp|Q54J66|SYTC1_DICDI_Probable_threonine--tRNA_ligase_1,_cytoplasmic_OS=Dictyostelium_discoideum_GN=thrS1_PE=3_SV=1	0	[illegible]	[illegible]
comp21162_c0_seq1.p1	sp|Q99K82|SMOX_MOUSE_Spermine_oxidase_OS=Mus_musculus_GN=Smox_PE=1_SV=1	1.00E-15	[illegible]	[illegible]
comp21165_c0_seq1.p1				
comp21167_c0_seq1.p1	sp|A8FLY1|PCKA_CAMJ8_Phosphoenolpyruvate_carboxykinase_[ATP]_OS=Campylobacter_jejuni_subsp._jejuni_serotype_O:6_(strain_81116_/_NCTC_11828)_GN=pckA_PE=3_SV=1	0	[illegible]	[illegible]
comp21169_c0_seq1.p1	sp|Q9LEJ0|ENO1_HEVBR_Enolase_1_OS=Hevea_brasiliensis_GN=ENO1_PE=1_SV=1	3.00E-72	[illegible]	[illegible]
comp21169_c0_seq2.p1	sp|Q43130|ENO_MESCR_Enolase_OS=Mesembryanthemum_crystallinum_GN=PGH1_PE=2_SV=1	2.00E-173	[illegible]	[illegible]
comp21171_c0_seq1.p1	sp|O04450|TCPE_ARATH_T-complex_protein_1_subunit_epsilon_OS=Arabidopsis_thaliana_GN=At1g24510_PE=2_SV=1	0	[illegible]	[illegible]
comp21172_c0_seq1.p1	sp|A1USR3|RL15_BARBK_50S_ribosomal_protein_L15_OS=Bartonella_bacilliformis_(strain_ATCC_35685_/_KC583)_GN=rplO_PE=3_SV=1	1.00E-14	[illegible]	[illegible]
comp21173_c0_seq1.p1	sp|Q9S7Q2|PP124_ARATH_Pentatricopeptide_repeat-containing_protein_At1g74850,_chloroplastic_OS=Arabidopsis_thaliana_GN=PTAC2_PE=2_SV=1	2.00E-49	[illegible]	[illegible]
comp21173_c0_seq1.p2				
comp21175_c0_seq1.p1	sp|Q9CR11|YETS4_MOUSE_YEATS_domain-containing_protein_4_OS=Mus_musculus_GN=Yeats4_PE=2_SV=1	3.00E-36	[illegible]	[illegible]
comp21180_c0_seq1.p1	sp|P37766|YDIF_ECOLI_Uncharacterized_protein_ydiF_OS=Escherichia_coli_(strain_K12)_GN=ydiF_PE=4_SV=3	1.00E-113	[illegible]	[illegible]
comp21181_c0_seq1.p2				
comp21182_c0_seq1.p1	sp|P19821|DPO1_THEAQ_DNA_polymerase_I,_thermostable_OS=Thermus_aquaticus_GN=polA_PE=1_SV=1	2.00E-50	[illegible]	[illegible]
comp21185_c0_seq1.p1				
comp21186_c0_seq1.p2	sp|Q9ZS91|MSRB5_ARATH_Peptide_methionine_sulfoxide_reductase_B5_OS=Arabidopsis_thaliana_GN=MSRB5_PE=2_SV=1	3.00E-43	[illegible]	[illegible]
comp21191_c0_seq1.p1				
comp21191_c0_seq2.p1				
comp21191_c0_seq3.p1	sp|Q9JK42|PDK2_MOUSE_[Pyruvate_dehydrogenase_[lipoamide]]_kinase_isozyme_2,_mitochondrial_OS=Mus_musculus_GN=Pdk2_PE=1_SV=2	6.00E-36	[illegible]	[illegible]
comp21192_c0_seq1.p2				
comp21194_c0_seq1.p1				
comp21194_c0_seq2.p1				
comp21195_c0_seq2.p1				
comp21196_c0_seq1.p1	sp|Q6DJG6|BABA1_XENLA_BRISC_and_BRCA1-A_complex_member_1_OS=Xenopus_laevis_GN=babam1_PE=2_SV=1	5.00E-17	[illegible]	[illegible]
comp21197_c0_seq1.p1	sp|Q9FUM8|HMT3_MAIZE_Homocysteine_S-methyltransferase_3_OS=Zea_mays_GN=HMT-3_PE=2_SV=1	6.00E-52	[illegible]	[illegible]
comp21197_c0_seq2.p1	sp|Q9FUM7|HMT4_MAIZE_Homocysteine_S-methyltransferase_4_OS=Zea_mays_GN=HMT-4_PE=2_SV=1	3.00E-45	[illegible]	[illegible]
comp21199_c0_seq1.p1	sp|Q9XFG3|TBG_PHYPA_Tubulin_gamma_chain_OS=Physcomitrella_patens_subsp._patens_GN=TUBG1_PE=3_SV=1	0	[illegible]	[illegible]
comp21199_c0_seq1.p2				
comp21203_c0_seq1.p1	sp|Q54JC0|CMBB_DICDI_Calmodulin-binding_protein_CmbB_OS=Dictyostelium_discoideum_GN=cmbB_PE=1_SV=1	1.00E-14	[illegible]	[illegible]
comp21204_c0_seq1.p1	sp|Q6NY34|AS1BB_DANRE_Histone_chaperone_asf1b-B_OS=Danio_rerio_GN=asf1bb_PE=2_SV=1	6.00E-50	[illegible]	[illegible]
comp21205_c0_seq1.p1				
comp21209_c0_seq1.p1				
comp21209_c0_seq3.p1				
comp21211_c0_seq1.p1	sp|Q00472|PNPP_SCHPO_4-nitrophenylphosphatase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=pho2_PE=2_SV=2	4.00E-57	[illegible]	[illegible]
comp21212_c0_seq2.p1	sp|Q9LZM3|PPCS2_ARATH_Phosphopantothenate--cysteine_ligase_2_OS=Arabidopsis_thaliana_GN=PPCS2_PE=2_SV=2	3.00E-32	[illegible]	[illegible]
comp21212_c0_seq2.p3				
comp21214_c0_seq1.p4				
comp21214_c0_seq2.p1	sp|Q9CY45|N6MT2_MOUSE_N(6)-adenine-specific_DNA_methyltransferase_2_OS=Mus_musculus_GN=N6amt2_PE=2_SV=1	9.00E-13	[illegible]	[illegible]
comp21215_c0_seq1.p1				
comp21217_c0_seq2.p1				
comp21218_c0_seq1.p1	sp|Q40296|FCPB_MACPY_Fucoxanthin-chlorophyll_a-c_binding_protein_B,_chloroplastic_OS=Macrocystis_pyrifera_GN=FCPB_PE=2_SV=1	6.00E-79	[illegible]	[illegible]
comp21218_c2_seq1.p2	sp|Q0WQF7|ODP21_ARATH_Dihydrolipoyllysine-residue_acetyltransferase_component_1_of_pyruvate_dehydrogenase_complex,_mitochondrial_OS=Arabidopsis_thaliana_GN=LTA3_PE=1_SV=2	2.00E-11	[illegible]	[illegible]
comp21220_c0_seq1.p1	sp|Q8L5U0|CSN4_ARATH_COP9_signalosome_complex_subunit_4_OS=Arabidopsis_thaliana_GN=CSN4_PE=1_SV=2	2.00E-77	[illegible]	[illegible]
comp21222_c0_seq1.p1				
comp21222_c1_seq1.p1				
comp21223_c0_seq1.p2				
comp21225_c0_seq1.p1	sp|A5WUY6|CA201_DANRE_UPF0490_protein_C1orf201_homolog_OS=Danio_rerio_GN=si:dkey-218f9.1_PE=2_SV=1	4.00E-15	[illegible]	[illegible]
comp21225_c0_seq2.p1	sp|Q3KQ80|CA201_XENLA_UPF0490_protein_C1orf201_homolog_OS=Xenopus_laevis_PE=2_SV=1	2.00E-14	[illegible]	[illegible]
comp21227_c0_seq1.p1	sp|P53007|TXTP_HUMAN_Tricarboxylate_transport_protein,_mitochondrial_OS=Homo_sapiens_GN=SLC25A1_PE=1_SV=2	4.00E-65	[illegible]	[illegible]
comp21229_c0_seq1.p1				
comp21229_c0_seq1.p2				
comp21235_c0_seq2.p2				
comp21236_c0_seq2.p1	sp|Q8BTS4|NUP54_MOUSE_Nuclear_pore_complex_protein_Nup54_OS=Mus_musculus_GN=Nup54_PE=1_SV=1	1.00E-14	[illegible]	[illegible]
comp21237_c0_seq4.p1	sp|Q4KLQ5|WDR76_XENLA_WD_repeat-containing_protein_76_OS=Xenopus_laevis_GN=wdr76_PE=2_SV=1	2.00E-52		
comp21238_c0_seq1.p1				
comp21239_c0_seq1.p1	sp|Q9SSR1|Y1259_ARATH_DCC_family_protein_At1g52590,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g52590_PE=1_SV=1	4.00E-17	[illegible]	[illegible]
comp21239_c0_seq2.p1	sp|Q9SSR1|Y1259_ARATH_DCC_family_protein_At1g52590,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g52590_PE=1_SV=1	4.00E-17	[illegible]	[illegible]
comp2124_c0_seq1.p1	sp|Q7ZV82|RL27_DANRE_60S_ribosomal_protein_L27_OS=Danio_rerio_GN=rpl27_PE=2_SV=3	2.00E-26	[illegible]	[illegible]
comp21240_c0_seq1.p1	sp|Q27177|CATR1_PARTE_Caltractin_ICL1a_OS=Paramecium_tetraurelia_GN=Icl1a_PE=1_SV=2	3.00E-64	[illegible]	[illegible]
comp21240_c0_seq1.p3				
comp21242_c0_seq2.p1				
comp21244_c0_seq1.p1	sp|Q39757|1433_FUCVE_14-3-3-like_protein_OS=Fucus_vesiculosus_PE=2_SV=1	3.00E-167	GO:0019904	[illegible]
comp21244_c0_seq2.p1	sp|Q39757|1433_FUCVE_14-3-3-like_protein_OS=Fucus_vesiculosus_PE=2_SV=1	7.00E-81	GO:0019904	[illegible]
comp21245_c0_seq1.p1	sp|P79987|HIRA_CHICK_Protein_HIRA_OS=Gallus_gallus_GN=HIRA_PE=1_SV=2	1.00E-77	[illegible]	[illegible]
comp21245_c0_seq1.p2				
comp21247_c0_seq2.p1	sp|Q6AXS0|NCKX6_RAT_Sodium/potassium/calcium_exchanger_6_OS=Rattus_norvegicus_GN=Slc24a6_PE=1_SV=1	3.00E-22	[illegible]	[illegible]
comp21247_c0_seq3.p1	sp|Q6AXS0|NCKX6_RAT_Sodium/potassium/calcium_exchanger_6_OS=Rattus_norvegicus_GN=Slc24a6_PE=1_SV=1	2.00E-21	[illegible]	[illegible]
comp21248_c0_seq1.p1	sp|Q3UJV1|CCD61_MOUSE_Coiled-coil_domain-containing_protein_61_OS=Mus_musculus_GN=Ccdc61_PE=2_SV=1	5.00E-22	[illegible]	[illegible]
comp21249_c0_seq1.p1				
comp21250_c0_seq2.p1				
comp21251_c0_seq1.p1	sp|P36428|SYA_ARATH_Alanine--tRNA_ligase_OS=Arabidopsis_thaliana_GN=ALATS_PE=1_SV=3	0	[illegible]	[illegible]
comp21252_c0_seq1.p1				
comp21255_c0_seq1.p1	sp|Q9LIG6|NIFU4_ARATH_NifU-like_protein_4,_mitochondrial_OS=Arabidopsis_thaliana_GN=NIFU4_PE=2_SV=1	5.00E-55	[illegible]	[illegible]
comp21255_c0_seq2.p1	sp|Q9LIG6|NIFU4_ARATH_NifU-like_protein_4,_mitochondrial_OS=Arabidopsis_thaliana_GN=NIFU4_PE=2_SV=1	5.00E-55	[illegible]	[illegible]
comp21257_c0_seq1.p1	sp|Q5PPI9|TTLL1_RAT_Probable_tubulin_polyglutamylase_TTLL1_OS=Rattus_norvegicus_GN=Ttll1_PE=2_SV=1	3.00E-167	[illegible]	[illegible]
comp21257_c0_seq1.p3				
comp21258_c1_seq1.p1	sp|Q566V3|RML1A_DANRE_RNA_methyltransferase-like_protein_1A_OS=Danio_rerio_GN=rnmtl1a_PE=2_SV=1	5.00E-31	[illegible]	[illegible]
comp21259_c0_seq1.p1	sp|Q9CWX9|DDX47_MOUSE_Probable_ATP-dependent_RNA_helicase_DDX47_OS=Mus_musculus_GN=Ddx47_PE=2_SV=2	0	[illegible]	[illegible]
comp21260_c0_seq1.p1				
comp21261_c0_seq1.p1	sp|Q5TDH0|DDI2_HUMAN_Protein_DDI1_homolog_2_OS=Homo_sapiens_GN=DDI2_PE=1_SV=1	2.00E-26	[illegible]	[illegible]
comp21261_c0_seq2.p1	sp|P0CS14|DDI1_CRYNJ_DNA_damage-inducible_protein_1_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=DDI1_PE=3_SV=1	2.00E-37	[illegible]	[illegible]
comp21262_c0_seq2.p2				
comp21263_c0_seq1.p1	sp|Q9FY46|SUT41_ARATH_Sulfate_transporter_4.1,_chloroplastic_OS=Arabidopsis_thaliana_GN=SULTR4;1_PE=2_SV=1	1.00E-76	[illegible]	[illegible]
comp21266_c0_seq2.p1	sp|Q91Y26|NOC3L_CRIGR_Nucleolar_complex_protein_3_homolog_OS=Cricetulus_griseus_GN=NOC3L_PE=2_SV=1	3.00E-40	GO:0005634,GO:0005730	[illegible]
comp21267_c0_seq1.p2				
comp21268_c0_seq1.p1				
comp21272_c0_seq1.p1				
comp21273_c0_seq1.p1				
comp21275_c0_seq1.p1				
comp21276_c0_seq1.p2				
comp21278_c0_seq1.p1	sp|P31752|ASNS_ASPOF_Asparagine_synthetase_[glutamine-hydrolyzing]_OS=Asparagus_officinalis_PE=2_SV=2	0	[illegible]	[illegible]
comp21279_c0_seq2.p1				
comp21281_c0_seq1.p1	sp|Q54GN8|NSA2_DICDI_Ribosome_biogenesis_protein_NSA2_homolog_OS=Dictyostelium_discoideum_GN=nsa2_PE=3_SV=1	7.00E-133	[illegible]	[illegible]
comp21282_c0_seq1.p1				
comp21285_c0_seq1.p1				
comp21285_c0_seq2.p1				
comp21286_c0_seq1.p1				
comp21287_c0_seq1.p1	sp|Q6NVL7|CHM2B_XENTR_Charged_multivesicular_body_protein_2b_OS=Xenopus_tropicalis_GN=chmp2b_PE=2_SV=1	1.00E-32	[illegible]	[illegible]
comp21288_c0_seq2.p1	sp|Q5U317|FIP1_RAT_Pre-mRNA_3'-end-processing_factor_FIP1_OS=Rattus_norvegicus_GN=Fip1l1_PE=1_SV=1	2.00E-13	[illegible]	[illegible]
comp21289_c0_seq1.p1	sp|Q4V8A2|CDC27_RAT_Cell_division_cycle_protein_27_homolog_OS=Rattus_norvegicus_GN=Cdc27_PE=2_SV=1	7.00E-15	[illegible]	[illegible]
comp21289_c0_seq2.p1	sp|Q4V8A2|CDC27_RAT_Cell_division_cycle_protein_27_homolog_OS=Rattus_norvegicus_GN=Cdc27_PE=2_SV=1	6.00E-15	[illegible]	[illegible]
comp21290_c0_seq1.p1	sp|A4XD40|KMO_SALTO_Kynurenine_3-monooxygenase_OS=Salinispora_tropica_(strain_ATCC_BAA-916_/_DSM_44818_/_CNB-440)_GN=kmo_PE=3_SV=1	1.00E-20	[illegible]	[illegible]
comp21291_c0_seq1.p1				
comp21292_c0_seq1.p5	sp|P00057|CYC_RICCO_Cytochrome_c_OS=Ricinus_communis_PE=1_SV=1	2.00E-53	[illegible]	[illegible]
comp21294_c0_seq1.p1	sp|Q8RWS8|PP199_ARATH_Pentatricopeptide_repeat-containing_protein_At2g41720_OS=Arabidopsis_thaliana_GN=EMB2654_PE=2_SV=1	2.00E-23		
comp21294_c0_seq2.p1	sp|Q9S7Q2|PP124_ARATH_Pentatricopeptide_repeat-containing_protein_At1g74850,_chloroplastic_OS=Arabidopsis_thaliana_GN=PTAC2_PE=2_SV=1	1.00E-30	[illegible]	[illegible]
comp21295_c0_seq1.p1	sp|P37221|MAOM_SOLTU_NAD-dependent_malic_enzyme_62_kDa_isoform,_mitochondrial_OS=Solanum_tuberosum_PE=1_SV=1	2.00E-144	[illegible]	[illegible]
comp21298_c0_seq2.p1				
comp21300_c0_seq1.p1				
comp21301_c0_seq1.p1	sp|Q8RXK2|SDN3_ARATH_Small_RNA_degrading_nuclease_3_OS=Arabidopsis_thaliana_GN=SDN3_PE=1_SV=1	1.00E-26	[illegible]	[illegible]
comp21302_c0_seq2.p1				
comp21303_c0_seq1.p1				
comp21305_c0_seq1.p2				
comp21305_c0_seq4.p1				
comp21306_c0_seq2.p1	sp|Q28IL6|RL22_XENTR_60S_ribosomal_protein_L22_OS=Xenopus_tropicalis_GN=rpl22_PE=2_SV=3	9.00E-28	[illegible]	[illegible]
comp21307_c0_seq1.p1				
comp21307_c0_seq2.p1				
comp21308_c0_seq1.p1				
comp21309_c0_seq1.p1	sp|P37624|YHIH_ECOLI_Uncharacterized_ABC_transporter_ATP-binding_protein_YhiH_OS=Escherichia_coli_(strain_K12)_GN=yhiH_PE=3_SV=3	0	[illegible]	[illegible]
comp21309_c1_seq1.p1	sp|P37624|YHIH_ECOLI_Uncharacterized_ABC_transporter_ATP-binding_protein_YhiH_OS=Escherichia_coli_(strain_K12)_GN=yhiH_PE=3_SV=3	1.00E-109	[illegible]	[illegible]
comp21310_c0_seq1.p1	sp|Q6GNI4|EIF3K_XENLA_Eukaryotic_translation_initiation_factor_3_subunit_K_OS=Xenopus_laevis_GN=eif3k_PE=2_SV=1	3.00E-23	[illegible]	[illegible]
comp21312_c1_seq1.p1	sp|Q54M29|Y6239_DICDI_Serine_hydrolase-like_protein_DDB_G0286239_OS=Dictyostelium_discoideum_GN=DDB_G0286239_PE=3_SV=2	1.00E-45	GO:0008152,GO:0016787	[illegible]
comp21313_c0_seq1.p2	sp|Q9FMY5|U2AFB_ARATH_Splicing_factor_U2af_small_subunit_B_OS=Arabidopsis_thaliana_GN=U2AF35B_PE=2_SV=1	3.00E-77	[illegible]	[illegible]
comp21315_c0_seq2.p2				
comp21316_c0_seq1.p1				
comp21316_c0_seq1.p2				
comp21318_c0_seq3.p1				
comp21319_c0_seq1.p1				
comp2132_c0_seq1.p1				
comp21320_c0_seq1.p1				
comp21322_c0_seq1.p1				
comp21323_c0_seq2.p1	sp|Q5E9W3|PYRD_BOVIN_Dihydroorotate_dehydrogenase_(quinone),_mitochondrial_OS=Bos_taurus_GN=DHODH_PE=1_SV=1	2.00E-124	[illegible]	[illegible]
comp21328_c0_seq1.p1				
comp21328_c0_seq2.p1				
comp21329_c0_seq1.p1	sp|P23818|GRIA1_MOUSE_Glutamate_receptor_1_OS=Mus_musculus_GN=Gria1_PE=1_SV=1	6.00E-14	[illegible]	[illegible]
comp21330_c0_seq1.p1				
comp21331_c0_seq1.p1				
comp21332_c0_seq2.p1	sp|P27522|CB13_SOLLC_Chlorophyll_a-b_binding_protein_8,_chloroplastic_OS=Solanum_lycopersicum_GN=CAB8_PE=3_SV=1	6.00E-18	[illegible]	[illegible]
comp21332_c0_seq2.p2				
comp21333_c0_seq1.p1	sp|B2RS91|RRN3_MOUSE_RNA_polymerase_I-specific_transcription_initiation_factor_RRN3_OS=Mus_musculus_GN=Rrn3_PE=1_SV=1	6.00E-33	[illegible]	[illegible]
comp21334_c0_seq1.p1	sp|P25323|MYLKA_DICDI_Myosin_light_chain_kinase_A_OS=Dictyostelium_discoideum_GN=mlkA_PE=1_SV=2	2.00E-64	[illegible]	[illegible]
comp21334_c0_seq1.p3				
comp21337_c0_seq1.p1				
comp21338_c0_seq1.p1	sp|Q13367|AP3B2_HUMAN_AP-3_complex_subunit_beta-2_OS=Homo_sapiens_GN=AP3B2_PE=1_SV=2	6.00E-12	[illegible]	[illegible]
comp21338_c0_seq3.p1	sp|Q13367|AP3B2_HUMAN_AP-3_complex_subunit_beta-2_OS=Homo_sapiens_GN=AP3B2_PE=1_SV=2	5.00E-120	[illegible]	[illegible]
comp2134_c0_seq1.p1	sp|Q3Z3L4|AROA_SHISS_3-phosphoshikimate_1-carboxyvinyltransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=aroA_PE=3_SV=1	2.00E-70	[illegible]	[illegible]
comp21342_c0_seq1.p2	sp|Q9FLP6|SUMO2_ARATH_Small_ubiquitin-related_modifier_2_OS=Arabidopsis_thaliana_GN=SUMO2_PE=1_SV=1	2.00E-20	[illegible]	[illegible]
comp21347_c0_seq1.p1	sp|Q941R4|GONS1_ARATH_GDP-mannose_transporter_GONST1_OS=Arabidopsis_thaliana_GN=GONST1_PE=1_SV=2	1.00E-50	[illegible]	[illegible]
comp21348_c0_seq1.p1				
comp21348_c0_seq1.p2				
comp21349_c0_seq1.p1	sp|Q6ICB0|PPDE2_HUMAN_PPPDE_peptidase_domain-containing_protein_2_OS=Homo_sapiens_GN=PPPDE2_PE=1_SV=1	9.00E-34	[illegible]	[illegible]
comp21350_c0_seq1.p1				
comp21352_c0_seq1.p1	sp|Q3UX61|NAA11_MOUSE_N-alpha-acetyltransferase_11_OS=Mus_musculus_GN=Naa11_PE=2_SV=1	5.00E-33	[illegible]	[illegible]
comp21355_c0_seq1.p1				
comp21356_c1_seq1.p2	sp|O23920|HPPD_DAUCA_4-hydroxyphenylpyruvate_dioxygenase_OS=Daucus_carota_PE=2_SV=1	9.00E-39	[illegible]	[illegible]
comp21356_c1_seq1.p3				
comp21363_c0_seq2.p1				
comp21364_c0_seq1.p1				
comp21366_c0_seq1.p1				
comp21368_c0_seq2.p1	sp|Q9M076|K6PF6_ARATH_6-phosphofructokinase_6_OS=Arabidopsis_thaliana_GN=PFK6_PE=1_SV=1	2.00E-101	[illegible]	[illegible]
comp21370_c0_seq1.p1	sp|Q2JKE8|METE_SYNJB_5-methyltetrahydropteroyltriglutamate--homocysteine_methyltransferase_OS=Synechococcus_sp._(strain_JA-2-3B'a(2-13))_GN=metE_PE=3_SV=1	0	[illegible]	[illegible]
comp21371_c0_seq1.p1	sp|Q28F07|ANM1_XENTR_Protein_arginine_N-methyltransferase_1_OS=Xenopus_tropicalis_GN=prmt1_PE=2_SV=1	2.00E-130	[illegible]	[illegible]
comp21372_c0_seq1.p1				
comp21374_c0_seq1.p1				
comp21376_c0_seq1.p1	sp|Q5ZJ17|RBG1L_CHICK_Rab_GTPase-activating_protein_1-like_OS=Gallus_gallus_GN=RABGAP1L_PE=2_SV=1	2.00E-17	[illegible]	[illegible]
comp21377_c0_seq1.p1	sp|A2BGL3|WSCD2_DANRE_WSC_domain-containing_protein_2_OS=Danio_rerio_GN=wscd2_PE=3_SV=1	5.00E-16	[illegible]	[illegible]
comp21379_c0_seq1.p1				
comp21379_c0_seq2.p1				
comp21380_c0_seq1.p1				
comp21382_c0_seq1.p1				
comp21385_c0_seq4.p1				
comp21390_c0_seq1.p1	sp|Q42290|MPPB_ARATH_Probable_mitochondrial-processing_peptidase_subunit_beta_OS=Arabidopsis_thaliana_GN=At3g02090_PE=1_SV=2	4.00E-60	[illegible]	[illegible]
comp21391_c0_seq1.p1	sp|P53798|FDFT_MOUSE_Squalene_synthase_OS=Mus_musculus_GN=Fdft1_PE=2_SV=2	4.00E-93	[illegible]	[illegible]
comp21394_c0_seq1.p1	sp|Q6P963|GLO2_DANRE_Hydroxyacylglutathione_hydrolase,_mitochondrial_OS=Danio_rerio_GN=hagh_PE=2_SV=2	2.00E-79	[illegible]	[illegible]
comp21394_c0_seq2.p1	sp|O24496|GLO2C_ARATH_Hydroxyacylglutathione_hydrolase_cytoplasmic_OS=Arabidopsis_thaliana_GN=GLX2-2_PE=1_SV=2	1.00E-64	[illegible]	[illegible]
comp21397_c0_seq1.p1				
comp21399_c0_seq1.p1	sp|Q8KG38|GLMS_CHLTE_Glucosamine--fructose-6-phosphate_aminotransferase_[isomerizing]_OS=Chlorobium_tepidum_(strain_ATCC_49652_/_DSM_12025_/_TLS)_GN=glmS_PE=3_SV=3	3.00E-110	[illegible]	[illegible]
comp21400_c0_seq2.p1				
comp21402_c0_seq1.p1				
comp21403_c0_seq1.p1				
comp21403_c0_seq2.p1				
comp21407_c0_seq1.p1	sp|Q6GQE1|T184C_XENLA_Transmembrane_protein_184C_OS=Xenopus_laevis_GN=tmem184c_PE=2_SV=1	2.00E-61	[illegible]	[illegible]
comp21408_c0_seq1.p1				
comp21409_c0_seq1.p1	sp|Q54UB1|TRM6_DICDI_tRNA_(adenine(58)-N(1))-methyltransferase_non-catalytic_subunit_trm6_OS=Dictyostelium_discoideum_GN=trmt6_PE=3_SV=1	9.00E-19	[illegible]	[illegible]
comp21409_c0_seq2.p1	sp|Q54UB1|TRM6_DICDI_tRNA_(adenine(58)-N(1))-methyltransferase_non-catalytic_subunit_trm6_OS=Dictyostelium_discoideum_GN=trmt6_PE=3_SV=1	6.00E-60	[illegible]	[illegible]
comp21413_c0_seq1.p1	sp|Q49X73|RECA_STAS1_Protein_RecA_OS=Staphylococcus_saprophyticus_subsp._saprophyticus_(strain_ATCC_15305_/_DSM_20229)_GN=recA_PE=3_SV=1	2.00E-109	[illegible]	[illegible]
comp21413_c0_seq1.p2	sp|O15905|SODF_BABBO_Superoxide_dismutase_[Fe]_OS=Babesia_bovis_GN=SODB_PE=2_SV=1	4.00E-75	[illegible]	[illegible]
comp21415_c0_seq3.p1				
comp21417_c0_seq1.p2	sp|Q9W2D6|TIM10_DROME_Mitochondrial_import_inner_membrane_translocase_subunit_Tim10_OS=Drosophila_melanogaster_GN=Tim10_PE=2_SV=1	2.00E-15	[illegible]	[illegible]
comp21418_c0_seq1.p1	sp|Q8YSU5|Y2987_NOSS1_UPF0187_protein_alr2987_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=alr2987_PE=3_SV=1	6.00E-30	[illegible]	[illegible]
comp21419_c0_seq1.p1				
comp21419_c0_seq1.p3				
comp21424_c0_seq1.p1				
comp21425_c0_seq2.p1	sp|B2SY78|PDXH_BURPP_Pyridoxine/pyridoxamine_5'-phosphate_oxidase_OS=Burkholderia_phytofirmans_(strain_DSM_17436_/_PsJN)_GN=pdxH_PE=3_SV=1	8.00E-65	[illegible]	[illegible]
comp21426_c0_seq1.p1	sp|P49695|PKWA_THECU_Probable_serine/threonine-protein_kinase_pkwA_OS=Thermomonospora_curvata_GN=pkwA_PE=3_SV=1	6.00E-17	[illegible]	[illegible]
comp21427_c0_seq1.p1				
comp21428_c0_seq1.p1				
comp21429_c0_seq3.p1				
comp21430_c1_seq1.p1	sp|A5GW73|PGK_SYNR3_Phosphoglycerate_kinase_OS=Synechococcus_sp._(strain_RCC307)_GN=pgk_PE=3_SV=1	7.00E-159	[illegible]	[illegible]
comp21430_c1_seq2.p1	sp|Q42961|PGKH_TOBAC_Phosphoglycerate_kinase,_chloroplastic_OS=Nicotiana_tabacum_PE=2_SV=1	6.00E-132	[illegible]	[illegible]
comp21430_c1_seq2.p3	sp|B0JT86|PGK_MICAN_Phosphoglycerate_kinase_OS=Microcystis_aeruginosa_(strain_NIES-843)_GN=pgk_PE=3_SV=1	9.00E-26	[illegible]	[illegible]
comp21431_c0_seq1.p1				
comp21431_c0_seq1.p3				
comp21431_c0_seq1.p4				
comp21433_c0_seq1.p1				
comp21436_c0_seq2.p2				
comp21437_c0_seq1.p1				
comp21437_c0_seq1.p4				
comp21438_c0_seq2.p1				
comp21439_c0_seq1.p1	sp|Q5N643|SYR_SYNP6_Arginine--tRNA_ligase_OS=Synechococcus_sp._(strain_ATCC_27144_/_PCC_6301_/_SAUG_1402/1)_GN=argS_PE=3_SV=1	7.00E-159	[illegible]	[illegible]
comp21440_c0_seq1.p1	sp|Q09704|RRP4_SCHPO_Exosome_complex_component_rrp4_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rrp4_PE=2_SV=1	6.00E-68	[illegible]	[illegible]
comp21442_c0_seq1.p1	sp|Q9LHG8|ELC_ARATH_Protein_ELC_OS=Arabidopsis_thaliana_GN=ELC_PE=1_SV=1	7.00E-35	[illegible]	[illegible]

comp21443_c0_seq1.p1	sp|O34499|YKGB_BACSU_Uncharacterized_protein_YkgB_OS=Bacillus_subtilis_GN=ykgB_PE=3_SV=1	6.00E-40	GO:0005975,GO:0006006,GO:0006098,GO:0016787,GO:0017057	carbohydrate metabolic process,glucose metabolic process,pentose-phosphate shunt,hydrolase activity,6-phosphogluconolactonase activity
comp21444_c0_seq1.p1	sp|Q8IZN3|ZDH14_HUMAN_Probable_palmitoyltransferase_ZDHHC14_OS=Homo_sapiens_GN=ZDHHC14_PE=1_SV=1	1.00E-12	GO:0005783,GO:0008270,GO:0016020,GO:0016020,GO:0016021,GO:0016409,GO:0016740,GO:0016746,GO:0018345,GO:0019706,GO:0046872	endoplasmic reticulum,zinc ion binding,membrane,membrane,integral component of membrane,palmitoyltransferase activity,transferase activity,transferase activity, transferring acyl groups,protein palmitoylation,protein-cysteine S-palmitoyltransferase activity,metal ion binding
comp21446_c0_seq1.p1	sp|Q29RK2|PYC_BOVIN_Pyruvate_carboxylase,_mitochondrial_OS=Bos_taurus_GN=PC_PE=2_SV=2	0	GO:0000166,GO:0003677,GO:0003824,GO:0003824,GO:0004075,GO:0004736,GO:0004736,GO:0005524,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005759,GO:0006094,GO:0006094,GO:0006094,GO:0006629,GO:0008152,GO:0008152,GO:0016874,GO:0016874,GO:0046872,GO:0046872	nucleotide binding,DNA binding,catalytic activity,catalytic activity,biotin carboxylase activity,pyruvate carboxylase activity,pyruvate carboxylase activity,ATP binding,ATP binding,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial matrix,gluconeogenesis,gluconeogenesis,gluconeogenesis,lipid metabolic process,metabolic process,metabolic process,ligase activity,ligase activity,metal ion binding,metal ion binding
comp21448_c0_seq2.p1	sp|Q9ST27|PHOT2_ORYSJ_Phototropin-2_OS=Oryza_sativa_subsp._japonica_GN=PHOT2_PE=1_SV=1	1.00E-24	GO:0000023,GO:0000155,GO:0000155,GO:0000160,GO:0000160,GO:0000166,GO:0000166,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004871,GO:0004871,GO:0005524,GO:0005524,GO:0005524,GO:0005794,GO:0005886,GO:0006364,GO:0006468,GO:0006468,GO:0007165,GO:0007165,GO:0009637,GO:0009638,GO:0009644,GO:0009744,GO:0009785,GO:0009881,GO:0009881,GO:0009882,GO:0009882,GO:0009902,GO:0010027,GO:0010103,GO:0010114,GO:0010118,GO:0010155,GO:0010181,GO:0010207,GO:0010218,GO:0010362,GO:0016020,GO:0016301,GO:0016301,GO:0016310,GO:0016310,GO:0016556,GO:0016740,GO:0016740,GO:0016772,GO:0016772,GO:0018298,GO:0018298,GO:0019252,GO:0019761,GO:0023014,GO:0034660,GO:0035304,GO:0042793,GO:0042802,GO:0043085,GO:0045893,GO:0046777,GO:0050896,GO:0050896	maltose metabolic process,phosphorelay sensor kinase activity,phosphorelay sensor kinase activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,nucleotide binding,protein kinase activity,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,signal transducer activity,signal transducer activity,ATP binding,ATP binding,ATP binding,Golgi apparatus,plasma membrane,rRNA processing,protein phosphorylation,protein phosphorylation,signal transduction,signal transduction,response to blue light,phototropism,response to high light intensity,response to sucrose,blue light signaling pathway,photoreceptor activity,photoreceptor activity,blue light photoreceptor activity,blue light photoreceptor activity,chloroplast relocation,thylakoid membrane organization,stomatal complex morphogenesis,response to red light,stomatal movement,regulation of proton transport,FMN binding,photosystem II assembly,response to far red light,negative regulation of anion channel activity by blue light,membrane,kinase activity,kinase activity,phosphorylation,phosphorylation,mRNA modification,transferase activity,transferase activity, transferring phosphorus-containing groups,transferase activity, transferring phosphorus-containing groups,protein-chromophore linkage,protein-chromophore linkage,starch biosynthetic process,glucosinolate biosynthetic process,signal transduction by phosphorylation,ncRNA metabolic process,regulation of protein dephosphorylation,transcription from plastid promoter,identical protein binding,positive regulation of catalytic activity,positive regulation of transcription, DNA-templated,protein autophosphorylation,response to stimulus,response to stimulus
comp21449_c0_seq1.p1	sp|Q3EC11|ZDHC2_ARATH_Probable_S-acyltransferase_At2g14255_OS=Arabidopsis_thaliana_GN=At2g14255_PE=2_SV=2	2.00E-30	GO:0000139,GO:0005794,GO:0005794,GO:0008150,GO:0008152,GO:0008152,GO:0008152,GO:0008270,GO:0016020,GO:0016021,GO:0016740,GO:0016746,GO:0019706,GO:0046872	Golgi membrane,Golgi apparatus,Golgi apparatus,biological_process,metabolic process,metabolic process,metabolic process,zinc ion binding,membrane,integral component of membrane,transferase activity,transferase activity, transferring acyl groups,protein-cysteine S-palmitoyltransferase activity,metal ion binding
comp21449_c0_seq1.p2				
comp21450_c0_seq1.p1				
comp21450_c0_seq2.p1	sp|Q94AX4|DLD_ARATH_D-lactate_dehydrogenase_[cytochrome],_mitochondrial_OS=Arabidopsis_thaliana_GN=DLD_PE=1_SV=1	3.00E-140	GO:0003824,GO:0004458,GO:0004458,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0008762,GO:0008891,GO:0016491,GO:0016491,GO:0016614,GO:0019154,GO:0042802,GO:0050660,GO:0050660,GO:0051596,GO:0055114,GO:0055114	catalytic activity,D-lactate dehydrogenase (cytochrome) activity,D-lactate dehydrogenase (cytochrome) activity,ATP binding,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,UDP-N-acetylmuramate dehydrogenase activity,glycolate oxidase activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on CH-OH group of donors,glycolate dehydrogenase activity,identical protein binding,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,methylglyoxal catabolic process,oxidation-reduction process,oxidation-reduction process
comp21451_c0_seq1.p1				
comp21452_c0_seq1.p1	sp|P12783|PGKY_WHEAT_Phosphoglycerate_kinase,_cytosolic_OS=Triticum_aestivum_PE=2_SV=1	0	GO:0000166,GO:0004618,GO:0004618,GO:0005524,GO:0005737,GO:0005737,GO:0006096,GO:0006096,GO:0006096,GO:0016301,GO:0016310,GO:0016740	nucleotide binding,phosphoglycerate kinase activity,phosphoglycerate kinase activity,ATP binding,cytoplasm,cytoplasm,glycolytic process,glycolytic process,glycolytic process,kinase activity,phosphorylation,transferase activity
comp21452_c0_seq1.p5				
comp21453_c0_seq1.p1				
comp21454_c0_seq1.p1	sp|Q5RGJ5|C19L1_DANRE_CWF19-like_protein_1_OS=Danio_rerio_GN=cwf19l1_PE=2_SV=1	9.00E-36	GO:0003824,GO:0005575,GO:0008152	catalytic activity,cellular_component,metabolic process
comp21454_c0_seq4.p1	sp|Q5RGJ5|C19L1_DANRE_CWF19-like_protein_1_OS=Danio_rerio_GN=cwf19l1_PE=2_SV=1	8.00E-36	GO:0003824,GO:0005575,GO:0008152	catalytic activity,cellular_component,metabolic process
comp21455_c0_seq1.p1				
comp21456_c0_seq2.p1	sp|P50165|TRNH_DATST_Tropinone_reductase_homolog_OS=Datura_stramonium_PE=2_SV=1	3.00E-81	GO:0008152,GO:0016491,GO:0016491,GO:0055114	metabolic process,oxidoreductase activity,oxidoreductase activity,oxidation-reduction process
comp21457_c0_seq1.p1	sp|O94396|PUS1_SCHPO_tRNA_pseudouridine_synthase_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=pus1_PE=1_SV=1	4.00E-54	GO:0001522,GO:0003723,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0008033,GO:0009451,GO:0009982,GO:0009982,GO:0016853,GO:0031119,GO:0046872	pseudouridine synthesis,RNA binding,nucleus,nucleus,nucleus,nucleus,tRNA processing,RNA modification,pseudouridine synthase activity,pseudouridine synthase activity,isomerase activity,tRNA pseudouridine synthesis,metal ion binding
comp21458_c0_seq1.p2				
comp21459_c0_seq1.p1	sp|Q9UTK2|RM19_SCHPO_54S_ribosomal_protein_L19,_mitochondrial_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=mrpl19_PE=2_SV=1	2.00E-35	GO:0003735,GO:0003735,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0005739,GO:0005762,GO:0005840,GO:0005840,GO:0006412,GO:0030529,GO:0032543	structural constituent of ribosome,structural constituent of ribosome,cytoplasm,cytoplasm,cytoplasm,mitochondrion,mitochondrion,mitochondrial large ribosomal subunit,ribosome,ribosome,translation,ribonucleoprotein complex,mitochondrial translation
comp21461_c0_seq1.p1				
comp21461_c0_seq2.p1				
comp21462_c0_seq1.p3				
comp21463_c0_seq1.p1				
comp21465_c0_seq1.p1				
comp21466_c0_seq1.p1	sp|Q0WWQ1|ATG3_ARATH_Autophagy-related_protein_3_OS=Arabidopsis_thaliana_GN=ATG3_PE=2_SV=2	7.00E-51	GO:0000045,GO:0000153,GO:0000422,GO:0000902,GO:0005515,GO:0005737,GO:0005737,GO:0005829,GO:0006623,GO:0006810,GO:0006914,GO:0015031,GO:0016049,GO:0016192,GO:0019776,GO:0044804,GO:0048193	autophagic vacuole assembly,cytoplasmic ubiquitin ligase complex,mitochondrion degradation,cell morphogenesis,protein binding,cytoplasm,cytoplasm,cytosol,protein targeting to vacuole,transport,autophagy,protein transport,cell growth,vesicle-mediated transport,Atg8 ligase activity,nucleophagy,Golgi vesicle transport
comp21469_c0_seq1.p1	sp|Q9C9Z1|ZTP50_ARATH_Putative_zinc_transporter_At3g08650_OS=Arabidopsis_thaliana_GN=At3g08650_PE=2_SV=2	2.00E-41	GO:0006810,GO:0006811,GO:0006829,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0030001,GO:0046873,GO:0055085	transport,ion transport,zinc ion transport,membrane,membrane,membrane,integral component of membrane,metal ion transport,metal ion transmembrane transporter activity,transmembrane transport
comp2147_c0_seq1.p1				
comp21471_c0_seq1.p1				
comp21471_c0_seq2.p1				
comp21472_c0_seq1.p1				
comp21477_c0_seq1.p1	sp|P07363|CHEA_ECOLI_Chemotaxis_protein_CheA_OS=Escherichia_coli_(strain_K12)_GN=cheA_PE=1_SV=3	4.00E-57	GO:0000155,GO:0000160,GO:0000160,GO:0000160,GO:0000166,GO:0004673,GO:0004673,GO:0004871,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005622,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0005886,GO:0006935,GO:0006935,GO:0006935,GO:0007165,GO:0016301,GO:0016310,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0018106,GO:0018106,GO:0023014,GO:0031400,GO:0035307,GO:0046777,GO:0051649,GO:0051649	phosphorelay sensor kinase activity,phosphorelay signal transduction system,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,protein histidine kinase activity,protein histidine kinase activity,signal transducer activity,protein binding,protein binding,protein binding,protein binding,protein binding,ATP binding,intracellular,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytosol,plasma membrane,chemotaxis,chemotaxis,chemotaxis,signal transduction,kinase activity,phosphorylation,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-histidine phosphorylation,peptidyl-histidine phosphorylation,signal transduction by phosphorylation,negative regulation of protein modification process,positive regulation of protein dephosphorylation,protein autophosphorylation,establishment of localization in cell,establishment of localization in cell
comp21477_c1_seq1.p1	sp|P07363|CHEA_ECOLI_Chemotaxis_protein_CheA_OS=Escherichia_coli_(strain_K12)_GN=cheA_PE=1_SV=3	5.00E-79	GO:0000155,GO:0000160,GO:0000160,GO:0000160,GO:0000166,GO:0004673,GO:0004673,GO:0004871,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005622,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0005886,GO:0006935,GO:0006935,GO:0006935,GO:0007165,GO:0016301,GO:0016310,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0018106,GO:0018106,GO:0023014,GO:0031400,GO:0035307,GO:0046777,GO:0051649,GO:0051649	phosphorelay sensor kinase activity,phosphorelay signal transduction system,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,protein histidine kinase activity,protein histidine kinase activity,signal transducer activity,protein binding,protein binding,protein binding,protein binding,protein binding,ATP binding,intracellular,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytosol,plasma membrane,chemotaxis,chemotaxis,chemotaxis,signal transduction,kinase activity,phosphorylation,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-histidine phosphorylation,peptidyl-histidine phosphorylation,signal transduction by phosphorylation,negative regulation of protein modification process,positive regulation of protein dephosphorylation,protein autophosphorylation,establishment of localization in cell,establishment of localization in cell
comp21478_c0_seq1.p1				
comp21479_c0_seq1.p1				
comp21482_c0_seq2.p1				
comp21483_c0_seq1.p1				
comp21484_c0_seq2.p1	sp|A8E4L1|COX19_BOVIN_Cytochrome_c_oxidase_assembly_protein_COX19_OS=Bos_taurus_GN=COX19_PE=3_SV=1	4.00E-16	GO:0005737,GO:0005737,GO:0005829	cytoplasm,cytoplasm,cytosol
comp21486_c0_seq2.p1	sp|Q5NVK5|PGTA_PONAB_Geranylgeranyl_transferase_type-2_subunit_alpha_OS=Pongo_abelii_GN=RABGGTA_PE=2_SV=1	7.00E-46	GO:0004659,GO:0004663,GO:0004663,GO:0004663,GO:0005968,GO:0008270,GO:0008318,GO:0016740,GO:0017137,GO:0018342,GO:0018344	prenyltransferase activity,Rab geranylgeranyltransferase activity,Rab geranylgeranyltransferase activity,Rab geranylgeranyltransferase activity,Rab-protein geranylgeranyltransferase complex,zinc ion binding,protein prenyltransferase activity,transferase activity,Rab GTPase binding,protein prenylation,protein geranylgeranylation
comp21488_c0_seq1.p1				
comp21489_c0_seq3.p1	sp|P0DH91|ARF2B_ARATH_ADP-ribosylation_factor_2-B_OS=Arabidopsis_thaliana_GN=ARF2-B_PE=2_SV=1	1.00E-109	GO:0000166,GO:0005525,GO:0005525,GO:0005525,GO:0005525,GO:0005622,GO:0005773,GO:0005794,GO:0005794,GO:0005794,GO:0005886,GO:0006499,GO:0006810,GO:0007264,GO:0015031,GO:0016004,GO:0016192,GO:0043085,GO:0005829	nucleotide binding,GTP binding,GTP binding,GTP binding,GTP binding,intracellular,vacuole,Golgi apparatus,Golgi apparatus,Golgi apparatus,plasma membrane,N-terminal protein myristoylation,transport,small GTPase mediated signal transduction,protein transport,phospholipase activator activity,vesicle-mediated transport,positive regulation of catalytic activity,cytosol
comp21490_c0_seq2.p1	sp|Q9DA80|RSH3B_MOUSE_Radial_spoke_head_protein_3_homolog_B_OS=Mus_musculus_GN=Rsph3b_PE=2_SV=1	5.00E-26	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp21491_c0_seq1.p1	sp|B8GM40|RRAAH_THISH_Putative_regulator_of_ribonuclease_activity_OS=Thioalkalivibrio_sp._(strain_HL-EbGR7)_GN=Tgr7_2551_PE=3_SV=1	5.00E-52	GO:0008152,GO:0008152,GO:0008152,GO:0008428,GO:0008948,GO:0016829,GO:0043086,GO:0046872,GO:0047443,GO:0051252	metabolic process,metabolic process,metabolic process,ribonuclease inhibitor activity,oxaloacetate decarboxylase activity,lyase activity,negative regulation of catalytic activity,metal ion binding,4-hydroxy-4-methyl-2-oxoglutarate aldolase activity,regulation of RNA metabolic process
comp21492_c0_seq1.p2				
comp21492_c0_seq1.p3	sp|Q63396|TCP4_RAT_Activated_RNA_polymerase_II_transcriptional_coactivator_p15_OS=Rattus_norvegicus_GN=Sub1_PE=2_SV=3	6.00E-20	GO:0001205,GO:0003677,GO:0003677,GO:0003697,GO:0003713,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005667,GO:0005730,GO:0006351,GO:0006355,GO:0006355,GO:0006357,GO:0044822,GO:0045944,GO:0070062	RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription,DNA binding,DNA binding,single-stranded DNA binding,transcription coactivator activity,nucleus,nucleus,nucleus,nucleus,transcription factor complex,nucleolus,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription from RNA polymerase II promoter,poly(A) RNA binding,positive regulation of transcription from RNA polymerase II promoter,extracellular vesicular exosome
comp21494_c0_seq1.p1	sp|Q74EU2|UBIE_GEOSL_Ubiquinone/menaquinone_biosynthesis_methyltransferase_ubiE_OS=Geobacter_sulfurreducens_(strain_ATCC_51573_/_DSM_12127_/_PCA)_GN=ubiE_PE=3_SV=1	2.00E-28	GO:0006744,GO:0006744,GO:0008168,GO:0008168,GO:0008425,GO:0009060,GO:0009234,GO:0009234,GO:0009234,GO:0016740,GO:0032259	ubiquinone biosynthetic process,ubiquinone biosynthetic process,methyltransferase activity,methyltransferase activity,2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity,aerobic respiration,menaquinone biosynthetic process,menaquinone biosynthetic process,menaquinone biosynthetic process,transferase activity,methylation
comp21494_c0_seq1.p2	sp|P48598|IF4E_DROME_Eukaryotic_translation_initiation_factor_4E_OS=Drosophila_melanogaster_GN=eIF-4E_PE=1_SV=1	7.00E-24	GO:0000022,GO:0000339,GO:0000339,GO:0000340,GO:0000340,GO:0000340,GO:0000340,GO:0000932,GO:0001558,GO:0003723,GO:0003723,GO:0003743,GO:0003743,GO:0003743,GO:0003743,GO:0003743,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0005829,GO:0005845,GO:0005875,GO:0006325,GO:0006412,GO:0006412,GO:0006412,GO:0006413,GO:0006413,GO:0006413,GO:0006413,GO:0006417,GO:0007052,GO:0007067,GO:0007067,GO:0007076,GO:0016070,GO:0016281,GO:0016281,GO:0016281,GO:0016281,GO:0016321,GO:0022008,GO:0030307,GO:0031370,GO:0031370,GO:0031594,GO:0035071,GO:0048102,GO:0097482	mitotic spindle elongation,RNA cap binding,RNA cap binding,RNA 7-methylguanosine cap binding,RNA 7-methylguanosine cap binding,RNA 7-methylguanosine cap binding,RNA 7-methylguanosine cap binding,cytoplasmic mRNA processing body,regulation of cell growth,RNA binding,RNA binding,translation initiation factor activity,translation initiation factor activity,translation initiation factor activity,translation initiation factor activity,translation initiation factor activity,protein binding,protein binding,protein binding,protein binding,protein binding,cytoplasm,cytoplasm,cytoplasm,cytosol,cytosol,cytosol,mRNA cap binding complex,microtubule associated complex,chromatin organization,translation,translation,translation,translational initiation,translational initiation,translational initiation,translational initiation,regulation of translation,mitotic spindle organization,mitotic nuclear division,mitotic nuclear division,mitotic chromosome condensation,RNA metabolic process,eukaryotic translation initiation factor 4F complex,eukaryotic translation initiation factor 4F complex,eukaryotic translation initiation factor 4F complex,eukaryotic translation initiation factor 4F complex,female meiosis chromosome segregation,neurogenesis,positive regulation of cell growth,eukaryotic initiation factor 4G binding,eukaryotic initiation factor 4G binding,neuromuscular junction,salivary gland cell autophagic cell death,autophagic cell death,muscle cell postsynaptic density
comp21495_c0_seq1.p1				
comp21496_c0_seq2.p1				
comp21504_c0_seq1.p3				
comp21506_c0_seq3.p1				
comp21509_c0_seq1.p1	sp|Q6BLK0|RL44_DEBHA_60S_ribosomal_protein_L44_OS=Debaryomyces_hansenii_(strain_ATCC_36239_/_CBS_767_/_JCM_1990_/_NBRC_0083_/_IGC_2968)_GN=RPL44_PE=3_SV=3	6.00E-54	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0030529	structural constituent of ribosome,intracellular,ribosome,ribosome,translation,ribonucleoprotein complex
comp21510_c0_seq1.p1	sp|Q3TX08|TRM1_MOUSE_tRNA_(guanine(26)-N(2))-dimethyltransferase_OS=Mus_musculus_GN=Trmt1_PE=1_SV=2	1.00E-143	GO:0000049,GO:0003723,GO:0003723,GO:0004809,GO:0005575,GO:0008033,GO:0008033,GO:0008150,GO:0008168,GO:0016740,GO:0030488,GO:0032259,GO:0044822,GO:0046872,GO:0046872	tRNA binding,RNA binding,RNA binding,tRNA (guanine-N2-)-methyltransferase activity,cellular_component,tRNA processing,tRNA processing,biological_process,methyltransferase activity,transferase activity,tRNA methylation,methylation,poly(A) RNA binding,metal ion binding,metal ion binding
comp21511_c1_seq1.p1	sp|Q327M6|RSMC_SHIDS_Ribosomal_RNA_small_subunit_methyltransferase_C_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=rsmC_PE=3_SV=1	3.00E-84	GO:0003676,GO:0005737,GO:0005737,GO:0006364,GO:0006364,GO:0008168,GO:0008168,GO:0008649,GO:0008990,GO:0008990,GO:0016740,GO:0031167,GO:0032259,GO:0032259,GO:0052914	nucleic acid binding,cytoplasm,cytoplasm,rRNA processing,rRNA processing,methyltransferase activity,methyltransferase activity,rRNA methyltransferase activity,rRNA (guanine-N2-)-methyltransferase activity,rRNA (guanine-N2-)-methyltransferase activity,transferase activity,rRNA methylation,methylation,methylation,16S rRNA (guanine(1207)-N(2))-methyltransferase activity
comp21512_c0_seq1.p1				
comp21512_c0_seq2.p1				
comp21512_c0_seq2.p2	sp|P36241|RL19_DROME_60S_ribosomal_protein_L19_OS=Drosophila_melanogaster_GN=RpL19_PE=1_SV=2	1.00E-73	GO:0000022,GO:0003735,GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0005840,GO:0006412,GO:0030529,GO:0051298	mitotic spindle elongation,structural constituent of ribosome,structural constituent of ribosome,intracellular,ribosome,ribosome,ribosome,translation,ribonucleoprotein complex,centrosome duplication
comp21513_c0_seq2.p1	sp|Q9URM2|TKT_SCHPO_Probable_transketolase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC2G5.05_PE=2_SV=1	0	GO:0003824,GO:0004802,GO:0004802,GO:0004802,GO:0005634,GO:0005737,GO:0005829,GO:0008152,GO:0009052,GO:0016740,GO:0046872	catalytic activity,transketolase activity,transketolase activity,transketolase activity,nucleus,cytoplasm,cytosol,metabolic process,pentose-phosphate shunt, non-oxidative branch,transferase activity,metal ion binding
comp21517_c0_seq3.p1	sp|P96604|YDBI_BACSU_UPF0118_membrane_protein_ydbI_OS=Bacillus_subtilis_GN=ydbI_PE=3_SV=1	1.00E-23	GO:0005886,GO:0005886,GO:0016020,GO:0016021	plasma membrane,plasma membrane,membrane,integral component of membrane
comp21517_c0_seq3.p2				
comp21518_c0_seq1.p1	sp|Q80UX8|ABHDD_MOUSE_Abhydrolase_domain-containing_protein_13_OS=Mus_musculus_GN=Abhd13_PE=2_SV=1	1.00E-59	GO:0003674,GO:0008150,GO:0008152,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016787	molecular_function,biological_process,metabolic process,membrane,membrane,membrane,integral component of membrane,hydrolase activity
comp21519_c0_seq1.p1	sp|Q9LF41|UBE4_ARATH_Probable_ubiquitin_conjugation_factor_E4_OS=Arabidopsis_thaliana_GN=PUB1_PE=1_SV=1	3.00E-75	GO:0000151,GO:0004842,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0006511,GO:0010413,GO:0016567,GO:0016567,GO:0016874,GO:0034450,GO:0045492	ubiquitin ligase complex,ubiquitin-protein transferase activity,nucleus,nucleus,cytoplasm,cytoplasm,cytosol,ubiquitin-dependent protein catabolic process,glucuronoxylan metabolic process,protein ubiquitination,protein ubiquitination,ligase activity,ubiquitin-ubiquitin ligase activity,xylan biosynthetic process
comp21520_c0_seq1.p2	sp|Q9UUZ6|RLA2_ASPFU_60S_acidic_ribosomal_protein_P2_OS=Neosartorya_fumigata_(strain_ATCC_MYA-4609_/_Af293_/_CBS_101355_/_FGSC_A1100)_GN=AFUA_2G10100_PE=1_SV=2	3.00E-16	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0006414,GO:0030529	structural constituent of ribosome,intracellular,ribosome,ribosome,translation,translational elongation,ribonucleoprotein complex
comp21521_c0_seq2.p1	sp|Q10066|ARGI2_SCHPO_Arginase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=aru1_PE=2_SV=1	2.00E-68	GO:0000050,GO:0000050,GO:0004053,GO:0004053,GO:0004053,GO:0005634,GO:0005829,GO:0006525,GO:0006525,GO:0010121,GO:0016787,GO:0016813,GO:0019547,GO:0046872,GO:0046872	urea cycle,urea cycle,arginase activity,arginase activity,arginase activity,nucleus,cytosol,arginine metabolic process,arginine metabolic process,arginine catabolic process to proline via ornithine,hydrolase activity,hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines,arginine catabolic process to ornithine,metal ion binding,metal ion binding
comp21524_c0_seq2.p1	sp|Q6DFN1|NDUF3_XENTR_NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_assembly_factor_3_OS=Xenopus_tropicalis_GN=ndufaf3_PE=2_SV=1	4.00E-13	GO:0005634,GO:0005634,GO:0005739,GO:0005743,GO:0005743,GO:0016020	nucleus,nucleus,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,membrane
comp21524_c0_seq4.p1	sp|Q6DFN1|NDUF3_XENTR_NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_assembly_factor_3_OS=Xenopus_tropicalis_GN=ndufaf3_PE=2_SV=1	1.00E-20	GO:0005634,GO:0005634,GO:0005739,GO:0005743,GO:0005743,GO:0016020	nucleus,nucleus,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,membrane
comp21525_c0_seq1.p1	sp|P57106|MDHC2_ARATH_Malate_dehydrogenase,_cytoplasmic_2_OS=Arabidopsis_thaliana_GN=At5g43330_PE=2_SV=1	8.00E-53	GO:0003824,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0005829,GO:0005886,GO:0005975,GO:0006099,GO:0006108,GO:0009506,GO:0016491,GO:0016491,GO:0016615,GO:0016616,GO:0030060,GO:0030060,GO:0044262,GO:0048046,GO:0055114,GO:0055114	catalytic activity,protein binding,protein binding,protein binding,cytoplasm,cytoplasm,cytosol,plasma membrane,carbohydrate metabolic process,tricarboxylic acid cycle,malate metabolic process,plasmodesma,oxidoreductase activity,oxidoreductase activity,malate dehydrogenase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,L-malate dehydrogenase activity,L-malate dehydrogenase activity,cellular carbohydrate metabolic process,apoplast,oxidation-reduction process,oxidation-reduction process
comp21525_c0_seq2.p1	sp|P57106|MDHC2_ARATH_Malate_dehydrogenase,_cytoplasmic_2_OS=Arabidopsis_thaliana_GN=At5g43330_PE=2_SV=1	1.00E-48	GO:0003824,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0005829,GO:0005886,GO:0005975,GO:0006099,GO:0006108,GO:0009506,GO:0016491,GO:0016491,GO:0016615,GO:0016616,GO:0030060,GO:0030060,GO:0044262,GO:0048046,GO:0055114,GO:0055114	catalytic activity,protein binding,protein binding,protein binding,cytoplasm,cytoplasm,cytosol,plasma membrane,carbohydrate metabolic process,tricarboxylic acid cycle,malate metabolic process,plasmodesma,oxidoreductase activity,oxidoreductase activity,malate dehydrogenase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,L-malate dehydrogenase activity,L-malate dehydrogenase activity,cellular carbohydrate metabolic process,apoplast,oxidation-reduction process,oxidation-reduction process
comp21527_c0_seq2.p1	sp|O14880|MGST3_HUMAN_Microsomal_glutathione_S-transferase_3_OS=Homo_sapiens_GN=MGST3_PE=1_SV=1	3.00E-15	GO:0004364,GO:0004364,GO:0004364,GO:0004601,GO:0004602,GO:0005635,GO:0005783,GO:0005789,GO:0005789,GO:0006629,GO:0006805,GO:0006805,GO:0007165,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016740,GO:0031090,GO:0043231,GO:0043231,GO:0044281,GO:0055114,GO:0055114,GO:0070062,GO:1901687	glutathione transferase activity,glutathione transferase activity,glutathione transferase activity,peroxidase activity,glutathione peroxidase activity,nuclear envelope,endoplasmic reticulum,endoplasmic reticulum membrane,endoplasmic reticulum membrane,lipid metabolic process,xenobiotic metabolic process,xenobiotic metabolic process,signal transduction,membrane,membrane,membrane,integral component of membrane,transferase activity,organelle membrane,intracellular membrane-bounded organelle,intracellular membrane-bounded organelle,small molecule metabolic process,oxidation-reduction process,oxidation-reduction process,extracellular vesicular exosome,glutathione derivative biosynthetic process
comp21528_c0_seq2.p1	sp|P58616|GLK_NOSS1_Glucokinase_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=glk_PE=3_SV=1	9.00E-71	GO:0000166,GO:0004340,GO:0004340,GO:0004340,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0006096,GO:0006096,GO:0006096,GO:0016301,GO:0016310,GO:0016740,GO:0051156	nucleotide binding,glucokinase activity,glucokinase activity,glucokinase activity,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,glycolytic process,glycolytic process,glycolytic process,kinase activity,phosphorylation,transferase activity,glucose 6-phosphate metabolic process
comp21528_c0_seq2.p2				
comp21528_c0_seq2.p3				
comp21530_c0_seq1.p1	sp|Q32LE3|CETN1_BOVIN_Centrin-1_OS=Bos_taurus_GN=CETN1_PE=2_SV=1	4.00E-24	GO:0000922,GO:0003676,GO:0005509,GO:0005524,GO:0005737,GO:0005813,GO:0005813,GO:0005814,GO:0005815,GO:0005815,GO:0005856,GO:0006200,GO:0007049,GO:0007067,GO:0008017,GO:0008026,GO:0031683,GO:0032391,GO:0032795,GO:0034605,GO:0046872,GO:0051301	spindle pole,nucleic acid binding,calcium ion binding,ATP binding,cytoplasm,centrosome,centrosome,centriole,microtubule organizing center,microtubule organizing center,cytoskeleton,ATP catabolic process,cell cycle,mitotic nuclear division,microtubule binding,ATP-dependent helicase activity,G-protein beta/gamma-subunit complex binding,photoreceptor connecting cilium,heterotrimeric G-protein binding,cellular response to heat,metal ion binding,cell division
comp21530_c0_seq2.p1	sp|Q06827|CATR_SCHDU_Caltractin_OS=Scherffelia_dubia_PE=1_SV=1	5.00E-60	GO:0003676,GO:0005509,GO:0005524,GO:0006200,GO:0007049,GO:0007067,GO:0008026,GO:0046872,GO:0051301	nucleic acid binding,calcium ion binding,ATP binding,ATP catabolic process,cell cycle,mitotic nuclear division,ATP-dependent helicase activity,metal ion binding,cell division
comp21533_c0_seq1.p1	sp|Q8TCT7|SPP2B_HUMAN_Signal_peptide_peptidase-like_2B_OS=Homo_sapiens_GN=SPPL2B_PE=1_SV=2	1.00E-38	GO:0000139,GO:0004190,GO:0005515,GO:0005765,GO:0005794,GO:0005886,GO:0005886,GO:0005886,GO:0006508,GO:0006509,GO:0006509,GO:0008233,GO:0010008,GO:0016020,GO:0016021,GO:0016021,GO:0016787,GO:0030660,GO:0031293,GO:0031293,GO:0031293,GO:0031293,GO:0042500,GO:0042500,GO:0042803,GO:0042803,GO:0042803,GO:0050776,GO:0071458,GO:0071556,GO:0042500	Golgi membrane,aspartic-type endopeptidase activity,protein binding,lysosomal membrane,Golgi apparatus,plasma membrane,plasma membrane,plasma membrane,proteolysis,membrane protein ectodomain proteolysis,membrane protein ectodomain proteolysis,peptidase activity,endosome membrane,membrane,integral component of membrane,integral component of membrane,hydrolase activity,Golgi-associated vesicle membrane,membrane protein intracellular domain proteolysis,membrane protein intracellular domain proteolysis,membrane protein intracellular domain proteolysis,membrane protein intracellular domain proteolysis,aspartic endopeptidase activity, intramembrane cleaving,aspartic endopeptidase activity, intramembrane cleaving,protein homodimerization activity,protein homodimerization activity,protein homodimerization activity,regulation of immune response,integral component of cytoplasmic side of endoplasmic reticulum membrane,integral component of lumenal side of endoplasmic reticulum membrane,aspartic endopeptidase activity, intramembrane cleaving
comp21534_c0_seq1.p1				
comp21534_c0_seq2.p1				
comp21536_c0_seq1.p1				
comp21537_c0_seq1.p1	sp|Q6PAX2|ATD3B_XENLA_ATPase_family_AAA_domain-containing_protein_3-B_OS=Xenopus_laevis_GN=atad3-b_PE=2_SV=1	4.00E-150	GO:0000166,GO:0005524,GO:0005524,GO:0005739,GO:0005743,GO:0005743,GO:0016020,GO:0016021,GO:0042645,GO:0042645	nucleotide binding,ATP binding,ATP binding,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,membrane,integral component of membrane,mitochondrial nucleoid,mitochondrial nucleoid
comp21538_c0_seq1.p1	sp|Q04500|UTP14_YEAST_U3_small_nucleolar_RNA-associated_protein_14_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=UTP14_PE=1_SV=1	4.00E-18	GO:0000166,GO:0000447,GO:0000472,GO:0000480,GO:0003674,GO:0005524,GO:0005634,GO:0005730,GO:0005730,GO:0006364,GO:0006364,GO:0030529,GO:0032040,GO:0032040,GO:0042254	nucleotide binding,endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA),endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),molecular_function,ATP binding,nucleus,nucleolus,nucleolus,rRNA processing,rRNA processing,ribonucleoprotein complex,small-subunit processome,small-subunit processome,ribosome biogenesis
comp21539_c0_seq1.p1	sp|Q9NV35|NUD15_HUMAN_Probable_8-oxo-dGTP_diphosphatase_NUDT15_OS=Homo_sapiens_GN=NUDT15_PE=1_SV=1	5.00E-29	GO:0005829,GO:0005829,GO:0006184,GO:0006203,GO:0008413,GO:0016787,GO:0016787,GO:0034656,GO:0035539,GO:0044281,GO:0046872,GO:0055086	cytosol,cytosol,GTP catabolic process,dGTP catabolic process,8-oxo-7,8-dihydroguanosine triphosphate pyrophosphatase activity,hydrolase activity,hydrolase activity,nucleobase-containing small molecule catabolic process,8-oxo-7,8-dihydrodeoxyguanosine triphosphate pyrophosphatase activity,small molecule metabolic process,metal ion binding,nucleobase-containing small molecule metabolic process
comp21540_c0_seq2.p1	sp|Q9NVG8|TBC13_HUMAN_TBC1_domain_family_member_13_OS=Homo_sapiens_GN=TBC1D13_PE=1_SV=3	5.00E-17	GO:0005096,GO:0005097,GO:0032313,GO:0032851,GO:0043547,GO:1902017	GTPase activator activity,Rab GTPase activator activity,regulation of Rab GTPase activity,positive regulation of Rab GTPase activity,positive regulation of GTPase activity,regulation of cilium assembly
comp21540_c0_seq3.p1	sp|Q8R3D1|TBC13_MOUSE_TBC1_domain_family_member_13_OS=Mus_musculus_GN=Tbc1d13_PE=2_SV=1	9.00E-56	GO:0005096,GO:0005097,GO:0005515,GO:0005575,GO:0008150,GO:0032313,GO:0032851,GO:0043547	GTPase activator activity,Rab GTPase activator activity,protein binding,cellular_component,biological_process,regulation of Rab GTPase activity,positive regulation of Rab GTPase activity,positive regulation of GTPase activity
comp21543_c0_seq1.p1	sp|O81770|MGDG1_ARATH_Monogalactosyldiacylglycerol_synthase_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=MGD1_PE=1_SV=1	7.00E-91	GO:0005975,GO:0008194,GO:0009247,GO:0009247,GO:0009507,GO:0009528,GO:0009536,GO:0009536,GO:0009611,GO:0009620,GO:0009695,GO:0009706,GO:0009706,GO:0009753,GO:0009793,GO:0009941,GO:0009941,GO:0009941,GO:0010027,GO:0010027,GO:0016020,GO:0016740,GO:0016757,GO:0016758,GO:0030246,GO:0030259,GO:0035250,GO:0046509,GO:0046509	carbohydrate metabolic process,UDP-glycosyltransferase activity,glycolipid biosynthetic process,glycolipid biosynthetic process,chloroplast,plastid inner membrane,plastid,plastid,response to wounding,response to fungus,jasmonic acid biosynthetic process,chloroplast inner membrane,chloroplast inner membrane,response to jasmonic acid,embryo development ending in seed dormancy,chloroplast envelope,chloroplast envelope,chloroplast envelope,thylakoid membrane organization,thylakoid membrane organization,membrane,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups,carbohydrate binding,lipid glycosylation,UDP-galactosyltransferase activity,1,2-diacylglycerol 3-beta-galactosyltransferase activity,1,2-diacylglycerol 3-beta-galactosyltransferase activity
comp21545_c0_seq1.p1				
comp21545_c0_seq2.p1				
comp21546_c0_seq1.p1	sp|Q6ZIX2|SMT1_ORYSJ_Cycloartenol-C-24-methyltransferase_1_OS=Oryza_sativa_subsp._japonica_GN=Smt1-1_PE=2_SV=1	4.00E-94	GO:0003838,GO:0006629,GO:0006694,GO:0006694,GO:0008152,GO:0008168,GO:0008168,GO:0008202,GO:0016126,GO:0016126,GO:0016740,GO:0032259	sterol 24-C-methyltransferase activity,lipid metabolic process,steroid biosynthetic process,steroid biosynthetic process,metabolic process,methyltransferase activity,methyltransferase activity,steroid metabolic process,sterol biosynthetic process,sterol biosynthetic process,transferase activity,methylation
comp21546_c0_seq2.p1	sp|Q6ZIX2|SMT1_ORYSJ_Cycloartenol-C-24-methyltransferase_1_OS=Oryza_sativa_subsp._japonica_GN=Smt1-1_PE=2_SV=1	4.00E-104	GO:0003838,GO:0006629,GO:0006694,GO:0006694,GO:0008152,GO:0008168,GO:0008168,GO:0008202,GO:0016126,GO:0016126,GO:0016740,GO:0032259	sterol 24-C-methyltransferase activity,lipid metabolic process,steroid biosynthetic process,steroid biosynthetic process,metabolic process,methyltransferase activity,methyltransferase activity,steroid metabolic process,sterol biosynthetic process,sterol biosynthetic process,transferase activity,methylation
comp21548_c0_seq1.p1				
comp21550_c0_seq2.p1				
comp21552_c0_seq1.p1	sp|Q54KR1|SYCC_DICDI_Cysteine--tRNA_ligase,_cytoplasmic_OS=Dictyostelium_discoideum_GN=cysS_PE=3_SV=1	3.00E-160	GO:0000049,GO:0000166,GO:0000166,GO:0004812,GO:0004812,GO:0004817,GO:0004817,GO:0004817,GO:0004817,GO:0004817,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0006412,GO:0006418,GO:0006423,GO:0006423,GO:0006423,GO:0006423,GO:0016874,GO:0044351,GO:0045335,GO:0046872	tRNA binding,nucleotide binding,nucleotide binding,aminoacyl-tRNA ligase activity,aminoacyl-tRNA ligase activity,cysteine-tRNA ligase activity,cysteine-tRNA ligase activity,cysteine-tRNA ligase activity,cysteine-tRNA ligase activity,cysteine-tRNA ligase activity,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytosol,translation,tRNA aminoacylation for protein translation,cysteinyl-tRNA aminoacylation,cysteinyl-tRNA aminoacylation,cysteinyl-tRNA aminoacylation,cysteinyl-tRNA aminoacylation,ligase activity,macropinocytosis,phagocytic vesicle,metal ion binding
comp21552_c0_seq2.p1	sp|Q54KR1|SYCC_DICDI_Cysteine--tRNA_ligase,_cytoplasmic_OS=Dictyostelium_discoideum_GN=cysS_PE=3_SV=1	6.00E-163	GO:0000049,GO:0000166,GO:0000166,GO:0004812,GO:0004812,GO:0004817,GO:0004817,GO:0004817,GO:0004817,GO:0004817,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0006412,GO:0006418,GO:0006423,GO:0006423,GO:0006423,GO:0006423,GO:0016874,GO:0044351,GO:0045335,GO:0046872	tRNA binding,nucleotide binding,nucleotide binding,aminoacyl-tRNA ligase activity,aminoacyl-tRNA ligase activity,cysteine-tRNA ligase activity,cysteine-tRNA ligase activity,cysteine-tRNA ligase activity,cysteine-tRNA ligase activity,cysteine-tRNA ligase activity,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytosol,translation,tRNA aminoacylation for protein translation,cysteinyl-tRNA aminoacylation,cysteinyl-tRNA aminoacylation,cysteinyl-tRNA aminoacylation,cysteinyl-tRNA aminoacylation,ligase activity,macropinocytosis,phagocytic vesicle,metal ion binding
comp21553_c0_seq2.p1				
comp21558_c0_seq1.p1				
comp21563_c0_seq1.p1	sp|Q8BPB0|MOB1B_MOUSE_MOB_kinase_activator_1B_OS=Mus_musculus_GN=Mob1b_PE=1_SV=3	8.00E-69	GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0019209,GO:0019209,GO:0019900,GO:0019900,GO:0035329,GO:0042327,GO:0046777,GO:0046777,GO:0046872,GO:0070062	nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,cytoplasm,kinase activator activity,kinase activator activity,kinase binding,kinase binding,hippo signaling,positive regulation of phosphorylation,protein autophosphorylation,protein autophosphorylation,metal ion binding,extracellular vesicular exosome
comp21564_c0_seq1.p1	sp|Q05360|WHITE_LUCCU_Protein_white_OS=Lucilia_cuprina_GN=W_PE=2_SV=2	2.00E-67	GO:0000166,GO:0005524,GO:0005524,GO:0006200,GO:0006810,GO:0006810,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016887,GO:0031409	nucleotide binding,ATP binding,ATP binding,ATP catabolic process,transport,transport,membrane,membrane,membrane,integral component of membrane,ATPase activity,pigment binding
comp21564_c0_seq1.p3	sp|Q17320|WHITE_CERCA_Protein_white_OS=Ceratitis_capitata_GN=W_PE=2_SV=1	5.00E-52	GO:0000166,GO:0005524,GO:0005524,GO:0006200,GO:0006810,GO:0006810,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016887,GO:0031409	nucleotide binding,ATP binding,ATP binding,ATP catabolic process,transport,transport,membrane,membrane,membrane,integral component of membrane,ATPase activity,pigment binding
comp21564_c0_seq2.p1	sp|Q17320|WHITE_CERCA_Protein_white_OS=Ceratitis_capitata_GN=W_PE=2_SV=1	6.00E-132	GO:0000166,GO:0005524,GO:0005524,GO:0006200,GO:0006810,GO:0006810,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016887,GO:0031409	nucleotide binding,ATP binding,ATP binding,ATP catabolic process,transport,transport,membrane,membrane,membrane,integral component of membrane,ATPase activity,pigment binding
comp21566_c0_seq1.p1				
comp21567_c0_seq1.p1	sp|Q7Z2Z2|ETUD1_HUMAN_Elongation_factor_Tu_GTP-binding_domain-containing_protein_1_OS=Homo_sapiens_GN=EFTUD1_PE=1_SV=2	9.00E-121	GO:0000166,GO:0003746,GO:0003924,GO:0003924,GO:0005525,GO:0005525,GO:0006184,GO:0006412,GO:0006414,GO:0042254,GO:0042256,GO:0043022	nucleotide binding,translation elongation factor activity,GTPase activity,GTPase activity,GTP binding,GTP binding,GTP catabolic process,translation,translational elongation,ribosome biogenesis,mature ribosome assembly,ribosome binding
comp21568_c0_seq1.p1				
comp21570_c0_seq1.p1	sp|Q8HXX4|ECHB_MACFA_Trifunctional_enzyme_subunit_beta,_mitochondrial_OS=Macaca_fascicularis_GN=HADHB_PE=2_SV=1	4.00E-68	GO:0003824,GO:0003988,GO:0005739,GO:0005739,GO:0005741,GO:0005741,GO:0005741,GO:0005743,GO:0005743,GO:0005743,GO:0005783,GO:0005783,GO:0005783,GO:0006629,GO:0006631,GO:0006635,GO:0008152,GO:0016020,GO:0016740,GO:0016746,GO:0016747	catalytic activity,acetyl-CoA C-acyltransferase activity,mitochondrion,mitochondrion,mitochondrial outer membrane,mitochondrial outer membrane,mitochondrial outer membrane,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,lipid metabolic process,fatty acid metabolic process,fatty acid beta-oxidation,metabolic process,membrane,transferase activity,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups other than amino-acyl groups
comp21570_c0_seq2.p1	sp|Q99JY0|ECHB_MOUSE_Trifunctional_enzyme_subunit_beta,_mitochondrial_OS=Mus_musculus_GN=Hadhb_PE=1_SV=1	6.00E-125	GO:0000062,GO:0003824,GO:0003857,GO:0003988,GO:0003988,GO:0003988,GO:0003988,GO:0004300,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005741,GO:0005741,GO:0005741,GO:0005741,GO:0005743,GO:0005743,GO:0005743,GO:0005743,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0006629,GO:0006631,GO:0006635,GO:0006635,GO:0006635,GO:0008152,GO:0016020,GO:0016507,GO:0016507,GO:0016508,GO:0016509,GO:0016509,GO:0016740,GO:0016746,GO:0016747,GO:0032403,GO:0042645,GO:0044822,GO:0051287,GO:0070062	fatty-acyl-CoA binding,catalytic activity,3-hydroxyacyl-CoA dehydrogenase activity,acetyl-CoA C-acyltransferase activity,acetyl-CoA C-acyltransferase activity,acetyl-CoA C-acyltransferase activity,acetyl-CoA C-acyltransferase activity,enoyl-CoA hydratase activity,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrial outer membrane,mitochondrial outer membrane,mitochondrial outer membrane,mitochondrial outer membrane,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,lipid metabolic process,fatty acid metabolic process,fatty acid beta-oxidation,fatty acid beta-oxidation,fatty acid beta-oxidation,metabolic process,membrane,mitochondrial fatty acid beta-oxidation multienzyme complex,mitochondrial fatty acid beta-oxidation multienzyme complex,long-chain-enoyl-CoA hydratase activity,long-chain-3-hydroxyacyl-CoA dehydrogenase activity,long-chain-3-hydroxyacyl-CoA dehydrogenase activity,transferase activity,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups other than amino-acyl groups,protein complex binding,mitochondrial nucleoid,poly(A) RNA binding,NAD binding,extracellular vesicular exosome
comp21570_c0_seq2.p2	sp|Q54MB8|LEO1_DICDI_RNA_polymerase-associated_protein_LEO1_OS=Dictyostelium_discoideum_GN=leo1_PE=3_SV=1	3.00E-23	GO:0005634,GO:0005634,GO:0006351,GO:0006355	nucleus,nucleus,transcription, DNA-templated,regulation of transcription, DNA-templated
comp21571_c0_seq2.p1				
comp21573_c0_seq2.p1				
comp21573_c0_seq4.p1	sp|Q6NZJ6|IF4G1_MOUSE_Eukaryotic_translation_initiation_factor_4_gamma_1_OS=Mus_musculus_GN=Eif4g1_PE=1_SV=1	1.00E-35	GO:0003723,GO:0003723,GO:0003743,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0006412,GO:0006413,GO:0006417,GO:0006446,GO:0016020,GO:0044822	RNA binding,RNA binding,translation initiation factor activity,protein binding,protein binding,protein binding,protein binding,protein binding,cytoplasm,translation,translational initiation,regulation of translation,regulation of translational initiation,membrane,poly(A) RNA binding
comp21573_c0_seq4.p4				
comp21573_c0_seq4.p6				
comp21574_c0_seq1.p1	sp|P12277|KCRB_HUMAN_Creatine_kinase_B-type_OS=Homo_sapiens_GN=CKB_PE=1_SV=1	3.00E-109	GO:0000166,GO:0003824,GO:0004111,GO:0004111,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005737,GO:0005737,GO:0005739,GO:0005829,GO:0006600,GO:0007420,GO:0016301,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0021762,GO:0030644,GO:0034641,GO:0044281,GO:0070062,GO:0070062,GO:0070062,GO:0070062	nucleotide binding,catalytic activity,creatine kinase activity,creatine kinase activity,protein binding,protein binding,protein binding,ATP binding,cytoplasm,cytoplasm,mitochondrion,cytosol,creatine metabolic process,brain development,kinase activity,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,substantia nigra development,cellular chloride ion homeostasis,cellular nitrogen compound metabolic process,small molecule metabolic process,extracellular vesicular exosome,extracellular vesicular exosome,extracellular vesicular exosome,extracellular vesicular exosome
comp21575_c0_seq1.p1				
comp21576_c0_seq1.p1				
comp21577_c1_seq1.p1				
comp21577_c1_seq1.p2				
comp21577_c1_seq2.p1				
comp21578_c0_seq1.p1				
comp2158_c0_seq1.p2	sp|P69104|GBLP_TRYBR_Guanine_nucleotide-binding_protein_subunit_beta-like_protein_OS=Trypanosoma_brucei_rhodesiense_PE=2_SV=1	5.00E-108		
comp21580_c0_seq1.p1				
comp21582_c0_seq1.p1	sp|P28307|CSGA_ECOLI_Major_curlin_subunit_OS=Escherichia_coli_(strain_K12)_GN=csgA_PE=1_SV=3	8.00E-83	GO:0007155,GO:0007155,GO:0009289,GO:0009289,GO:0009289,GO:0009289,GO:0044010,GO:1990000	cell adhesion,cell adhesion,pilus,pilus,pilus,pilus,single-species biofilm formation,amyloid fibril formation
comp21583_c0_seq1.p1	sp|Q5DU56|NLRC3_MOUSE_Protein_NLRC3_OS=Mus_musculus_GN=Nlrc3_PE=2_SV=2	2.00E-23	GO:0000166,GO:0003674,GO:0005515,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0007249,GO:0031396,GO:0031396,GO:0032088,GO:0032496,GO:0042110,GO:0043124,GO:0043124	nucleotide binding,molecular_function,protein binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,I-kappaB kinase/NF-kappaB signaling,regulation of protein ubiquitination,regulation of protein ubiquitination,negative regulation of NF-kappaB transcription factor activity,response to lipopolysaccharide,T cell activation,negative regulation of I-kappaB kinase/NF-kappaB signaling,negative regulation of I-kappaB kinase/NF-kappaB signaling
comp21584_c0_seq1.p1	sp|Q8CFV9|RIFK_MOUSE_Riboflavin_kinase_OS=Mus_musculus_GN=Rfk_PE=2_SV=2	4.00E-25	GO:0000166,GO:0005515,GO:0005524,GO:0005737,GO:0005737,GO:0005739,GO:0006915,GO:0008531,GO:0008531,GO:0008531,GO:0009231,GO:0009398,GO:0016301,GO:0016310,GO:0016740,GO:0033864,GO:0033864,GO:0046872,GO:0072593	nucleotide binding,protein binding,ATP binding,cytoplasm,cytoplasm,mitochondrion,apoptotic process,riboflavin kinase activity,riboflavin kinase activity,riboflavin kinase activity,riboflavin biosynthetic process,FMN biosynthetic process,kinase activity,phosphorylation,transferase activity,positive regulation of NAD(P)H oxidase activity,positive regulation of NAD(P)H oxidase activity,metal ion binding,reactive oxygen species metabolic process
comp21585_c0_seq2.p1	sp|Q9VR91|HERC2_DROME_Probable_E3_ubiquitin-protein_ligase_HERC2_OS=Drosophila_melanogaster_GN=HERC2_PE=1_SV=3	1.00E-26	GO:0004842,GO:0004842,GO:0005575,GO:0005634,GO:0005737,GO:0005737,GO:0005814,GO:0005856,GO:0016567,GO:0016567,GO:0016874,GO:0020037,GO:0042787,GO:0046872	ubiquitin-protein transferase activity,ubiquitin-protein transferase activity,cellular_component,nucleus,cytoplasm,cytoplasm,centriole,cytoskeleton,protein ubiquitination,protein ubiquitination,ligase activity,heme binding,protein ubiquitination involved in ubiquitin-dependent protein catabolic process,metal ion binding
comp21586_c0_seq3.p1	sp|A6WXV2|GLPK_OCHA4_Glycerol_kinase_OS=Ochrobactrum_anthropi_(strain_ATCC_49188_/_DSM_6882_/_NCTC_12168)_GN=glpK_PE=3_SV=1	0	GO:0000166,GO:0004370,GO:0004370,GO:0004370,GO:0004370,GO:0005524,GO:0005524,GO:0005975,GO:0006071,GO:0006071,GO:0006072,GO:0006072,GO:0016301,GO:0016310,GO:0016740,GO:0016773,GO:0019563	nucleotide binding,glycerol kinase activity,glycerol kinase activity,glycerol kinase activity,glycerol kinase activity,ATP binding,ATP binding,carbohydrate metabolic process,glycerol metabolic process,glycerol metabolic process,glycerol-3-phosphate metabolic process,glycerol-3-phosphate metabolic process,kinase activity,phosphorylation,transferase activity,phosphotransferase activity, alcohol group as acceptor,glycerol catabolic process
comp21587_c0_seq1.p1				
comp21588_c0_seq1.p1				
comp21588_c0_seq2.p1				
comp21589_c0_seq3.p1				
comp2159_c0_seq1.p1				
comp21590_c1_seq1.p1				
comp21592_c0_seq1.p1				
comp21594_c0_seq1.p1				
comp21595_c0_seq1.p1				
comp21596_c0_seq1.p1				
comp21596_c0_seq3.p2				
comp21598_c0_seq1.p1				
comp21599_c0_seq1.p1				
comp21600_c0_seq1.p1	sp|O93796|EF3_CANGA_Elongation_factor_3_OS=Candida_glabrata_(strain_ATCC_2001_/_CBS_138_/_JCM_3761_/_NBRC_0622_/_NRRL_Y-65)_GN=TEF3_PE=3_SV=2	0	GO:0000166,GO:0003674,GO:0003723,GO:0003746,GO:0005524,GO:0005524,GO:0006200,GO:0006412,GO:0006414,GO:0006414,GO:0008150,GO:0016887	nucleotide binding,molecular_function,RNA binding,translation elongation factor activity,ATP binding,ATP binding,ATP catabolic process,translation,translational elongation,translational elongation,biological_process,ATPase activity
comp21601_c0_seq1.p1				
comp21603_c0_seq3.p1				
comp21606_c0_seq1.p3				
comp21606_c0_seq2.p2				
comp21606_c0_seq2.p4				
comp21611_c0_seq1.p1				
comp21613_c0_seq1.p1	sp|Q6P158|DHX57_HUMAN_Putative_ATP-dependent_RNA_helicase_DHX57_OS=Homo_sapiens_GN=DHX57_PE=1_SV=2	4.00E-77	GO:0000166,GO:0003676,GO:0004004,GO:0004386,GO:0004386,GO:0005524,GO:0005524,GO:0005739,GO:0006200,GO:0006200,GO:0006396,GO:0008026,GO:0016787,GO:0044822,GO:0044822,GO:0046872,GO:0046872,GO:0005634	nucleotide binding,nucleic acid binding,ATP-dependent RNA helicase activity,helicase activity,helicase activity,ATP binding,ATP binding,mitochondrion,ATP catabolic process,ATP catabolic process,RNA processing,ATP-dependent helicase activity,hydrolase activity,poly(A) RNA binding,poly(A) RNA binding,metal ion binding,metal ion binding,nucleus
comp21614_c0_seq1.p1	sp|O94606|JMJ4_SCHPO_JmjC_domain-containing_protein_4_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=jmj4_PE=1_SV=1	1.00E-37	GO:0000790,GO:0005634,GO:0005634,GO:0005634,GO:0006338,GO:0016577,GO:0032452,GO:0051321	nuclear chromatin,nucleus,nucleus,nucleus,chromatin remodeling,histone demethylation,histone demethylase activity,meiotic cell cycle
comp21615_c0_seq1.p2	sp|P20790|RAB8A_DICDI_Ras-related_protein_Rab-8A_OS=Dictyostelium_discoideum_GN=rab8A_PE=3_SV=1	1.00E-81	GO:0000166,GO:0000331,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0005525,GO:0005886,GO:0005886,GO:0006184,GO:0006810,GO:0006886,GO:0006904,GO:0007264,GO:0015031,GO:0015031,GO:0016020,GO:0016339,GO:0017157,GO:0019003,GO:0030036,GO:0030667,GO:0031157,GO:0032482,GO:0032794,GO:0033298,GO:0044351,GO:0050708	nucleotide binding,contractile vacuole,GTPase activity,GTP binding,GTP binding,GTP binding,GTP binding,plasma membrane,plasma membrane,GTP catabolic process,transport,intracellular protein transport,vesicle docking involved in exocytosis,small GTPase mediated signal transduction,protein transport,protein transport,membrane,calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules,regulation of exocytosis,GDP binding,actin cytoskeleton organization,secretory granule membrane,regulation of aggregate size involved in sorocarp development,Rab protein signal transduction,GTPase activating protein binding,contractile vacuole organization,macropinocytosis,regulation of protein secretion
comp21615_c0_seq2.p3	sp|P20791|RAB8B_DICDI_Ras-related_protein_Rab-8B_OS=Dictyostelium_discoideum_GN=rab8B_PE=2_SV=1	2.00E-31	GO:0000166,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0005525,GO:0005575,GO:0005886,GO:0005886,GO:0006184,GO:0006810,GO:0006886,GO:0006904,GO:0007264,GO:0009306,GO:0015031,GO:0015031,GO:0016020,GO:0016339,GO:0017157,GO:0019003,GO:0030667,GO:0031157,GO:0032482	nucleotide binding,GTPase activity,GTP binding,GTP binding,GTP binding,GTP binding,cellular_component,plasma membrane,plasma membrane,GTP catabolic process,transport,intracellular protein transport,vesicle docking involved in exocytosis,small GTPase mediated signal transduction,protein secretion,protein transport,protein transport,membrane,calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules,regulation of exocytosis,GDP binding,secretory granule membrane,regulation of aggregate size involved in sorocarp development,Rab protein signal transduction
comp21621_c1_seq1.p1				
comp21623_c0_seq1.p1	sp|P09110|THIK_HUMAN_3-ketoacyl-CoA_thiolase,_peroxisomal_OS=Homo_sapiens_GN=ACAA1_PE=1_SV=2	2.00E-44	GO:0000038,GO:0003824,GO:0003988,GO:0005515,GO:0005777,GO:0005777,GO:0005777,GO:0005777,GO:0005777,GO:0005777,GO:0005777,GO:0005782,GO:0005782,GO:0006629,GO:0006631,GO:0006631,GO:0006635,GO:0006635,GO:0008152,GO:0008206,GO:0016020,GO:0016401,GO:0016740,GO:0016746,GO:0016747,GO:0033540,GO:0033559,GO:0036109,GO:0043231,GO:0044255,GO:0044281	very long-chain fatty acid metabolic process,catalytic activity,acetyl-CoA C-acyltransferase activity,protein binding,peroxisome,peroxisome,peroxisome,peroxisome,peroxisome,peroxisome,peroxisome,peroxisomal matrix,peroxisomal matrix,lipid metabolic process,fatty acid metabolic process,fatty acid metabolic process,fatty acid beta-oxidation,fatty acid beta-oxidation,metabolic process,bile acid metabolic process,membrane,palmitoyl-CoA oxidase activity,transferase activity,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups other than amino-acyl groups,fatty acid beta-oxidation using acyl-CoA oxidase,unsaturated fatty acid metabolic process,alpha-linolenic acid metabolic process,intracellular membrane-bounded organelle,cellular lipid metabolic process,small molecule metabolic process
comp21634_c0_seq1.p1				
comp21634_c0_seq2.p1				
comp21640_c0_seq1.p1	sp|Q9UTA3|YL8H_SCHPO_Probable_intramembrane_protease_C25B8.17_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC25B8.17_PE=2_SV=1	8.00E-19	GO:0000139,GO:0004190,GO:0005783,GO:0005783,GO:0005789,GO:0005794,GO:0005794,GO:0006465,GO:0006508,GO:0008233,GO:0016020,GO:0016021,GO:0016021,GO:0016787	Golgi membrane,aspartic-type endopeptidase activity,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,Golgi apparatus,Golgi apparatus,signal peptide processing,proteolysis,peptidase activity,membrane,integral component of membrane,integral component of membrane,hydrolase activity
comp21640_c0_seq2.p1	sp|Q9UTA3|YL8H_SCHPO_Probable_intramembrane_protease_C25B8.17_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC25B8.17_PE=2_SV=1	5.00E-25	GO:0000139,GO:0004190,GO:0005783,GO:0005783,GO:0005789,GO:0005794,GO:0005794,GO:0006465,GO:0006508,GO:0008233,GO:0016020,GO:0016021,GO:0016021,GO:0016787	Golgi membrane,aspartic-type endopeptidase activity,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,Golgi apparatus,Golgi apparatus,signal peptide processing,proteolysis,peptidase activity,membrane,integral component of membrane,integral component of membrane,hydrolase activity
comp21643_c0_seq1.p2	sp|Q5U3U3|CPT2_DANRE_Carnitine_O-palmitoyltransferase_2,_mitochondrial_OS=Danio_rerio_GN=cpt2_PE=2_SV=2	1.00E-18	GO:0004095,GO:0005739,GO:0005743,GO:0005743,GO:0006629,GO:0006631,GO:0006635,GO:0006810,GO:0016020,GO:0016740,GO:0016746,GO:0016746	carnitine O-palmitoyltransferase activity,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,lipid metabolic process,fatty acid metabolic process,fatty acid beta-oxidation,transport,membrane,transferase activity,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups
comp21643_c0_seq3.p1	sp|Q5U3U3|CPT2_DANRE_Carnitine_O-palmitoyltransferase_2,_mitochondrial_OS=Danio_rerio_GN=cpt2_PE=2_SV=2	2.00E-24	GO:0004095,GO:0005739,GO:0005743,GO:0005743,GO:0006629,GO:0006631,GO:0006635,GO:0006810,GO:0016020,GO:0016740,GO:0016746,GO:0016746	carnitine O-palmitoyltransferase activity,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,lipid metabolic process,fatty acid metabolic process,fatty acid beta-oxidation,transport,membrane,transferase activity,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups
comp21646_c0_seq1.p1	sp|Q8LAD0|PDX2_ARATH_Pyridoxal_biosynthesis_protein_PDX2_OS=Arabidopsis_thaliana_GN=PDX2_PE=1_SV=1	6.00E-28	GO:0004359,GO:0004359,GO:0005737,GO:0005737,GO:0005829,GO:0006541,GO:0006543,GO:0008615,GO:0016740,GO:0016740,GO:0042819,GO:0042819,GO:0042819,GO:0042823,GO:0042823,GO:0046982	glutaminase activity,glutaminase activity,cytoplasm,cytoplasm,cytosol,glutamine metabolic process,glutamine catabolic process,pyridoxine biosynthetic process,transferase activity,transferase activity,vitamin B6 biosynthetic process,vitamin B6 biosynthetic process,vitamin B6 biosynthetic process,pyridoxal phosphate biosynthetic process,pyridoxal phosphate biosynthetic process,protein heterodimerization activity
comp21646_c0_seq2.p1	sp|Q8LAD0|PDX2_ARATH_Pyridoxal_biosynthesis_protein_PDX2_OS=Arabidopsis_thaliana_GN=PDX2_PE=1_SV=1	3.00E-55	GO:0004359,GO:0004359,GO:0005737,GO:0005737,GO:0005829,GO:0006541,GO:0006543,GO:0008615,GO:0016740,GO:0016740,GO:0042819,GO:0042819,GO:0042819,GO:0042823,GO:0042823,GO:0046982	glutaminase activity,glutaminase activity,cytoplasm,cytoplasm,cytosol,glutamine metabolic process,glutamine catabolic process,pyridoxine biosynthetic process,transferase activity,transferase activity,vitamin B6 biosynthetic process,vitamin B6 biosynthetic process,vitamin B6 biosynthetic process,pyridoxal phosphate biosynthetic process,pyridoxal phosphate biosynthetic process,protein heterodimerization activity
comp21649_c0_seq1.p1				
comp21649_c1_seq1.p1				
comp21651_c0_seq1.p1				
comp21654_c0_seq1.p1				
comp21662_c0_seq1.p1				
comp21667_c0_seq1.p1	sp|A7ZTP5|CBRA_ECO24_Protein_CbrA_OS=Escherichia_coli_O139:H28_(strain_E24377A_/_ETEC)_GN=cbrA_PE=3_SV=1	2.00E-75	GO:0008152,GO:0016491,GO:0055114	metabolic process,oxidoreductase activity,oxidation-reduction process
comp21672_c0_seq2.p1				
comp21674_c0_seq1.p1	sp|Q8WXB1|MT21A_HUMAN_Methyltransferase-like_protein_21A_OS=Homo_sapiens_GN=METTL21A_PE=2_SV=2	9.00E-14	GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0006479,GO:0008168,GO:0016279,GO:0016279,GO:0016740,GO:0018022,GO:0030544,GO:0030544,GO:0030544,GO:0030544,GO:0032259,GO:0051117,GO:0051117,GO:0051117,GO:0051117,GO:0043462	protein binding,protein binding,protein binding,cytoplasm,cytoplasm,protein methylation,methyltransferase activity,protein-lysine N-methyltransferase activity,protein-lysine N-methyltransferase activity,transferase activity,peptidyl-lysine methylation,Hsp70 protein binding,Hsp70 protein binding,Hsp70 protein binding,Hsp70 protein binding,methylation,ATPase binding,ATPase binding,ATPase binding,ATPase binding,regulation of ATPase activity
comp21674_c0_seq2.p1	sp|Q8WXB1|MT21A_HUMAN_Methyltransferase-like_protein_21A_OS=Homo_sapiens_GN=METTL21A_PE=2_SV=2	2.00E-13	GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0006479,GO:0008168,GO:0016279,GO:0016279,GO:0016740,GO:0018022,GO:0030544,GO:0030544,GO:0030544,GO:0030544,GO:0032259,GO:0051117,GO:0051117,GO:0051117,GO:0051117,GO:0043462	protein binding,protein binding,protein binding,cytoplasm,cytoplasm,protein methylation,methyltransferase activity,protein-lysine N-methyltransferase activity,protein-lysine N-methyltransferase activity,transferase activity,peptidyl-lysine methylation,Hsp70 protein binding,Hsp70 protein binding,Hsp70 protein binding,Hsp70 protein binding,methylation,ATPase binding,ATPase binding,ATPase binding,ATPase binding,regulation of ATPase activity
comp21674_c0_seq3.p2				
comp21676_c0_seq1.p1				

comp2215_c1_seq1.p1	sp|Q32K70|LSPA_SHIDS_Lipoprotein_signal_peptidase_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=lspA_PE=3_SV=1	2.00E-79
comp22150_c0_seq1.p1	sp|O84100|RS1_CHLTR_30S_ribosomal_protein_S1_OS=Chlamydia_trachomatis_(strain_D/UW-3/Cx)_GN=rpsA_PE=3_SV=1	6.00E-44
comp22152_c0_seq2.p1		
comp22152_c0_seq2.p2		
comp22164_c0_seq1.p1		
comp22164_c0_seq2.p1		
comp22164_c0_seq2.p2		
comp22167_c0_seq2.p1		
comp2217_c0_seq1.p1	sp|Q3YXE2|SSTT_SHISS_Serine/threonine_transporter_sstT_OS=Shigella_sonnei_(strain_Ss046)_GN=sstT_PE=3_SV=1	1.00E-55
comp2217_c1_seq1.p1	sp|Q3YXE2|SSTT_SHISS_Serine/threonine_transporter_sstT_OS=Shigella_sonnei_(strain_Ss046)_GN=sstT_PE=3_SV=1	9.00E-58
comp22172_c0_seq1.p1		
comp22174_c0_seq1.p2		
comp22175_c0_seq1.p1		
comp22175_c0_seq2.p2		
comp2218_c0_seq1.p1		
comp22183_c0_seq1.p1		
comp22183_c0_seq2.p1		
comp22188_c0_seq1.p1		
comp2219_c0_seq1.p1	sp|P39172|ZNUA_ECOLI_High-affinity_zinc_uptake_system_protein_znuA_OS=Escherichia_coli_(strain_K12)_GN=znuA_PE=1_SV=4	2.00E-49
comp22190_c0_seq1.p2	sp|Q9DG68|RLA0_RANSY_60S_acidic_ribosomal_protein_P0_OS=Rana_sylvatica_GN=RPLP0_PE=2_SV=1	6.00E-88
comp22195_c1_seq1.p1		
comp22199_c0_seq3.p1		
comp22200_c0_seq1.p1		
comp22201_c0_seq1.p1	sp|O65282|CH10C_ARATH_20_kDa_chaperonin,_chloroplastic_OS=Arabidopsis_thaliana_GN=CPN21_PE=1_SV=2	7.00E-29
comp22203_c0_seq2.p3		
comp22205_c0_seq1.p1		
comp22209_c0_seq1.p1	sp|Q92354|RL24A_SCHPO_60S_ribosomal_protein_L24-A_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpl24a_PE=2_SV=1	7.00E-23
comp22210_c0_seq1.p1	sp|P11988|BGLB_ECOLI_6-phospho-beta-glucosidase_BglB_OS=Escherichia_coli_(strain_K12)_GN=bglB_PE=3_SV=2	2.00E-84
comp22211_c0_seq1.p1		
comp22213_c1_seq1.p2	sp|P0ABU4|ENGD_SHIFL_GTP-dependent_nucleic_acid-binding_protein_engD_OS=Shigella_flexneri_GN=engD_PE=3_SV=2	2.00E-106
comp22214_c0_seq1.p2	sp|P36580|ALF_SCHPO_Fructose-bisphosphate_aldolase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=fba1_PE=1_SV=2	2.00E-24
comp22219_c0_seq1.p1	sp|Q6IN36|WIPF1_RAT_WAS/WASL-interacting_protein_family_member_1_OS=Rattus_norvegicus_GN=Wipf1_PE=1_SV=2	3.00E-13
comp2222_c0_seq1.p1	sp|P23883|PUUC_ECOLI_Aldehyde_dehydrogenase_PuuC_OS=Escherichia_coli_(strain_K12)_GN=puuC_PE=1_SV=2	6.00E-73
comp22221_c0_seq1.p1		
comp22226_c0_seq4.p1		
comp22236_c0_seq1.p1	sp|Q6DEY8|WDR67_XENTR_WD_repeat-containing_protein_67_OS=Xenopus_tropicalis_GN=wdr67_PE=2_SV=1	1.00E-46
comp22236_c0_seq2.p1	sp|Q6DEY8|WDR67_XENTR_WD_repeat-containing_protein_67_OS=Xenopus_tropicalis_GN=wdr67_PE=2_SV=1	1.00E-44
comp22247_c0_seq1.p1	sp|A7S8T5|CCD42_NEMVE_Coiled-coil_domain-containing_protein_42_homolog_OS=Nematostella_vectensis_GN=v1g187067_PE=3_SV=1	2.00E-18
comp22257_c0_seq1.p1		
comp22261_c0_seq1.p1		
comp22263_c0_seq1.p1	sp|Q9ET30|TM9S3_MOUSE_Transmembrane_9_superfamily_member_3_OS=Mus_musculus_GN=Tm9sf3_PE=1_SV=1	1.00E-42
comp22264_c0_seq1.p1		
comp22266_c0_seq1.p1	sp|O18158|OGT1_CAEEL_UDP-N-acetylglucosamine--peptide_N-acetylglucosaminyltransferase_OS=Caenorhabditis_elegans_GN=ogt-1_PE=1_SV=2	3.00E-38
comp22266_c1_seq1.p1	sp|Q9M8Y0|SEC_ARATH_Probable_UDP-N-acetylglucosamine--peptide_N-acetylglucosaminyltransferase_SEC_OS=Arabidopsis_thaliana_GN=SEC_PE=2_SV=1	1.00E-44
comp22268_c0_seq1.p1		
comp2227_c0_seq1.p1	sp|Q3YWE6|NEPI_SHISS_Purine_ribonucleoside_efflux_pump_nepI_OS=Shigella_sonnei_(strain_Ss046)_GN=nepI_PE=3_SV=2	6.00E-63
comp22277_c0_seq1.p1	sp|P25906|YDBC_ECOLI_Putative_oxidoreductase_YdbC_OS=Escherichia_coli_(strain_K12)_GN=ydbC_PE=1_SV=1	2.00E-98
comp22278_c0_seq1.p1		
comp22278_c0_seq2.p2	sp|Q8WW35|TC1D2_HUMAN_Tctex1_domain-containing_protein_2_OS=Homo_sapiens_GN=TCTEX1D2_PE=1_SV=2	1.00E-25
comp22287_c0_seq1.p1	sp|P05458|PTRA_ECOLI_Protease_3_OS=Escherichia_coli_(strain_K12)_GN=ptrA_PE=1_SV=1	2.00E-140
comp22292_c0_seq1.p1		
comp22292_c0_seq2.p1		
comp22300_c0_seq2.p1		
comp22302_c0_seq1.p1		
comp22303_c0_seq3.p3		
comp22310_c0_seq2.p1	sp|Q08BG1|TMPPE_DANRE_Transmembrane_protein_with_metallophosphoesterase_domain_OS=Danio_rerio_GN=tmppe_PE=2_SV=1	5.00E-43
comp22313_c0_seq3.p1	sp|P93798|SNAA_VITVI_Alpha-soluble_NSF_attachment_protein_OS=Vitis_vinifera_PE=2_SV=1	2.00E-51
comp22315_c0_seq1.p1		
comp22317_c0_seq1.p1		
comp22321_c0_seq1.p1	sp|P77260|YDFI_ECOLI_Uncharacterized_oxidoreductase_ydfI_OS=Escherichia_coli_(strain_K12)_GN=ydfI_PE=3_SV=1	0
comp22321_c1_seq1.p2	sp|P0ACM4|YDFH_SHIFL_Uncharacterized_HTH-type_transcriptional_regulator_ydfH_OS=Shigella_flexneri_GN=ydfH_PE=4_SV=1	5.00E-64
comp22334_c0_seq1.p1		
comp22338_c0_seq1.p1	sp|Q552M6|ZDHC7_DICDI_Putative_ZDHHC-type_palmitoyltransferase_7_OS=Dictyostelium_discoideum_GN=DDB_G0276017_PE=2_SV=1	3.00E-20
comp22338_c0_seq2.p1		
comp22365_c0_seq1.p1	sp|Q9SCC7|CBBX_GUITH_Protein_cbbX_homolog,_chloroplastic_OS=Guillardia_theta_GN=cbbX_PE=3_SV=1	2.00E-125
comp22365_c0_seq1.p2	sp|Q6P0I8|EXOS6_DANRE_Exosome_complex_component_MTR3_OS=Danio_rerio_GN=exosc6_PE=2_SV=2	3.00E-42
comp22365_c0_seq2.p1	sp|Q9SCC7|CBBX_GUITH_Protein_cbbX_homolog,_chloroplastic_OS=Guillardia_theta_GN=cbbX_PE=3_SV=1	8.00E-149
comp22365_c0_seq2.p2	sp|Q6P0I8|EXOS6_DANRE_Exosome_complex_component_MTR3_OS=Danio_rerio_GN=exosc6_PE=2_SV=2	3.00E-42
comp22366_c1_seq1.p1	sp|P0AAE8|CADB_ECOLI_Probable_cadaverine/lysine_antiporter_OS=Escherichia_coli_(strain_K12)_GN=cadB_PE=2_SV=1	0
comp22376_c0_seq1.p2	sp|Q99MN9|PCCB_MOUSE_Propionyl-CoA_carboxylase_beta_chain,_mitochondrial_OS=Mus_musculus_GN=Pccb_PE=1_SV=2	2.00E-125
comp22378_c0_seq1.p1		
comp22386_c0_seq3.p1		
comp22386_c0_seq4.p1		
comp22386_c0_seq5.p1		
comp22386_c0_seq5.p3		
comp22388_c0_seq1.p2	sp|P0AFI4|PARC_SHIFL_DNA_topoisomerase_4_subunit_A_OS=Shigella_flexneri_GN=parC_PE=3_SV=1	1.00E-60
comp22388_c0_seq2.p1	sp|P0AFI4|PARC_SHIFL_DNA_topoisomerase_4_subunit_A_OS=Shigella_flexneri_GN=parC_PE=3_SV=1	0
comp22393_c0_seq1.p1		
comp22395_c1_seq1.p1		
comp22398_c0_seq1.p2		
comp22404_c0_seq1.p1		
comp22416_c0_seq1.p1		
comp22420_c0_seq2.p1		
comp22421_c0_seq1.p1		
comp22424_c0_seq1.p1		
comp22435_c1_seq2.p1		
comp22435_c1_seq3.p1		
comp22437_c0_seq1.p1	sp|Q9P6P9|PDK_SCHPO_[Pyruvate_dehydrogenase_[lipoamide]]_kinase,_mitochondrial_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC644.11c_PE=2_SV=1	3.00E-11
comp22438_c0_seq1.p1		
comp22440_c0_seq1.p2		
comp22442_c0_seq1.p1	sp|P58021|TM9S2_MOUSE_Transmembrane_9_superfamily_member_2_OS=Mus_musculus_GN=Tm9sf2_PE=2_SV=1	4.00E-32
comp22444_c0_seq1.p1		
comp2245_c0_seq1.p1	sp|O13326|CYSD_SCHPO_O-acetylhomoserine_(thiol)-lyase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC428.11_PE=2_SV=1	1.00E-25
comp22455_c1_seq1.p1	sp|Q54T82|Y1931_DICDI_Putative_leucine-rich_repeat-containing_protein_DDB_G0281931_OS=Dictyostelium_discoideum_GN=DDB_G0281931_PE=4_SV=1	1.00E-13
comp22456_c0_seq1.p1		
comp22459_c0_seq1.p1		
comp22467_c0_seq1.p1		
comp22470_c0_seq1.p1	sp|Q8LKS5|LACS7_ARATH_Long_chain_acyl-CoA_synthetase_7,_peroxisomal_OS=Arabidopsis_thaliana_GN=LACS7_PE=1_SV=2	7.00E-18
comp22473_c0_seq1.p1		
comp22473_c1_seq1.p1		
comp22473_c2_seq1.p2		
comp22475_c0_seq1.p1		
comp22476_c0_seq1.p1		
comp2248_c0_seq1.p1	sp|Q3Z5V8|RSMA_SHISS_Ribosomal_RNA_small_subunit_methyltransferase_A_OS=Shigella_sonnei_(strain_Ss046)_GN=rsmA_PE=3_SV=1	5.00E-160
comp2248_c1_seq1.p1	sp|Q3Z5V7|PDXA_SHISS_4-hydroxythreonine-4-phosphate_dehydrogenase_OS=Shigella_sonnei_(strain_Ss046)_GN=pdxA_PE=3_SV=1	1.00E-98
comp22495_c0_seq3.p1		
comp22495_c0_seq3.p5		
comp22498_c0_seq1.p1	sp|Q96SZ6|CK5P1_HUMAN_CDK5_regulatory_subunit-associated_protein_1_OS=Homo_sapiens_GN=CDK5RAP1_PE=1_SV=2	8.00E-27
comp22498_c0_seq2.p1		
comp22498_c0_seq3.p1	sp|Q8A2W0|MIAB_BACTN_(Dimethylallyl)adenosine_tRNA_methylthiotransferase_MiaB_OS=Bacteroides_thetaiotaomicron_(strain_ATCC_29148_/_DSM_2079_/_NCTC_10582_/_E50_/_VPI-5482)_GN=miaB_PE=3_SV=1	1.00E-15
comp22503_c0_seq1.p1	sp|P15111|DHE4_SALTY_NADP-specific_glutamate_dehydrogenase_OS=Salmonella_typhimurium_GN=gdhA_PE=3_SV=2	2.00E-113
comp22513_c0_seq2.p1		
comp22513_c0_seq3.p1		
comp22521_c0_seq1.p1	sp|P35055|HEM6_SOYBN_Coproporphyrinogen-III_oxidase,_chloroplastic_OS=Glycine_max_GN=CPX_PE=2_SV=1	2.00E-14
comp22522_c0_seq1.p1		
comp22526_c0_seq1.p1	sp|Q5RKH0|GLYR1_RAT_Putative_oxidoreductase_GLYR1_OS=Rattus_norvegicus_GN=Glyr1_PE=2_SV=1	3.00E-63
comp22526_c0_seq2.p1		
comp22527_c0_seq1.p1		
comp22532_c0_seq1.p1		
comp22555_c0_seq2.p1		
comp22555_c0_seq3.p2		
comp22563_c0_seq1.p1	sp|O77033|CYC8_DICDI_General_transcriptional_corepressor_trfA_OS=Dictyostelium_discoideum_GN=trfA_PE=2_SV=1	1.00E-120
comp22569_c0_seq1.p1		
comp22588_c0_seq1.p1		
comp22598_c0_seq2.p1	sp|Q3US41|ESRP1_MOUSE_Epithelial_splicing_regulatory_protein_1_OS=Mus_musculus_GN=Esrp1_PE=2_SV=2	1.00E-44
comp22599_c0_seq1.p2	sp|P04107|TBB_TRYBR_Tubulin_beta_chain_OS=Trypanosoma_brucei_rhodesiense_PE=3_SV=1	3.00E-170
comp22602_c0_seq1.p1		
comp22605_c0_seq2.p1	sp|Q6PBQ2|CHMP7_DANRE_Charged_multivesicular_body_protein_7_OS=Danio_rerio_GN=chmp7_PE=2_SV=1	9.00E-12
comp22609_c0_seq1.p1	sp|P62282|RS11_RAT_40S_ribosomal_protein_S11_OS=Rattus_norvegicus_GN=Rps11_PE=1_SV=3	1.00E-77
comp22632_c1_seq1.p1		
comp22642_c0_seq1.p2	sp|P0AC32|FTSX_SHIFL_Cell_division_protein_FtsX_OS=Shigella_flexneri_GN=ftsX_PE=3_SV=1	8.00E-88
comp22642_c2_seq1.p1	sp|P0AGB3|RP32_ECOLI_RNA_polymerase_sigma-32_factor_OS=Escherichia_coli_(strain_K12)_GN=rpoH_PE=1_SV=1	8.00E-80
comp22645_c0_seq1.p1		
comp22657_c0_seq1.p1		
comp22660_c1_seq1.p1		
comp22661_c0_seq1.p1		
comp22668_c0_seq1.p1	sp|P0DJ19|RL27_TETTH_60S_ribosomal_protein_L27_OS=Tetrahymena_thermophila_GN=RPL27_PE=1_SV=1	4.00E-32
comp22671_c0_seq2.p1		
comp22677_c0_seq1.p1		
comp22677_c0_seq2.p1		
comp22679_c0_seq1.p1		
comp22681_c0_seq1.p1		
comp22682_c0_seq2.p1		
comp22682_c0_seq3.p1		
comp22684_c0_seq1.p1		
comp22686_c0_seq1.p1		
comp22686_c0_seq2.p1		
comp22686_c1_seq1.p1		
comp22689_c0_seq1.p1	sp|C9ZN16|FAZ1_TRYB9_Flagellar_attachment_zone_protein_1_OS=Trypanosoma_brucei_gambiense_(strain_MHOM/CI/86/DAL972)_GN=TbgDal_IV3690_PE=3_SV=1	2.00E-12
comp22695_c0_seq1.p2	sp|P77735|YAJO_ECOLI_Uncharacterized_oxidoreductase_YajO_OS=Escherichia_coli_(strain_K12)_GN=yajO_PE=3_SV=2	5.00E-92
comp22710_c0_seq1.p1		
comp22711_c0_seq2.p1	sp|Q40255|ALDH_LINUS_Probable_aldehyde_dehydrogenase_OS=Linum_usitatissimum_GN=FIS1_PE=2_SV=1	0
comp22712_c0_seq1.p1		
comp22714_c0_seq1.p2		
comp22718_c0_seq1.p2		
comp22718_c0_seq1.p3		
comp22723_c0_seq2.p1		
comp2273_c0_seq1.p1	sp|P0AGL4|TDCF_SHIFL_Putative_reactive_intermediate_deaminase_TdcF_OS=Shigella_flexneri_GN=tdcF_PE=3_SV=1	9.00E-86
comp2273_c0_seq1.p2	sp|P42632|TDCE_ECOLI_PFL-like_enzyme_TdcE_OS=Escherichia_coli_(strain_K12)_GN=tdcE_PE=1_SV=2	5.00E-93
comp22731_c0_seq1.p1	sp|O84068|TLC1_CHLTR_ADP,ATP_carrier_protein_1_OS=Chlamydia_trachomatis_(strain_D/UW-3/Cx)_GN=tlcA_PE=3_SV=1	2.00E-105
comp22731_c0_seq2.p1	sp|O84068|TLC1_CHLTR_ADP,ATP_carrier_protein_1_OS=Chlamydia_trachomatis_(strain_D/UW-3/Cx)_GN=tlcA_PE=3_SV=1	7.00E-86
comp22734_c0_seq2.p1		
comp22735_c0_seq2.p2		
comp22737_c0_seq1.p1	sp|Q6I5Y0|CDKC1_ORYSJ_Cyclin-dependent_kinase_C-1_OS=Oryza_sativa_subsp._japonica_GN=CDKC-1_PE=2_SV=1	1.00E-78
comp22737_c0_seq2.p1	sp|Q6I5Y0|CDKC1_ORYSJ_Cyclin-dependent_kinase_C-1_OS=Oryza_sativa_subsp._japonica_GN=CDKC-1_PE=2_SV=1	1.00E-78
comp22737_c0_seq2.p2		
comp22742_c0_seq1.p1	sp|Q3SZ90|RL13A_BOVIN_60S_ribosomal_protein_L13a_OS=Bos_taurus_GN=RPL13A_PE=2_SV=3	6.00E-65
comp22748_c0_seq1.p1		
comp22749_c0_seq1.p1		
comp22752_c0_seq1.p1		
comp22752_c0_seq1.p2		
comp22753_c0_seq1.p1		
comp22753_c0_seq2.p1		
comp22756_c0_seq1.p1		
comp22756_c0_seq2.p1		
comp22756_c0_seq3.p1		
comp22757_c1_seq1.p1		
comp22758_c0_seq1.p1	sp|Q03346|MPPB_RAT_Mitochondrial-processing_peptidase_subunit_beta_OS=Rattus_norvegicus_GN=Pmpcb_PE=1_SV=3	6.00E-112
comp22759_c0_seq1.p1		
comp22761_c0_seq1.p1		
comp22765_c0_seq1.p1		
comp22772_c0_seq2.p1	sp|P91791|PPIA_HEMPU_Peptidyl-prolyl_cis-trans_isomerase_OS=Hemicentrotus_pulcherrimus_PE=2_SV=1	8.00E-32
comp22773_c0_seq1.p1		
comp22777_c0_seq1.p1		
comp22777_c0_seq2.p2		
comp22777_c0_seq2.p3		
comp22783_c0_seq1.p1		
comp22784_c0_seq1.p1		
comp22787_c0_seq1.p1	sp|P30870|GLNE_ECOLI_Glutamate-ammonia-ligase_adenylyltransferase_OS=Escherichia_coli_(strain_K12)_GN=glnE_PE=1_SV=2	1.00E-119
comp22787_c1_seq1.p1	sp|P30871|YGIF_ECOLI_Uncharacterized_protein_ygiF_OS=Escherichia_coli_(strain_K12)_GN=ygiF_PE=4_SV=1	4.00E-56
comp2279_c0_seq1.p1		
comp2279_c1_seq1.p1	sp|Q7SBD5|RL7_NEUCR_60S_ribosomal_protein_L7_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=rpl-7_PE=3_SV=2	1.00E-22
comp22790_c0_seq1.p1	sp|B7NGX8|UXUA_ECOLU_Mannonate_dehydratase_OS=Escherichia_coli_O17:K52:H18_(strain_UMN026_/_ExPEC)_GN=uxuA_PE=3_SV=1	0
comp22790_c1_seq1.p1	sp|P69786|PTGCB_ECOLI_PTS_system_glucose-specific_EIICB_component_OS=Escherichia_coli_(strain_K12)_GN=ptsG_PE=1_SV=1	5.00E-102
comp22790_c2_seq1.p1	sp|P69786|PTGCB_ECOLI_PTS_system_glucose-specific_EIICB_component_OS=Escherichia_coli_(strain_K12)_GN=ptsG_PE=1_SV=1	2.00E-74
comp22803_c0_seq1.p3	sp|Q7T2E3|KC1DA_DANRE_Casein_kinase_I_isoform_delta-A_OS=Danio_rerio_GN=csnk1da_PE=2_SV=1	7.00E-19
comp22803_c1_seq1.p2	sp|P40235|HHP1_SCHPO_Casein_kinase_I_homolog_hhp1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=hhp1_PE=2_SV=1	1.00E-79
comp22809_c1_seq1.p1		
comp2281_c0_seq1.p1	sp|P31224|ACRB_ECOLI_Acriflavine_resistance_protein_B_OS=Escherichia_coli_(strain_K12)_GN=acrB_PE=1_SV=1	1.00E-109
comp2281_c1_seq1.p1	sp|P31224|ACRB_ECOLI_Acriflavine_resistance_protein_B_OS=Escherichia_coli_(strain_K12)_GN=acrB_PE=1_SV=1	1.00E-75
comp22817_c0_seq1.p1	sp|P77360|YPHC_ECOLI_Uncharacterized_zinc-type_alcohol_dehydrogenase-like_protein_YphC_OS=Escherichia_coli_(strain_K12)_GN=yphC_PE=3_SV=2	5.00E-50
comp22818_c0_seq3.p2		
comp22819_c0_seq1.p1		
comp22825_c0_seq1.p1		
comp22826_c0_seq1.p1		
comp22831_c0_seq1.p1		
comp22831_c1_seq1.p1		
comp22831_c1_seq1.p2		
comp22836_c1_seq1.p1		
comp22843_c0_seq1.p1	sp|P30749|MOAE_ECOLI_Molybdopterin_synthase_catalytic_subunit_OS=Escherichia_coli_(strain_K12)_GN=moaE_PE=1_SV=3	4.00E-107
comp22847_c0_seq1.p1		
comp22848_c0_seq1.p1	sp|Q8LBU2|GPX8_ARATH_Probable_glutathione_peroxidase_8_OS=Arabidopsis_thaliana_GN=GPX8_PE=2_SV=1	2.00E-33
comp22857_c0_seq2.p1		
comp22870_c0_seq1.p1		
comp22872_c0_seq1.p1		
comp22876_c1_seq1.p1		
comp22877_c0_seq1.p2	sp|P0DJ13|RL7_TETTH_60S_ribosomal_protein_L7_OS=Tetrahymena_thermophila_GN=RPL7_PE=1_SV=1	5.00E-66
comp22880_c0_seq1.p1	sp|Q54RA4|Y3291_DICDI_Probable_iron/ascorbate_oxidoreductase_DDB_G0283291_OS=Dictyostelium_discoideum_GN=DDB_G0283291_PE=3_SV=1	1.00E-15
comp22889_c0_seq1.p1	sp|Q5UP39|YR873_MIMIV_Putative_ankyrin_repeat_protein_R873_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R873_PE=4_SV=1	8.00E-15
comp22894_c0_seq1.p2	sp|Q28CN3|UBP33_XENTR_Ubiquitin_carboxyl-terminal_hydrolase_33_OS=Xenopus_tropicalis_GN=usp33_PE=2_SV=1	6.00E-15
comp22896_c0_seq1.p1	sp|Q58D72|ATLA1_BOVIN_Atlastin-1_OS=Bos_taurus_GN=ATL1_PE=2_SV=2	1.00E-31
comp22896_c0_seq1.p4		
comp2290_c0_seq1.p1		
comp22901_c0_seq1.p1		
comp22907_c0_seq1.p1		
comp22911_c0_seq1.p1	sp|P42037|RLA2_ALTAL_60S_acidic_ribosomal_protein_P2_OS=Alternaria_alternata_GN=ALTA5_PE=1_SV=1	4.00E-18
comp22911_c0_seq2.p1		
comp22919_c0_seq2.p1	sp|P0C5W5|INSD_ECOLX_Transposase_insD_for_insertion_element_IS2A/D/F/H/I/K_OS=Escherichia_coli_GN=insD_PE=3_SV=1	6.00E-136
comp22935_c0_seq1.p1		
comp22945_c0_seq3.p1		
comp22950_c0_seq1.p1		
comp22956_c0_seq1.p2	sp|Q9LUQ6|RL192_ARATH_60S_ribosomal_protein_L19-2_OS=Arabidopsis_thaliana_GN=RPL19B_PE=2_SV=1	1.00E-40
comp22958_c0_seq1.p1		
comp22969_c0_seq1.p1	sp|Q10PV9|RH47B_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_47B_OS=Oryza_sativa_subsp._japonica_GN=Os03g0219700_PE=2_SV=1	2.00E-36
comp22969_c0_seq1.p2		
comp2297_c0_seq1.p1		
comp22971_c0_seq1.p2		
comp22971_c1_seq1.p1		
comp22975_c0_seq1.p1		
comp22977_c0_seq1.p1		
comp22988_c0_seq1.p1		
comp2299_c1_seq1.p1	sp|P52062|YGGW_ECOLI_Oxygen-independent_coproporphyrinogen-III_oxidase-like_protein_YggW_OS=Escherichia_coli_(strain_K12)_GN=yggW_PE=3_SV=1	6.00E-67
comp22995_c0_seq3.p1	sp|Q40300|FCPF_MACPY_Fucoxanthin-chlorophyll_a-c_binding_protein_F,_chloroplastic_(Fragment)_OS=Macrocystis_pyrifera_GN=FCPF_PE=2_SV=1	1.00E-25
comp22995_c0_seq4.p1		
comp23000_c0_seq1.p1		
comp23000_c0_seq2.p1		
comp23001_c0_seq3.p1		
comp23002_c0_seq2.p1		
comp23003_c0_seq1.p1	sp|Q6Z437|MPK3_ORYSJ_Mitogen-activated_protein_kinase_3_OS=Oryza_sativa_subsp._japonica_GN=MPK3_PE=2_SV=1	6.00E-34
comp23008_c0_seq1.p1	sp|Q23868|TAGC_DICDI_Serine_protease/ABC_transporter_B_family_protein_tagC_OS=Dictyostelium_discoideum_GN=tagC_PE=2_SV=2	1.00E-12
comp23008_c0_seq1.p2		
comp2301_c0_seq1.p1		
comp23015_c0_seq1.p1	sp|Q8LBS4|GRS12_ARATH_Monothiol_glutaredoxin-S12,_chloroplastic_OS=Arabidopsis_thaliana_GN=GRXS12_PE=1_SV=2	5.00E-13
comp23021_c0_seq1.p1	sp|Q3Z5Y4|SYI_SHISS_Isoleucine--tRNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=ileS_PE=3_SV=1	1.00E-70
comp23021_c1_seq1.p1	sp|P69912|DCEB_SHIFL_Glutamate_decarboxylase_beta_OS=Shigella_flexneri_GN=gadB_PE=3_SV=1	0
comp23022_c0_seq1.p2		
comp23029_c0_seq1.p1	sp|Q9WUU7|CATZ_MOUSE_Cathepsin_Z_OS=Mus_musculus_GN=Ctsz_PE=2_SV=1	2.00E-57
comp23031_c1_seq1.p1	sp|P37682|YIAU_ECOLI_Uncharacterized_HTH-type_transcriptional_regulator_yiaU_OS=Escherichia_coli_(strain_K12)_GN=yiaU_PE=4_SV=1	3.00E-124
comp23032_c0_seq2.p1	sp|Q8HXY2|MCAT_MACFA_Mitochondrial_carnitine/acylcarnitine_carrier_protein_OS=Macaca_fascicularis_GN=SLC25A20_PE=2_SV=1	9.00E-22
comp23035_c0_seq1.p1		
comp2304_c0_seq1.p1	sp|P63284|CLPB_ECOLI_Chaperone_protein_ClpB_OS=Escherichia_coli_(strain_K12)_GN=clpB_PE=1_SV=1	5.00E-79
comp23042_c0_seq1.p1		
comp23042_c0_seq2.p1		
comp23043_c0_seq1.p1		
comp23045_c0_seq1.p1	sp|P37651|GUN_ECOLI_Endoglucanase_OS=Escherichia_coli_(strain_K12)_GN=bcsZ_PE=1_SV=1	3.00E-77
comp23045_c1_seq1.p1	sp|P37651|GUN_ECOLI_Endoglucanase_OS=Escherichia_coli_(strain_K12)_GN=bcsZ_PE=1_SV=1	9.00E-109
comp23049_c0_seq1.p1		
comp23051_c0_seq1.p1		
comp23060_c0_seq1.p1		
comp23061_c0_seq1.p1		
comp23061_c0_seq2.p1	sp|Q922S4|PDE2A_MOUSE_cGMP-dependent_3',5'-cyclic_phosphodiesterase_OS=Mus_musculus_GN=Pde2a_PE=1_SV=3	3.00E-11
comp23062_c0_seq1.p1		
comp23062_c1_seq1.p1		
comp23063_c2_seq1.p1		
comp23082_c0_seq1.p1		
comp23085_c0_seq1.p1	sp|Q11004|PPID_SCHPO_40_kDa_peptidyl-prolyl_cis-trans_isomerase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=wis2_PE=2_SV=1	3.00E-32
comp23101_c0_seq1.p1	sp|Q11118|WOS2_SCHPO_Protein_wos2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=wos2_PE=2_SV=1	3.00E-18
comp23104_c0_seq1.p1	sp|Q43362|VATL_PLECA_V-type_proton_ATPase_16_kDa_proteolipid_subunit_OS=Pleurochrysis_carterae_GN=VAP_PE=2_SV=1	7.00E-67
comp23110_c0_seq1.p1		
comp23110_c0_seq2.p1		
comp23112_c0_seq1.p1		
comp23116_c0_seq1.p1		
comp23118_c0_seq1.p1		
comp23118_c0_seq2.p2		
comp23120_c0_seq1.p1		
comp23126_c0_seq1.p2	sp|P0A910|OMPA_ECOLI_Outer_membrane_protein_A_OS=Escherichia_coli_(strain_K12)_GN=ompA_PE=1_SV=1	1.00E-84
comp23128_c0_seq1.p1	sp|P0ACQ3|RBSR_SHIFL_Ribose_operon_repressor_OS=Shigella_flexneri_GN=rbsR_PE=3_SV=2	1.00E-48
comp23128_c0_seq3.p1	sp|P0ACQ3|RBSR_SHIFL_Ribose_operon_repressor_OS=Shigella_flexneri_GN=rbsR_PE=3_SV=2	0
comp23132_c0_seq2.p1		
comp23132_c0_seq3.p1		
comp23133_c0_seq2.p1	sp|Q91820|AURAA_XENLA_Aurora_kinase_A-A_OS=Xenopus_laevis_GN=aurka-a_PE=1_SV=1	3.00E-124
comp2314_c0_seq1.p1		
comp2314_c0_seq2.p1		
comp23148_c0_seq2.p1		
comp23149_c0_seq2.p1		
comp23150_c0_seq1.p1		
comp23156_c0_seq1.p1		
comp23156_c0_seq2.p1		
comp23164_c0_seq1.p2		
comp23165_c0_seq1.p1		
comp23170_c0_seq1.p2		
comp23170_c0_seq1.p3		
comp23185_c0_seq3.p1		
comp23185_c0_seq3.p3		
comp23186_c0_seq1.p1		
comp23187_c0_seq1.p1		
comp23197_c0_seq1.p1		
comp23197_c0_seq3.p1	sp|Q8U0L6|PSA_PYRFU_Proteasome_subunit_alpha_OS=Pyrococcus_furiosus_(strain_ATCC_43587_/_DSM_3638_/_JCM_8422_/_Vc1)_GN=psmA_PE=3_SV=1	1.00E-21
comp23202_c0_seq1.p1		
comp23210_c0_seq1.p1		
comp23211_c0_seq3.p1		
comp23212_c0_seq1.p1	sp|Q9VLT5|POE_DROME_Protein_purity_of_essence_OS=Drosophila_melanogaster_GN=poe_PE=1_SV=1	5.00E-15
comp23217_c0_seq1.p1	sp|P43885|SERA_HAEIN_D-3-phosphoglycerate_dehydrogenase_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=serA_PE=3_SV=1	3.00E-17
comp23218_c0_seq1.p2		
comp23218_c0_seq2.p1		
comp23221_c0_seq1.p1		
comp23223_c0_seq1.p1		
comp23223_c0_seq2.p4		
comp23227_c0_seq2.p1	sp|P31433|YICH_ECOLI_Uncharacterized_protein_yicH_OS=Escherichia_coli_(strain_K12)_GN=yicH_PE=4_SV=2	1.00E-53
comp23228_c0_seq1.p1	sp|P52052|YGGR_ECOLI_Uncharacterized_protein_yggR_OS=Escherichia_coli_(strain_K12)_GN=yggR_PE=1_SV=1	4.00E-120
comp23238_c0_seq1.p1		
comp23238_c0_seq2.p1		
comp23238_c0_seq3.p1		
comp23248_c0_seq1.p1	sp|P49724|OAT_DROAN_Ornithine_aminotransferase,_mitochondrial_OS=Drosophila_ananassae_GN=Oat_PE=1_SV=1	1.00E-36
comp23248_c1_seq1.p1	sp|Q9VW26|OAT_DROME_Ornithine_aminotransferase,_mitochondrial_OS=Drosophila_melanogaster_GN=Oat_PE=2_SV=1	8.00E-140
comp23249_c0_seq2.p1		
comp23250_c0_seq1.p1		
comp23250_c0_seq1.p2		
comp23252_c0_seq1.p2		
comp23253_c0_seq1.p1		
comp23257_c0_seq1.p1	sp|Q9Z398|PMP9_CHLPN_Probable_outer_membrane_protein_pmp9_OS=Chlamydia_pneumoniae_GN=pmp9_PE=3_SV=1	7.00E-13
comp23258_c0_seq2.p1		
comp23259_c0_seq1.p1		
comp23261_c1_seq1.p1		
comp23270_c0_seq1.p1	sp|P37677|LYXK_ECOLI_L-xylulose/3-keto-L-gulonate_kinase_OS=Escherichia_coli_(strain_K12)_GN=lyx_PE=1_SV=1	6.00E-81
comp23281_c0_seq1.p1	sp|P75810|YBJJ_ECOLI_Inner_membrane_protein_ybjJ_OS=Escherichia_coli_(strain_K12)_GN=ybjJ_PE=1_SV=1	0
comp23282_c0_seq1.p1		
comp23289_c0_seq2.p1		
comp23302_c0_seq1.p1	sp|P32717|YJCS_ECOLI_Uncharacterized_protein_yjcS_OS=Escherichia_coli_(strain_K12)_GN=yjcS_PE=4_SV=2	9.00E-84
comp23309_c0_seq2.p1		
comp23309_c0_seq3.p1		
comp23310_c0_seq1.p1		
comp23327_c0_seq1.p2		
comp23329_c0_seq1.p1		
comp23362_c0_seq1.p1	sp|D0MVS1|KEX1_PHYIT_Pheromone-processing_carboxypeptidase_KEX1_OS=Phytophthora_infestans_(strain_T30-4)_GN=KEX1_PE=3_SV=1	6.00E-95
comp23362_c0_seq2.p1	sp|D0MVS1|KEX1_PHYIT_Pheromone-processing_carboxypeptidase_KEX1_OS=Phytophthora_infestans_(strain_T30-4)_GN=KEX1_PE=3_SV=1	2.00E-54
comp23366_c0_seq4.p1		
comp23381_c0_seq1.p1	sp|P0CG86|RS271_HORVU_Ubiquitin-40S_ribosomal_protein_S27a_OS=Hordeum_vulgare_GN=MUB1_PE=3_SV=1	1.00E-40
comp23391_c0_seq1.p2	sp|O42820|EF1A_SCHCO_Elongation_factor_1-alpha_OS=Schizophyllum_commune_GN=TEF1_PE=3_SV=1	1.00E-90
comp23393_c0_seq1.p2		
comp23397_c0_seq1.p1		
comp23401_c0_seq2.p1	sp|Q3TYG6|F179A_MOUSE_Protein_FAM179A_OS=Mus_musculus_GN=Fam179a_PE=2_SV=1	1.00E-15
comp23402_c0_seq2.p1		
comp23422_c0_seq3.p1		
comp23424_c0_seq2.p1	sp|Q5UPJ7|SYY_MIMIV_Tyrosine--tRNA_ligase_OS=Acanthamoeba_polyphaga_mimivirus_GN=YARS_PE=1_SV=1	3.00E-87
comp23424_c0_seq2.p2	sp|Q40784|AAPC_CENCI_Putative_glucose-6-phosphate_1-epimerase_OS=Cenchrus_ciliaris_PE=2_SV=1	7.00E-31
comp23429_c0_seq2.p1		
comp23430_c0_seq1.p1		
comp23432_c0_seq2.p1	sp|B8JAX1|GPDA_ANAD2_Glycerol-3-phosphate_dehydrogenase_[NAD(P)+]_OS=Anaeromyxobacter_dehalogenans_(strain_2CP-1_/_ATCC_BAA-258)_GN=gpsA_PE=3_SV=1	4.00E-93
comp23436_c0_seq1.p1	sp|P54697|MYOJ_DICDI_Myosin-J_heavy_chain_OS=Dictyostelium_discoideum_GN=myoJ_PE=4_SV=2	1.00E-22
comp23438_c0_seq1.p1		
comp23448_c0_seq1.p1		
comp23455_c0_seq1.p1	sp|Q03409|RS25_DICDI_40S_ribosomal_protein_S25_OS=Dictyostelium_discoideum_GN=rps25_PE=3_SV=1	9.00E-11
comp23462_c0_seq1.p1		

comp23467_c0_seq1.p1				
comp23467_c0_seq2.p1	sp|Q54YZ0|UGPA2_DICDI_UTP--glucose-1-phosphate_uridylyltransferase_2_OS=Dictyostelium_discoideum_GN=ugpB_PE=2_SV=1	5.00E-140	[illegible]	[illegible]
comp23470_c0_seq1.p1	sp|Q9LYR5|FKB19_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP19,_chloroplastic_OS=Arabidopsis_thaliana_GN=FKBP19_PE=1_SV=1	1.00E-10	[illegible]	[illegible]
comp23470_c0_seq2.p1	sp|Q9LYR5|FKB19_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP19,_chloroplastic_OS=Arabidopsis_thaliana_GN=FKBP19_PE=1_SV=1	7.00E-11	[illegible]	[illegible]
comp23474_c0_seq1.p1				
comp23483_c0_seq1.p1	sp|P26616|MAO1_ECOLI_NAD-dependent_malic_enzyme_OS=Escherichia_coli_(strain_K12)_GN=maeA_PE=1_SV=4	1.00E-121	[illegible]	[illegible]
comp23487_c0_seq1.p2				
comp23487_c0_seq3.p2				
comp23487_c0_seq4.p1				
comp23504_c0_seq1.p1	sp|A5UZX0|GAL1_ROSS1_Galactokinase_OS=Roseiflexus_sp._(strain_RS-1)_GN=galK_PE=3_SV=1	2.00E-20	[illegible]	[illegible]
comp23504_c1_seq1.p1				
comp23504_c2_seq1.p1	sp|P51570|GALK1_HUMAN_Galactokinase_OS=Homo_sapiens_GN=GALK1_PE=1_SV=1	2.00E-38	[illegible]	[illegible]
comp23508_c0_seq1.p1				
comp23508_c0_seq2.p1				
comp23521_c0_seq1.p2				
comp23521_c0_seq2.p1				
comp23524_c0_seq3.p2				
comp23525_c0_seq1.p1				
comp23525_c0_seq2.p1				
comp23525_c0_seq4.p1				
comp23529_c0_seq2.p1				
comp23531_c0_seq3.p2				
comp23536_c0_seq2.p1	sp|P73960|LEU3_SYNY3_3-isopropylmalate_dehydrogenase_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=leuB_PE=3_SV=1	6.00E-150	[illegible]	[illegible]
comp23537_c0_seq3.p1	sp|D0NKK0|GUF1_PHYIT_Translation_factor_GUF1_homolog,_mitochondrial_OS=Phytophthora_infestans_(strain_T30-4)_GN=PITG_12454_PE=3_SV=1	0	[illegible]	[illegible]
comp23542_c0_seq1.p1				
comp23549_c0_seq1.p1	sp|P0AFJ7|PITA_ECOLI_Low-affinity_inorganic_phosphate_transporter_1_OS=Escherichia_coli_(strain_K12)_GN=pitA_PE=1_SV=1	6.00E-78	[illegible]	[illegible]
comp23549_c1_seq1.p1	sp|P0AFJ7|PITA_ECOLI_Low-affinity_inorganic_phosphate_transporter_1_OS=Escherichia_coli_(strain_K12)_GN=pitA_PE=1_SV=1	5.00E-114	[illegible]	[illegible]
comp23555_c0_seq1.p1	sp|P32176|FDOG_ECOLI_Formate_dehydrogenase-O_major_subunit_OS=Escherichia_coli_(strain_K12)_GN=fdoG_PE=1_SV=5	0	[illegible]	[illegible]
comp23570_c0_seq1.p1	sp|Q2UTL1|GMT_ASPOR_GDP-mannose_transporter_OS=Aspergillus_oryzae_(strain_ATCC_42149_/_RIB_40)_GN=gmt1_PE=3_SV=2	3.00E-42	[illegible]	[illegible]
comp23582_c0_seq1.p1	sp|B4I0K4|RTEL1_DROSE_Regulator_of_telomere_elongation_helicase_1_homolog_OS=Drosophila_sechellia_GN=GM12432_PE=3_SV=1	1.00E-14	[illegible]	[illegible]
comp23583_c0_seq1.p1	sp|P0ACA6|SSPA_SHIFL_Stringent_starvation_protein_A_OS=Shigella_flexneri_GN=sspA_PE=3_SV=2	3.00E-133		
comp23588_c0_seq1.p2				
comp23592_c0_seq2.p1				
comp23593_c0_seq1.p1				
comp23595_c0_seq1.p1				
comp23595_c0_seq2.p1				
comp23598_c0_seq1.p1	sp|Q6BRY4|ACEA_DEBHA_Isocitrate_lyase_OS=Debaryomyces_hansenii_(strain_ATCC_36239_/_CBS_767_/_JCM_1990_/_NBRC_0083_/_IGC_2968)_GN=ICL1_PE=3_SV=1	7.00E-176	[illegible]	[illegible]
comp23603_c1_seq1.p1	sp|Q20065|P4HA2_CAEEL_Prolyl_4-hydroxylase_subunit_alpha-2_OS=Caenorhabditis_elegans_GN=phy-2_PE=1_SV=1	8.00E-22	[illegible]	[illegible]
comp23607_c0_seq1.p1				
comp23607_c1_seq1.p1				
comp23614_c0_seq1.p1				
comp23614_c0_seq1.p2				
comp2362_c0_seq1.p1	sp|A2PYH4|HFM1_HUMAN_Probable_ATP-dependent_DNA_helicase_HFM1_OS=Homo_sapiens_GN=HFM1_PE=1_SV=2	6.00E-16	[illegible]	[illegible]
comp23621_c0_seq2.p1	sp|Q5ZLS7|GLYR1_CHICK_Putative_oxidoreductase_GLYR1_OS=Gallus_gallus_GN=GLYR1_PE=2_SV=1	5.00E-52	[illegible]	[illegible]
comp23622_c0_seq1.p1				
comp23629_c0_seq1.p1	sp|P35685|RL7A_ORYSJ_60S_ribosomal_protein_L7a_OS=Oryza_sativa_subsp._japonica_GN=RPL7A_PE=2_SV=1	4.00E-71	[illegible]	[illegible]
comp23636_c0_seq2.p1				
comp23639_c1_seq2.p1	sp|Q8T2H0|FAM49_DICDI_Protein_FAM49_homolog_OS=Dictyostelium_discoideum_GN=fam49_PE=3_SV=2	5.00E-37	[illegible]	[illegible]
comp23640_c0_seq2.p1				
comp23641_c0_seq1.p1				
comp23643_c0_seq1.p1	sp|P09152|NARG_ECOLI_Respiratory_nitrate_reductase_1_alpha_chain_OS=Escherichia_coli_(strain_K12)_GN=narG_PE=1_SV=4	8.00E-126	[illegible]	[illegible]
comp23650_c0_seq1.p1				
comp23654_c0_seq1.p1	sp|Q9P6C8|ADH1_NEUCR_Alcohol_dehydrogenase_1_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=adh-1_PE=3_SV=1	7.00E-56	[illegible]	[illegible]
comp23654_c1_seq1.p2	sp|Q9P6C8|ADH1_NEUCR_Alcohol_dehydrogenase_1_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=adh-1_PE=3_SV=1	1.00E-60	[illegible]	[illegible]
comp23659_c0_seq1.p2				
comp23668_c0_seq1.p1	sp|P62752|RL23A_RAT_60S_ribosomal_protein_L23a_OS=Rattus_norvegicus_GN=Rpl23a_PE=2_SV=1	1.00E-33	[illegible]	[illegible]
comp23673_c0_seq1.p1	sp|Q11KJ6|DNAK_MESSB_Chaperone_protein_DnaK_OS=Mesorhizobium_sp._(strain_BNC1)_GN=dnaK_PE=3_SV=1	5.00E-76	[illegible]	[illegible]
comp23675_c0_seq2.p2				
comp23677_c0_seq1.p1				
comp23677_c1_seq1.p1				
comp23685_c0_seq3.p1				
comp23687_c0_seq1.p1	sp|P11801|KPSH1_HUMAN_Serine/threonine-protein_kinase_H1_OS=Homo_sapiens_GN=PSKH1_PE=1_SV=4	2.00E-12	[illegible]	[illegible]
comp23687_c0_seq1.p3	sp|Q9DB30|PHKG2_MOUSE_Phosphorylase_b_kinase_gamma_catalytic_chain,_testis/liver_isoform_OS=Mus_musculus_GN=Phkg2_PE=2_SV=2	3.00E-21	[illegible]	[illegible]
comp23688_c0_seq1.p1	sp|P34334|RL21_CAEEL_60S_ribosomal_protein_L21_OS=Caenorhabditis_elegans_GN=rpl-21_PE=1_SV=3	1.00E-48	[illegible]	[illegible]
comp23689_c0_seq1.p1				
comp23691_c0_seq1.p1				
comp23691_c0_seq4.p1				
comp23708_c0_seq1.p1	sp|P66025|RF2_SHIFL_Peptide_chain_release_factor_2_OS=Shigella_flexneri_GN=prfB_PE=3_SV=1	0	[illegible]	[illegible]
comp23712_c0_seq1.p1	sp|P76585|YPHG_ECOLI_Uncharacterized_protein_yphG_OS=Escherichia_coli_(strain_K12)_GN=yphG_PE=4_SV=2	8.00E-74		
comp23713_c0_seq1.p1				
comp23713_c0_seq1.p3	sp|Q5ZJN0|ASND1_CHICK_Asparagine_synthetase_domain-containing_protein_1_OS=Gallus_gallus_GN=ASNSD1_PE=2_SV=1	2.00E-34	[illegible]	[illegible]
comp23713_c0_seq2.p1	sp|Q5ZJN0|ASND1_CHICK_Asparagine_synthetase_domain-containing_protein_1_OS=Gallus_gallus_GN=ASNSD1_PE=2_SV=1	4.00E-39	[illegible]	[illegible]
comp23730_c0_seq3.p1				
comp23738_c0_seq1.p2				
comp23746_c0_seq1.p1	sp|Q65ML1|BIOF_BACLD_Putative_8-amino-7-oxononanoate_synthase_OS=Bacillus_licheniformis_(strain_DSM_13_/_ATCC_14580)_GN=bioF_PE=3_SV=1	6.00E-53	[illegible]	[illegible]
comp23746_c0_seq2.p1	sp|Q65ML1|BIOF_BACLD_Putative_8-amino-7-oxononanoate_synthase_OS=Bacillus_licheniformis_(strain_DSM_13_/_ATCC_14580)_GN=bioF_PE=3_SV=1	1.00E-51	[illegible]	[illegible]
comp23748_c0_seq1.p1				
comp23754_c0_seq1.p2				
comp23759_c0_seq1.p1				
comp23759_c0_seq2.p1				
comp23759_c0_seq3.p1				
comp23765_c1_seq1.p1	sp|P06864|BGA2_ECOLI_Evolved_beta-galactosidase_subunit_alpha_OS=Escherichia_coli_(strain_K12)_GN=ebgA_PE=1_SV=4	3.00E-100	[illegible]	[illegible]
comp23774_c0_seq2.p1				
comp23778_c0_seq1.p1				
comp23779_c0_seq1.p1				
comp23788_c0_seq2.p1				
comp23788_c0_seq2.p2				
comp23796_c0_seq1.p1				
comp23798_c0_seq1.p1				
comp23800_c0_seq1.p1	sp|A4F4L4|DNAL4_PIG_Dynein_light_chain_4,_axonemal_OS=Sus_scrofa_GN=DNAL4_PE=3_SV=1	3.00E-24	[illegible]	[illegible]
comp23803_c0_seq1.p1				
comp23809_c0_seq1.p1				
comp23809_c1_seq1.p1				
comp23817_c0_seq1.p1	sp|Q83IY4|GLMS_SHIFL_Glucosamine--fructose-6-phosphate_aminotransferase_[isomerizing]_OS=Shigella_flexneri_GN=glmS_PE=3_SV=3	0	[illegible]	[illegible]
comp23818_c0_seq1.p1	sp|A6SDT7|MCA1_BOTFB_Metacaspase-1_OS=Botryotinia_fuckeliana_(strain_B05.10)_GN=casA_PE=3_SV=1	6.00E-34	[illegible]	[illegible]
comp23824_c0_seq1.p1	sp|Q83R05|HIS7_SHIFL_Histidine_biosynthesis_bifunctional_protein_hisB_OS=Shigella_flexneri_GN=hisB_PE=3_SV=2	7.00E-113	[illegible]	[illegible]
comp23843_c0_seq1.p1				
comp23844_c0_seq1.p2	sp|O09452|G3PA_GUITH_Glyceraldehyde-3-phosphate_dehydrogenase,_chloroplastic_OS=Guillardia_theta_GN=GAPC1_PE=2_SV=1	2.00E-90	[illegible]	[illegible]
comp23850_c0_seq1.p1				
comp23851_c0_seq1.p1				
comp23863_c0_seq1.p2				
comp23863_c1_seq1.p1				
comp23868_c0_seq1.p1				
comp23878_c0_seq1.p1	sp|Q54MZ3|CDC20_DICDI_Anaphase-promoting_complex_subunit_cdc20_OS=Dictyostelium_discoideum_GN=cdc20_PE=1_SV=1	2.00E-116	[illegible]	[illegible]
comp23878_c0_seq3.p1				
comp2388_c0_seq1.p1	sp|P0AA76|DGOT_ECOLI_D-galactonate_transporter_OS=Escherichia_coli_(strain_K12)_GN=dgoT_PE=1_SV=1	7.00E-77	[illegible]	[illegible]
comp23883_c0_seq2.p1				
comp23888_c0_seq1.p1				
comp23892_c0_seq1.p1				
comp23892_c0_seq2.p1	sp|Q99LT0|DPY30_MOUSE_Protein_dpy-30_homolog_OS=Mus_musculus_GN=Dpy30_PE=2_SV=1	1.00E-17	[illegible]	[illegible]
comp23901_c0_seq1.p1				
comp23904_c0_seq2.p1				
comp23904_c0_seq3.p2				
comp23914_c0_seq1.p1				
comp23915_c0_seq2.p1				
comp23916_c0_seq1.p1	sp|Q9URB4|ALF_CANAL_Fructose-bisphosphate_aldolase_OS=Candida_albicans_(strain_SC5314_/_ATCC_MYA-2876)_GN=FBA1_PE=1_SV=2	1.00E-110	[illegible]	[illegible]
comp23917_c0_seq1.p1				
comp23917_c0_seq2.p1				
comp23926_c0_seq1.p1				
comp23933_c0_seq1.p1				
comp23934_c0_seq1.p1				
comp23970_c1_seq1.p1	sp|B7LU47|DAPF_ESCF3_Diaminopimelate_epimerase_OS=Escherichia_fergusonii_(strain_ATCC_35469_/_DSM_13698_/_CDC_0568-73)_GN=dapF_PE=3_SV=1	5.00E-96	[illegible]	[illegible]
comp23975_c0_seq1.p1				
comp23976_c0_seq1.p1				
comp23979_c0_seq1.p1	sp|O04386|TBB_CHLIN_Tubulin_beta_chain_OS=Chlamydomonas_incerta_GN=TUBB_PE=3_SV=1	2.00E-70	[illegible]	[illegible]
comp23979_c0_seq2.p2	sp|P86221|TBB4B_MESAU_Tubulin_beta-4B_chain_(Fragments)_OS=Mesocricetus_auratus_GN=TUBB4B_PE=1_SV=1	2.00E-67	[illegible]	[illegible]
comp23982_c0_seq2.p1				
comp23983_c0_seq1.p1	sp|O35547|ACSL4_RAT_Long-chain-fatty-acid--CoA_ligase_4_OS=Rattus_norvegicus_GN=Acsl4_PE=2_SV=1	7.00E-72	[illegible]	[illegible]
comp23998_c0_seq1.p1				
comp23998_c0_seq2.p1				
comp24001_c0_seq1.p2	sp|P06715|GSHR_ECOLI_Glutathione_reductase_OS=Escherichia_coli_(strain_K12)_GN=gor_PE=1_SV=1	2.00E-58	[illegible]	[illegible]
comp24002_c0_seq3.p1				
comp24002_c0_seq5.p1				
comp24004_c0_seq1.p2				
comp24005_c0_seq1.p1				
comp24006_c0_seq1.p1				
comp24006_c0_seq3.p1				
comp24013_c0_seq1.p1	sp|P76272|YEBT_ECOLI_Uncharacterized_protein_yebT_OS=Escherichia_coli_(strain_K12)_GN=yebT_PE=3_SV=2	9.00E-124	[illegible]	[illegible]
comp24013_c1_seq1.p1	sp|P76272|YEBT_ECOLI_Uncharacterized_protein_yebT_OS=Escherichia_coli_(strain_K12)_GN=yebT_PE=3_SV=2	1.00E-59	[illegible]	[illegible]
comp24014_c0_seq2.p1				
comp24015_c0_seq3.p1				
comp24015_c0_seq4.p1				
comp24021_c0_seq1.p1	sp|P49076|ARF_MAIZE_ADP-ribosylation_factor_OS=Zea_mays_GN=ARF1_PE=2_SV=2	5.00E-108	[illegible]	[illegible]
comp24025_c0_seq1.p1	sp|P45332|LPTG_HAEIN_Lipopolysaccharide_export_system_permease_protein_lptG_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=lptG_PE=3_SV=1	1.00E-12	[illegible]	[illegible]
comp24026_c0_seq2.p1				
comp24027_c0_seq1.p1				
comp24029_c0_seq2.p1	sp|Q9FZ59|PEPR2_ARATH_Leucine-rich_repeat_receptor-like_protein_kinase_PEPR2_OS=Arabidopsis_thaliana_GN=PEPR2_PE=1_SV=1	2.00E-27	[illegible]	[illegible]
comp2403_c0_seq1.p1	sp|Q8NK13|SKP1_NEUCR_E3_ubiquitin_ligase_complex_SCF_subunit_scon-3_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=scon-3_PE=1_SV=1	2.00E-16	[illegible]	[illegible]
comp24036_c0_seq1.p1				
comp24037_c0_seq2.p1				
comp24038_c0_seq2.p1	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	4.00E-37	[illegible]	[illegible]
comp24044_c0_seq1.p1				
comp24047_c0_seq1.p1	sp|B1LPG6|PUR9_ECOSM_Bifunctional_purine_biosynthesis_protein_PurH_OS=Escherichia_coli_(strain_SMS-3-5_/_SECEC)_GN=purH_PE=3_SV=1	3.00E-135	[illegible]	[illegible]
comp24051_c0_seq2.p1	sp|Q65S97|SYV_MANSM_Valine--tRNA_ligase_OS=Mannheimia_succiniciproducens_(strain_MBEL55E)_GN=valS_PE=3_SV=1	7.00E-172	[illegible]	[illegible]
comp24051_c0_seq7.p1	sp|Q81LD3|SYV_BACAN_Valine--tRNA_ligase_OS=Bacillus_anthracis_GN=valS_PE=3_SV=1	0	[illegible]	[illegible]
comp24053_c0_seq1.p1	sp|P76298|FLHA_ECOLI_Flagellar_biosynthesis_protein_flhA_OS=Escherichia_coli_(strain_K12)_GN=flhA_PE=1_SV=1	2.00E-40	[illegible]	[illegible]
comp24055_c0_seq1.p1				
comp24055_c0_seq2.p2				
comp24064_c1_seq1.p1	sp|Q3Z5H6|LPXB_SHISS_Lipid-A-disaccharide_synthase_OS=Shigella_sonnei_(strain_Ss046)_GN=lpxB_PE=3_SV=1	0	[illegible]	[illegible]
comp24064_c1_seq1.p2	sp|B1IQF8|RNH2_ECOLC_Ribonuclease_HII_OS=Escherichia_coli_(strain_ATCC_8739_/_DSM_1576_/_Crooks)_GN=rnhB_PE=3_SV=1	2.00E-63	[illegible]	[illegible]
comp24064_c2_seq1.p1	sp|Q3Z5H7|LPXA_SHISS_Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine_O-acyltransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=lpxA_PE=3_SV=1	1.00E-109	[illegible]	[illegible]
comp24065_c0_seq1.p1				
comp24065_c0_seq2.p1				
comp24065_c1_seq2.p2				
comp24065_c1_seq3.p1				
comp24068_c0_seq1.p1				
comp24072_c0_seq3.p1	sp|Q3TLP5|ECHD2_MOUSE_Enoyl-CoA_hydratase_domain-containing_protein_2,_mitochondrial_OS=Mus_musculus_GN=Echdc2_PE=2_SV=2	3.00E-75	[illegible]	[illegible]
comp24076_c0_seq1.p2				
comp24090_c1_seq2.p1	sp|Q8I7P9|POL5_DROME_Retrovirus-related_Pol_polyprotein_from_transposon_opus_OS=Drosophila_melanogaster_GN=pol_PE=4_SV=1	2.00E-14	[illegible]	[illegible]
comp24092_c0_seq1.p1				
comp24092_c0_seq2.p1				
comp24093_c0_seq3.p1	sp|Q6CU71|GUAA_KLULA_GMP_synthase_[glutamine-hydrolyzing]_OS=Kluyveromyces_lactis_(strain_ATCC_8585_/_CBS_2359_/_DSM_70799_/_NBRC_1267_/_NRRL_Y-1140_/_WM37)_GN=GUA1_PE=3_SV=1	0	[illegible]	[illegible]
comp24105_c0_seq2.p1	sp|Q8L9J9|CAES_ARATH_Probable_carbohydrate_esterase_At4g34215_OS=Arabidopsis_thaliana_GN=At4g34215_PE=1_SV=2	2.00E-35	[illegible]	[illegible]
comp24116_c0_seq1.p1	sp|O94768|ST17B_HUMAN_Serine/threonine-protein_kinase_17B_OS=Homo_sapiens_GN=STK17B_PE=1_SV=1	3.00E-14	[illegible]	[illegible]
comp24118_c0_seq1.p1	sp|Q8C8R3|ANK2_MOUSE_Ankyrin-2_OS=Mus_musculus_GN=Ank2_PE=1_SV=2	2.00E-17	[illegible]	[illegible]
comp24120_c0_seq1.p1	sp|A7S1L6|FUCT1_NEMVE_GDP-fucose_transporter_1_OS=Nematostella_vectensis_GN=slc35c1_PE=3_SV=1	3.00E-12	[illegible]	[illegible]
comp24122_c0_seq1.p1	sp|P28624|HIS7_PHYPR_Imidazoleglycerol-phosphate_dehydratase_OS=Phytophthora_parasitica_GN=HIS3_PE=3_SV=1	4.00E-152	[illegible]	[illegible]
comp24124_c0_seq1.p1				
comp24125_c0_seq1.p1				
comp24125_c0_seq2.p1				
comp24125_c0_seq2.p3	sp|O94675|MAM33_SCHPO_Mitochondrial_acidic_protein_mam33_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC776.07_PE=2_SV=1	8.00E-12	[illegible]	[illegible]
comp24127_c0_seq1.p2	sp|Q9SQT4|NDA8A_ARATH_NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_8-A_OS=Arabidopsis_thaliana_GN=At3g06310_PE=2_SV=1	3.00E-16	[illegible]	[illegible]
comp24129_c0_seq1.p1	sp|Q9FGW9|GTE10_ARATH_Transcription_factor_GTE10_OS=Arabidopsis_thaliana_GN=GTE10_PE=1_SV=2	1.00E-18	[illegible]	[illegible]
comp24130_c0_seq1.p2	sp|A4L691|PINX1_RAT_PIN2/TERF1-interacting_telomerase_inhibitor_1_OS=Rattus_norvegicus_GN=Pinx1_PE=2_SV=1	4.00E-18	[illegible]	[illegible]
comp24132_c0_seq2.p1	sp|Q6MZZ7|CAN13_HUMAN_Calpain-13_OS=Homo_sapiens_GN=CAPN13_PE=1_SV=2	3.00E-36	[illegible]	[illegible]
comp24132_c0_seq3.p1	sp|Q78EJ9|CAN8_RAT_Calpain-8_OS=Rattus_norvegicus_GN=Capn8_PE=2_SV=1	2.00E-22	[illegible]	[illegible]
comp24132_c0_seq3.p3				
comp24133_c0_seq2.p1	sp|P36096|TUL1_YEAST_Transmembrane_E3_ubiquitin-protein_ligase_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TUL1_PE=1_SV=1	2.00E-12	[illegible]	[illegible]
comp24135_c0_seq1.p1				
comp24136_c0_seq3.p1				
comp24136_c0_seq5.p1				
comp24137_c0_seq1.p1	sp|P32490|MKK1_YEAST_MAP_kinase_kinase_MKK1/SSP32_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=MKK1_PE=1_SV=1	2.00E-22	[illegible]	[illegible]
comp24138_c0_seq1.p1	sp|Q86VU5|CMTD1_HUMAN_Catechol_O-methyltransferase_domain-containing_protein_1_OS=Homo_sapiens_GN=COMTD1_PE=1_SV=1	2.00E-27	[illegible]	[illegible]
comp24138_c0_seq2.p1	sp|Q86VU5|CMTD1_HUMAN_Catechol_O-methyltransferase_domain-containing_protein_1_OS=Homo_sapiens_GN=COMTD1_PE=1_SV=1	5.00E-13	[illegible]	[illegible]
comp24138_c0_seq2.p2				
comp24139_c0_seq1.p1				
comp24140_c0_seq1.p1				
comp24141_c0_seq1.p1	sp|P59889|S39A1_DANRE_Zinc_transporter_ZIP1_OS=Danio_rerio_GN=slc39a1_PE=2_SV=1	1.00E-19	[illegible]	[illegible]
comp24142_c0_seq1.p1				
comp24143_c0_seq1.p1				
comp24143_c0_seq2.p1				
comp24145_c0_seq1.p1	sp|Q54F30|NARF_DICDI_Probable_cytosolic_Fe-S_cluster_assembly_factor_narfl_OS=Dictyostelium_discoideum_GN=narfl_PE=3_SV=1	1.00E-39	[illegible]	[illegible]
comp24146_c0_seq2.p2				
comp24146_c0_seq3.p1				
comp24147_c0_seq1.p1				
comp24150_c1_seq1.p1	sp|P19769|INSK_ECOLI_Putative_transposase_InsK_for_insertion_sequence_element_IS150_OS=Escherichia_coli_(strain_K12)_GN=insK_PE=3_SV=2	1.00E-69	[illegible]	[illegible]
comp24151_c0_seq2.p1	sp|Q86US8|EST1A_HUMAN_Telomerase-binding_protein_EST1A_OS=Homo_sapiens_GN=SMG6_PE=1_SV=2	5.00E-23	[illegible]	[illegible]
comp24152_c0_seq2.p2	sp|Q5M934|TRUB1_RAT_Probable_tRNA_pseudouridine_synthase_1_OS=Rattus_norvegicus_GN=Trub1_PE=2_SV=1	1.00E-46	[illegible]	[illegible]
comp24152_c0_seq4.p1	sp|Q8WWH5|TRUB1_HUMAN_Probable_tRNA_pseudouridine_synthase_1_OS=Homo_sapiens_GN=TRUB1_PE=1_SV=1	4.00E-53	[illegible]	[illegible]
comp24153_c0_seq1.p2	sp|P39409|YJJW_ECOLI_Uncharacterized_protein_yjjW_OS=Escherichia_coli_(strain_K12)_GN=yjjW_PE=3_SV=1	7.00E-73	[illegible]	[illegible]
comp24153_c0_seq2.p1	sp|P76569|YFGD_ECOLI_Uncharacterized_protein_YfgD_OS=Escherichia_coli_(strain_K12)_GN=yfgD_PE=1_SV=1	1.00E-77	[illegible]	[illegible]
comp24153_c1_seq1.p1	sp|P0AGM7|URAA_ECOLI_Uracil_permease_OS=Escherichia_coli_(strain_K12)_GN=uraA_PE=1_SV=1	9.00E-116	[illegible]	[illegible]
comp24154_c0_seq1.p1				
comp24156_c0_seq1.p1				
comp24157_c0_seq1.p1				
comp24158_c0_seq2.p1				
comp24158_c0_seq2.p2	sp|Q5U680|SAMC_MOUSE_S-adenosylmethionine_mitochondrial_carrier_protein_OS=Mus_musculus_GN=Slc25a26_PE=2_SV=2	8.00E-57	[illegible]	[illegible]
comp24159_c0_seq1.p1				
comp24160_c0_seq1.p1	sp|Q8BLR9|HIF1N_MOUSE_Hypoxia-inducible_factor_1-alpha_inhibitor_OS=Mus_musculus_GN=Hif1an_PE=1_SV=2	9.00E-12	[illegible]	[illegible]
comp24162_c0_seq1.p1	sp|P34943|NDUA9_BOVIN_NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_9,_mitochondrial_OS=Bos_taurus_GN=NDUFA9_PE=1_SV=1	9.00E-53	[illegible]	[illegible]
comp24163_c0_seq1.p1				
comp24163_c0_seq2.p1	sp|Q9Y6D9|MD1L1_HUMAN_Mitotic_spindle_assembly_checkpoint_protein_MAD1_OS=Homo_sapiens_GN=MAD1L1_PE=1_SV=2	4.00E-17	[illegible]	[illegible]
comp24165_c1_seq2.p1	sp|P58559|G3P3_NOSS1_Glyceraldehyde-3-phosphate_dehydrogenase_3_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=gap3_PE=2_SV=1	5.00E-134	[illegible]	[illegible]
comp24167_c0_seq2.p1				
comp24167_c0_seq5.p1				
comp24169_c0_seq2.p1				
comp24169_c0_seq3.p1	sp|Q9Z2E9|BSCL2_MOUSE_Seipin_OS=Mus_musculus_GN=Bscl2_PE=2_SV=2	9.00E-18	[illegible]	[illegible]
comp24169_c0_seq5.p2				
comp24170_c0_seq1.p1	sp|Q16526|CRY1_HUMAN_Cryptochrome-1_OS=Homo_sapiens_GN=CRY1_PE=1_SV=1	3.00E-164	[illegible]	[illegible]
comp24173_c0_seq1.p1				
comp24173_c0_seq2.p1				
comp24174_c0_seq3.p1				
comp24179_c0_seq1.p1				
comp24179_c0_seq1.p2	sp|Q54PN3|MED6_DICDI_Putative_mediator_of_RNA_polymerase_II_transcription_subunit_6_OS=Dictyostelium_discoideum_GN=med6_PE=3_SV=1	1.00E-24	[illegible]	[illegible]
comp24181_c0_seq3.p1				
comp24182_c0_seq2.p1	sp|Q54XX9|PX24B_DICDI_PXMP2/4_family_protein_2_OS=Dictyostelium_discoideum_GN=DDB_G0278529_PE=3_SV=1	1.00E-17	[illegible]	[illegible]
comp24184_c0_seq1.p1	sp|Q84M92|ARP4_ARATH_Actin-related_protein_4_OS=Arabidopsis_thaliana_GN=ARP4_PE=1_SV=1	3.00E-84	[illegible]	[illegible]
comp24185_c0_seq1.p1	sp|Q9SLD2|DGAT1_ARATH_Diacylglycerol_O-acyltransferase_1_OS=Arabidopsis_thaliana_GN=DGAT1_PE=1_SV=2	2.00E-77	[illegible]	[illegible]
comp24185_c0_seq2.p1	sp|Q9SLD2|DGAT1_ARATH_Diacylglycerol_O-acyltransferase_1_OS=Arabidopsis_thaliana_GN=DGAT1_PE=1_SV=2	4.00E-53	[illegible]	[illegible]
comp24185_c0_seq3.p1				
comp24186_c0_seq1.p1				
comp24187_c0_seq1.p1	sp|Q9CI64|DBH_LACLA_DNA-binding_protein_HU_OS=Lactococcus_lactis_subsp._lactis_(strain_IL1403)_GN=hup_PE=3_SV=1	1.00E-24	[illegible]	[illegible]
comp24187_c0_seq2.p1	sp|Q9CI64|DBH_LACLA_DNA-binding_protein_HU_OS=Lactococcus_lactis_subsp._lactis_(strain_IL1403)_GN=hup_PE=3_SV=1	5.00E-25	[illegible]	[illegible]
comp24188_c0_seq1.p1	sp|P22675|ARLY_CHLRE_Argininosuccinate_lyase_OS=Chlamydomonas_reinhardtii_GN=ARG7_PE=2_SV=2	0	[illegible]	[illegible]
comp24189_c0_seq1.p1				
comp24190_c0_seq2.p1				
comp24190_c0_seq2.p2				
comp24191_c0_seq3.p3				
comp24191_c0_seq3.p4				
comp24191_c0_seq4.p2				
comp24191_c0_seq4.p4				
comp24194_c0_seq1.p1				
comp24196_c0_seq1.p1	sp|Q557H7|ATG4_DICDI_Cysteine_protease_atg4_OS=Dictyostelium_discoideum_GN=atg4-1_PE=3_SV=1	3.00E-21	[illegible]	[illegible]
comp24197_c0_seq1.p1	sp|Q5PQX0|UXS1_RAT_UDP-glucuronic_acid_decarboxylase_1_OS=Rattus_norvegicus_GN=Uxs1_PE=1_SV=1	8.00E-122	[illegible]	[illegible]
comp24197_c0_seq1.p2				
comp24197_c0_seq2.p1	sp|Q5PQX0|UXS1_RAT_UDP-glucuronic_acid_decarboxylase_1_OS=Rattus_norvegicus_GN=Uxs1_PE=1_SV=1	1.00E-104	[illegible]	[illegible]
comp24199_c0_seq2.p1	sp|Q9ZU52|ALFC3_ARATH_Probable_fructose-bisphosphate_aldolase_3,_chloroplastic_OS=Arabidopsis_thaliana_GN=FBA3_PE=1_SV=1	2.00E-145	[illegible]	[illegible]
comp24200_c0_seq1.p1	sp|Q6YS30|RH5_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_5_OS=Oryza_sativa_subsp._japonica_GN=Os07g0301200_PE=2_SV=1	1.00E-136	[illegible]	[illegible]
comp24200_c0_seq2.p1				
comp24201_c0_seq1.p1	sp|P81178|ALDH2_MESAU_Aldehyde_dehydrogenase,_mitochondrial_OS=Mesocricetus_auratus_GN=ALDH2_PE=1_SV=1	0	[illegible]	[illegible]
comp24202_c0_seq1.p1				
comp24203_c0_seq1.p2	sp|Q9ESP1|SDF2L_MOUSE_Stromal_cell-derived_factor_2-like_protein_1_OS=Mus_musculus_GN=Sdf2l1_PE=2_SV=2	4.00E-42	[illegible]	[illegible]
comp24203_c0_seq1.p5				
comp24204_c0_seq1.p1	sp|Q13888|TF2H2_HUMAN_General_transcription_factor_IIH_subunit_2_OS=Homo_sapiens_GN=GTF2H2_PE=1_SV=1	9.00E-99	[illegible]	[illegible]
comp24205_c0_seq1.p1				
comp24205_c0_seq1.p2	sp|Q7SY07|EIF1A_DANRE_Probable_RNA-binding_protein_EIF1AD_OS=Danio_rerio_GN=eif1ad_PE=2_SV=1	1.00E-18	[illegible]	[illegible]
comp24208_c0_seq1.p1	sp|Q7TYX8|FAC15_MYCBO_Long-chain-fatty-acid--CoA_ligase_FadD15_OS=Mycobacterium_bovis_GN=fadD15_PE=3_SV=2	1.00E-63	[illegible]	[illegible]
comp24209_c0_seq1.p1	sp|P49191|ELO3_CAEEL_Putative_fatty_acid_elongation_protein_3_OS=Caenorhabditis_elegans_GN=elo-3_PE=1_SV=2	1.00E-43	[illegible]	[illegible]
comp24210_c0_seq2.p1	sp|Q3AFD0|TPIS_CARHZ_Triosephosphate_isomerase_OS=Carboxydothermus_hydrogenoformans_(strain_Z-2901_/_DSM_6008)_GN=tpiA_PE=3_SV=1	3.00E-80	[illegible]	[illegible]
comp24210_c0_seq2.p4				
comp24211_c0_seq1.p1				
comp24213_c1_seq1.p1	sp|Q78PG9|CCD25_MOUSE_Coiled-coil_domain-containing_protein_25_OS=Mus_musculus_GN=Ccdc25_PE=1_SV=1	7.00E-63	[illegible]	[illegible]
comp24213_c1_seq2.p1	sp|Q78PG9|CCD25_MOUSE_Coiled-coil_domain-containing_protein_25_OS=Mus_musculus_GN=Ccdc25_PE=1_SV=1	1.00E-62	[illegible]	[illegible]
comp24216_c0_seq1.p1	sp|P02730|B3AT_HUMAN_Band_3_anion_transport_protein_OS=Homo_sapiens_GN=SLC4A1_PE=1_SV=3	3.00E-63	[illegible]	[illegible]
comp24216_c0_seq2.p1	sp|Q80ZA5|S4A10_RAT_Sodium-driven_chloride_bicarbonate_exchanger_OS=Rattus_norvegicus_GN=Slc4a10_PE=2_SV=1	3.00E-42	[illegible]	[illegible]
comp24216_c0_seq2.p2	sp|Q80ZA5|S4A10_RAT_Sodium-driven_chloride_bicarbonate_exchanger_OS=Rattus_norvegicus_GN=Slc4a10_PE=2_SV=1	7.00E-34	[illegible]	[illegible]
comp24218_c0_seq1.p1	sp|B4KD90|NMDA1_DROMO_Glutamate_[NMDA]_receptor_subunit_1_OS=Drosophila_mojavensis_GN=Nmdar1_PE=3_SV=1	3.00E-23	[illegible]	[illegible]
comp24219_c0_seq1.p1	sp|C3Z724|UBE2S_BRAFL_Ubiquitin-conjugating_enzyme_E2_S_OS=Branchiostoma_floridae_GN=BRAFLDRAFT_259979_PE=3_SV=1	1.00E-53	[illegible]	[illegible]
comp24220_c0_seq3.p1	sp|A4FPM8|EFG_SACEN_Elongation_factor_G_OS=Saccharopolyspora_erythraea_(strain_NRRL_23338)_GN=fusA_PE=3_SV=1	2.00E-111	[illegible]	[illegible]
comp24221_c0_seq1.p1	sp|Q5RAP1|TCPQ_PONAB_T-complex_protein_1_subunit_theta_OS=Pongo_abelii_GN=CCT8_PE=2_SV=3	0	[illegible]	[illegible]
comp24223_c0_seq1.p1	sp|O88738|BIRC6_MOUSE_Baculoviral_IAP_repeat-containing_protein_6_OS=Mus_musculus_GN=Birc6_PE=1_SV=2	9.00E-65	[illegible]	[illegible]
comp24224_c0_seq3.p2				
comp24225_c0_seq2.p1	sp|Q01976|ADPP_YEAST_ADP-ribose_pyrophosphatase_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YSA1_PE=1_SV=2	2.00E-43	[illegible]	[illegible]
comp24226_c0_seq1.p1				
comp24227_c0_seq1.p1				
comp24228_c0_seq1.p1				
comp24228_c0_seq2.p1	sp|Q8GWE0|PP314_ARATH_Pentatricopeptide_repeat-containing_protein_At4g16390,_chloroplastic_OS=Arabidopsis_thaliana_GN=P67_PE=1_SV=3	5.00E-13	[illegible]	[illegible]
comp24230_c0_seq1.p1				

comp24231_c0_seq1.p1	sp|P12617|DCMC_ANSAN_Malonyl-CoA_decarboxylase,_mitochondrial_OS=Anser_anser_anser_GN=MLYCD_PE=1_SV=2	6.00E-40	[illegible]	[illegible]
comp24231_c0_seq2.p1				
comp24232_c0_seq1.p1	sp|Q2S1W0|DCUP_SALRD_Uroporphyrinogen_decarboxylase_OS=Salinibacter_ruber_(strain_DSM_13855_/_M31)_GN=hemE_PE=3_SV=1	1.00E-94	[illegible]	[illegible]
comp24233_c0_seq1.p1	sp|Q0P5C0|LMF1_BOVIN_Lipase_maturation_factor_1_OS=Bos_taurus_GN=LMF1_PE=2_SV=1	7.00E-42	[illegible]	[illegible]
comp24233_c0_seq2.p1	sp|Q0P5C0|LMF1_BOVIN_Lipase_maturation_factor_1_OS=Bos_taurus_GN=LMF1_PE=2_SV=1	3.00E-135	[illegible]	[illegible]
comp24234_c0_seq1.p1				
comp24234_c0_seq4.p1				
comp24237_c0_seq2.p1	sp|O15865|CDPK2_PLAFK_Calcium-dependent_protein_kinase_2_OS=Plasmodium_falciparum_(isolate_K1_/_Thailand)_GN=CPK2_PE=1_SV=3	2.00E-82	[illegible]	[illegible]
comp24238_c0_seq1.p1	sp|P46276|F16P2_SOLTU_Fructose-1,6-bisphosphatase,_cytosolic_OS=Solanum_tuberosum_PE=2_SV=1	3.00E-105	[illegible]	[illegible]
comp24239_c0_seq1.p1				
comp24242_c0_seq2.p1				
comp24243_c0_seq1.p1	sp|Q9KCU7|DPO41_BACHD_DNA_polymerase_IV_1_OS=Bacillus_halodurans_(strain_ATCC_BAA-125_/_DSM_18197_/_FERM_7344_/_JCM_9153_/_C-125)_GN=dinB1_PE=3_SV=1	8.00E-12	[illegible]	[illegible]
comp24243_c0_seq2.p1				
comp24243_c0_seq2.p2	sp|Q9JJN0|POLH_MOUSE_DNA_polymerase_eta_OS=Mus_musculus_GN=Polh_PE=1_SV=1	1.00E-12	[illegible]	[illegible]
comp24248_c0_seq1.p1				
comp24248_c1_seq1.p1				
comp24248_c2_seq1.p1				
comp24249_c0_seq1.p1				
comp24249_c0_seq2.p2				
comp24250_c0_seq1.p2				
comp24251_c0_seq1.p1				
comp24252_c0_seq1.p1	sp|Q9NZN4|EHD2_HUMAN_EH_domain-containing_protein_2_OS=Homo_sapiens_GN=EHD2_PE=1_SV=2	1.00E-26	[illegible]	[illegible]
comp24252_c0_seq3.p1	sp|Q9NZN4|EHD2_HUMAN_EH_domain-containing_protein_2_OS=Homo_sapiens_GN=EHD2_PE=1_SV=2	4.00E-27	[illegible]	[illegible]
comp24253_c0_seq1.p1				
comp24255_c0_seq1.p1	sp|Q53I77|XPO6A_XENLA_Exportin-6-A_OS=Xenopus_laevis_GN=xpo6-a_PE=1_SV=1	2.00E-29	[illegible]	[illegible]
comp24255_c0_seq1.p2	sp|P54985|PPIA_BLAGE_Peptidyl-prolyl_cis-trans_isomerase_OS=Blattella_germanica_GN=CYPA_PE=2_SV=1	2.00E-71	[illegible]	[illegible]
comp24256_c0_seq1.p1				
comp24257_c1_seq2.p1	sp|P21538|REB1_YEAST_DNA-binding_protein_REB1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=REB1_PE=1_SV=2	6.00E-14	[illegible]	[illegible]
comp24257_c1_seq3.p1	sp|Q66HG1|DMTF1_RAT_Cyclin-D-binding_Myb-like_transcription_factor_1_OS=Rattus_norvegicus_GN=Dmtf1_PE=2_SV=2	2.00E-16	[illegible]	[illegible]
comp24257_c1_seq4.p1	sp|P21538|REB1_YEAST_DNA-binding_protein_REB1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=REB1_PE=1_SV=2	6.00E-14	[illegible]	[illegible]
comp24260_c0_seq2.p1				
comp24260_c0_seq3.p1	sp|P26024|NODC_BRAJA_N-acetylglucosaminyltransferase_OS=Bradyrhizobium_japonicum_(strain_USDA_110)_GN=nodC_PE=3_SV=2	6.00E-12	[illegible]	[illegible]
comp24262_c0_seq1.p1	sp|A1CEK7|PAN2_ASPCL_PAB-dependent_poly(A)-specific_ribonuclease_subunit_pan2_OS=Aspergillus_clavatus_(strain_ATCC_1007_/_CBS_513.65_/_DSM_816_/_NCTC_3887_/_NRRL_1)_GN=pan2_PE=3_SV=1	2.00E-19	[illegible]	[illegible]
comp24262_c0_seq1.p3				
comp24263_c0_seq1.p1	sp|Q8VY21|TLP3_ARATH_Tubby-like_F-box_protein_3_OS=Arabidopsis_thaliana_GN=TULP3_PE=2_SV=1	4.00E-18	[illegible]	[illegible]
comp24263_c0_seq1.p5	sp|O49313|NDADB_ARATH_NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_13-B_OS=Arabidopsis_thaliana_GN=At2g33220_PE=2_SV=1	1.00E-16	[illegible]	[illegible]
comp24265_c0_seq1.p1	sp|Q5BLD8|MT21A_DANRE_Methyltransferase-like_protein_21A_OS=Danio_rerio_GN=mettl21a_PE=2_SV=1	3.00E-19	[illegible]	[illegible]
comp24265_c0_seq2.p1	sp|Q5BLD8|MT21A_DANRE_Methyltransferase-like_protein_21A_OS=Danio_rerio_GN=mettl21a_PE=2_SV=1	2.00E-16	[illegible]	[illegible]
comp24272_c0_seq1.p1	sp|Q2JII9|GLMU_SYNJB_Bifunctional_protein_GlmU_OS=Synechococcus_sp._(strain_JA-2-3B'a(2-13))_GN=glmU_PE=3_SV=1	4.00E-22	[illegible]	[illegible]
comp24272_c0_seq1.p2				
comp24274_c0_seq1.p1	sp|Q5U680|SAMC_MOUSE_S-adenosylmethionine_mitochondrial_carrier_protein_OS=Mus_musculus_GN=Slc25a26_PE=2_SV=2	1.00E-25	[illegible]	[illegible]
comp24276_c0_seq1.p1				
comp24279_c0_seq1.p1	sp|Q17QG2|NUDC_BOVIN_Nuclear_migration_protein_nudC_OS=Bos_taurus_GN=NUDC_PE=2_SV=1	3.00E-78	[illegible]	[illegible]
comp24280_c0_seq1.p1	sp|Q05981|DNAK_BRUO2_Chaperone_protein_DnaK_OS=Brucella_ovis_(strain_ATCC_25840_/_63/290_/_NCTC_10512)_GN=dnaK_PE=2_SV=2	0	[illegible]	[illegible]
comp24282_c0_seq1.p1	sp|P51427|RS52_ARATH_40S_ribosomal_protein_S5-2_OS=Arabidopsis_thaliana_GN=RPS5B_PE=1_SV=2	4.00E-105	[illegible]	[illegible]
comp24283_c0_seq1.p1	sp|P44747|TYRPB_HAEIN_Tyrosine-specific_transport_protein_2_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=tyrP-B_PE=3_SV=1	7.00E-18	[illegible]	[illegible]
comp24283_c0_seq1.p2	sp|P17057|CRTK_RHOCB_Protein_CrtK_OS=Rhodobacter_capsulatus_(strain_ATCC_BAA-309_/_NBRC_16581_/_SB1003)_GN=crtK_PE=3_SV=1	9.00E-14	[illegible]	[illegible]
comp24284_c0_seq1.p1	sp|Q18515|C1GLT_CAEEL_Glycoprotein-N-acetylgalactosamine_3-beta-galactosyltransferase_1_OS=Caenorhabditis_elegans_GN=C38H2.2_PE=2_SV=2	9.00E-45	[illegible]	[illegible]
comp24286_c0_seq1.p1				
comp24286_c0_seq3.p1				
comp24287_c0_seq3.p1	sp|Q55CD9|NDH_DICDI_Probable_NADH_dehydrogenase_OS=Dictyostelium_discoideum_GN=DDB_G0270104_PE=3_SV=2	2.00E-99	[illegible]	[illegible]
comp24288_c0_seq1.p1				
comp24289_c0_seq2.p1				
comp24290_c0_seq2.p1				
comp24291_c0_seq1.p1				
comp24292_c0_seq1.p1				
comp24293_c0_seq2.p1	sp|Q8W4M7|ERCC2_ARATH_DNA_repair_helicase_UVH6_OS=Arabidopsis_thaliana_GN=UVH6_PE=1_SV=1	0	[illegible]	[illegible]
comp24295_c0_seq2.p1	sp|Q8L6Z7|EXO1_ARATH_Exonuclease_1_OS=Arabidopsis_thaliana_GN=EXO1_PE=2_SV=2	6.00E-89	[illegible]	[illegible]
comp24296_c0_seq1.p1	sp|Q499U8|TMCO4_RAT_Transmembrane_and_coiled-coil_domain-containing_protein_4_OS=Rattus_norvegicus_GN=Tmco4_PE=2_SV=1	2.00E-33	[illegible]	[illegible]
comp24297_c0_seq1.p1				
comp24297_c0_seq2.p1				
comp24298_c0_seq1.p1				
comp24298_c0_seq1.p2	sp|Q86HW6|Y6461_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0276461_OS=Dictyostelium_discoideum_GN=DDB_G0276461_PE=3_SV=1	6.00E-41	[illegible]	[illegible]
comp24301_c0_seq1.p1				
comp24303_c0_seq2.p2				
comp24303_c0_seq3.p1				
comp24303_c0_seq4.p1				
comp24304_c0_seq1.p1	sp|A9HRD8|ACP_GLUDA_Acyl_carrier_protein_OS=Gluconacetobacter_diazotrophicus_(strain_ATCC_49037_/_DSM_5601_/_PAl5)_GN=acpP_PE=3_SV=1	3.00E-19	[illegible]	[illegible]
comp24305_c0_seq2.p1				
comp24306_c0_seq1.p1	sp|Q07878|VPS13_YEAST_Vacuolar_protein_sorting-associated_protein_13_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=VPS13_PE=1_SV=2	4.00E-46	[illegible]	[illegible]
comp24307_c0_seq1.p1				
comp24311_c0_seq1.p1	sp|Q5UQF1|YL483_MIMIV_Putative_ankyrin_repeat_protein_L483_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L483_PE=4_SV=1	6.00E-23		
comp24312_c0_seq1.p1	sp|Q8R3N1|NOP14_MOUSE_Nucleolar_protein_14_OS=Mus_musculus_GN=Nop14_PE=1_SV=2	4.00E-52	[illegible]	[illegible]
comp24313_c0_seq1.p1				
comp24315_c0_seq1.p3	sp|Q8LF36|2A5T_ARATH_Serine/threonine_protein_phosphatase_2A_57_kDa_regulatory_subunit_B'_theta_isoform_OS=Arabidopsis_thaliana_GN=B'THETA_PE=2_SV=2	4.00E-11	[illegible]	[illegible]
comp24315_c0_seq2.p1	sp|O04376|2A5B_ARATH_Serine/threonine_protein_phosphatase_2A_57_kDa_regulatory_subunit_B'_beta_isoform_OS=Arabidopsis_thaliana_GN=B'BETA_PE=1_SV=1	2.00E-64	[illegible]	[illegible]
comp24315_c0_seq3.p3	sp|O04376|2A5B_ARATH_Serine/threonine_protein_phosphatase_2A_57_kDa_regulatory_subunit_B'_beta_isoform_OS=Arabidopsis_thaliana_GN=B'BETA_PE=1_SV=1	1.00E-75	[illegible]	[illegible]
comp24316_c0_seq1.p1				
comp24318_c0_seq1.p1	sp|Q01369|GBLP_NEUCR_Guanine_nucleotide-binding_protein_subunit_beta-like_protein_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=cpc-2_PE=3_SV=1	4.00E-68		
comp24319_c0_seq1.p1				
comp24319_c0_seq3.p1				
comp24319_c0_seq4.p1				
comp24320_c0_seq1.p1	sp|O14248|TEA3_SCHPO_Tip_elongation_aberrant_protein_3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=tea3_PE=1_SV=1	5.00E-11	[illegible]	[illegible]
comp24320_c0_seq1.p3				
comp24320_c0_seq2.p1	sp|Q8N653|LZTR1_HUMAN_Leucine-zipper-like_transcriptional_regulator_1_OS=Homo_sapiens_GN=LZTR1_PE=2_SV=2	2.00E-33	[illegible]	[illegible]
comp24321_c0_seq2.p2	sp|Q5QQ52|XYLT_CAEBR_Xylosyltransferase_sqv-6_OS=Caenorhabditis_briggsae_GN=sqv-6_PE=2_SV=1	2.00E-12	[illegible]	[illegible]
comp24322_c0_seq1.p1	sp|Q7SXT7|F164A_DANRE_Protein_FAM164A_OS=Danio_rerio_GN=fam164a_PE=2_SV=1	9.00E-17	[illegible]	[illegible]
comp24325_c0_seq2.p1				
comp24327_c0_seq1.p1				
comp24331_c0_seq4.p1				
comp24333_c0_seq2.p2				
comp24334_c0_seq2.p1				
comp24335_c0_seq1.p1	sp|Q9GKX6|GALM_PIG_Aldose_1-epimerase_OS=Sus_scrofa_GN=GALM_PE=2_SV=1	2.00E-64	[illegible]	[illegible]
comp24338_c0_seq1.p1	sp|Q14137|BOP1_HUMAN_Ribosome_biogenesis_protein_BOP1_OS=Homo_sapiens_GN=BOP1_PE=1_SV=2	1.00E-104	[illegible]	[illegible]
comp24338_c1_seq1.p1	sp|A4IHS2|BOP1_XENTR_Ribosome_biogenesis_protein_bop1_OS=Xenopus_tropicalis_GN=bop1_PE=2_SV=1	0	[illegible]	[illegible]
comp24339_c0_seq1.p1	sp|Q4UMT7|FTSZ_RICFE_Cell_division_protein_FtsZ_OS=Rickettsia_felis_(strain_ATCC_VR-1525_/_URRWXCal2)_GN=ftsZ_PE=3_SV=1	1.00E-90	[illegible]	[illegible]
comp24341_c0_seq1.p1				
comp24341_c0_seq1.p2				
comp24343_c0_seq1.p1	sp|Q9N0V7|CBS_RABIT_Cystathionine_beta-synthase_OS=Oryctolagus_cuniculus_GN=CBS_PE=2_SV=3	6.00E-175	[illegible]	[illegible]
comp24344_c0_seq1.p1				
comp24347_c0_seq2.p1	sp|Q9TTU2|KAD6_RABIT_Adenylate_kinase_isoenzyme_6_OS=Oryctolagus_cuniculus_GN=TAF9_PE=2_SV=1	5.00E-55	[illegible]	[illegible]
comp24348_c0_seq1.p1	sp|Q9FNS4|MBB1_CHLRE_PsbB_mRNA_maturation_factor_Mbb1,_chloroplastic_OS=Chlamydomonas_reinhardtii_GN=MBB1_PE=2_SV=1	7.00E-57	[illegible]	[illegible]
comp24348_c0_seq2.p1	sp|Q9FNS4|MBB1_CHLRE_PsbB_mRNA_maturation_factor_Mbb1,_chloroplastic_OS=Chlamydomonas_reinhardtii_GN=MBB1_PE=2_SV=1	7.00E-57	[illegible]	[illegible]
comp24351_c0_seq1.p1	sp|Q8AXS6|S35B1_XENTR_Solute_carrier_family_35_member_B1_OS=Xenopus_tropicalis_GN=slc35b1_PE=2_SV=2	6.00E-62	[illegible]	[illegible]
comp24352_c0_seq1.p1				
comp24353_c0_seq1.p1	sp|Q14690|RRP5_HUMAN_Protein_RRP5_homolog_OS=Homo_sapiens_GN=PDCD11_PE=1_SV=3	3.00E-64	[illegible]	[illegible]
comp24354_c0_seq1.p1				
comp24355_c0_seq1.p1	sp|Q9JJF3|NO66_MOUSE_Lysine-specific_demethylase_NO66_OS=Mus_musculus_GN=No66_PE=1_SV=2	2.00E-99	[illegible]	[illegible]
comp24357_c0_seq3.p1				
comp24357_c0_seq3.p2				
comp24357_c0_seq4.p1				
comp24357_c0_seq4.p2				
comp24358_c0_seq2.p1	sp|P16865|H2A3_VOLCA_Histone_H2A-III_OS=Volvox_carteri_PE=3_SV=1	3.00E-43	[illegible]	[illegible]
comp24360_c0_seq1.p1				
comp24360_c0_seq2.p1				
comp24363_c0_seq1.p1	sp|Q9STX5|ENPL_ARATH_Endoplasmin_homolog_OS=Arabidopsis_thaliana_GN=SHD_PE=1_SV=1	2.00E-98	[illegible]	[illegible]
comp24364_c0_seq1.p1	sp|B2VEC7|UNG_ERWT9_Uracil-DNA_glycosylase_OS=Erwinia_tasmaniensis_(strain_DSM_17950_/_Et1/99)_GN=ung_PE=3_SV=1	4.00E-70	[illegible]	[illegible]
comp24365_c0_seq1.p1				
comp24365_c0_seq1.p2				
comp24366_c0_seq1.p1	sp|Q84KI6|SQD1_SPIOL_UDP-sulfoquinovose_synthase,_chloroplastic_OS=Spinacia_oleracea_GN=SQD1_PE=1_SV=1	1.00E-101	[illegible]	[illegible]
comp24367_c0_seq2.p3				
comp24367_c0_seq2.p5				
comp24367_c0_seq3.p1	sp|A8N5J5|EFG1P_COPC7_rRNA-processing_protein_EFG1_OS=Coprinopsis_cinerea_(strain_Okayama-7_/_130_/_ATCC_MYA-4618_/_FGSC_9003)_GN=EFG1_PE=3_SV=1	1.00E-14	[illegible]	[illegible]
comp24369_c0_seq1.p1	sp|Q10LJ2|MTP2_ORYSJ_Metal_tolerance_protein_2_OS=Oryza_sativa_subsp._japonica_GN=MTP2_PE=2_SV=1	9.00E-39	[illegible]	[illegible]
comp24370_c0_seq1.p2				
comp24371_c0_seq1.p1	sp|Q9P6P9|PDK_SCHPO_[Pyruvate_dehydrogenase_[lipoamide]]_kinase,_mitochondrial_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC644.11c_PE=2_SV=1	7.00E-65	[illegible]	[illegible]
comp24371_c0_seq2.p1	sp|Q2KJG8|BCKD_BOVIN_[3-methyl-2-oxobutanoate_dehydrogenase_[lipoamide]]_kinase,_mitochondrial_OS=Bos_taurus_GN=BCKDK_PE=2_SV=1	1.00E-45	[illegible]	[illegible]
comp24374_c1_seq2.p1				
comp24375_c0_seq1.p1				
comp24376_c0_seq1.p1				
comp24378_c0_seq1.p1	sp|P25776|ORYA_ORYSJ_Oryzain_alpha_chain_OS=Oryza_sativa_subsp._japonica_GN=Os04g0650000_PE=1_SV=2	2.00E-79	[illegible]	[illegible]
comp24381_c0_seq2.p1				
comp24383_c0_seq1.p1				
comp24384_c0_seq2.p1				
comp24384_c0_seq3.p1				
comp24388_c0_seq3.p1	sp|P51094|UFOG_VITVI_Anthocyanidin_3-O-glucosyltransferase_2_OS=Vitis_vinifera_GN=UFGT_PE=1_SV=2	7.00E-14	[illegible]	[illegible]
comp24389_c0_seq1.p1				
comp24389_c0_seq2.p1				
comp24389_c0_seq4.p1				
comp24390_c0_seq1.p1	sp|Q07078|HSP83_ORYSJ_Heat_shock_protein_81-3_OS=Oryza_sativa_subsp._japonica_GN=HSP81-3_PE=2_SV=2	6.00E-166	[illegible]	[illegible]
comp24393_c0_seq1.p1				
comp24394_c0_seq3.p1	sp|Q9ES00|UBE4B_MOUSE_Ubiquitin_conjugation_factor_E4_B_OS=Mus_musculus_GN=Ube4b_PE=1_SV=3	1.00E-64	[illegible]	[illegible]
comp24396_c0_seq2.p1				
comp24397_c0_seq1.p1				
comp24398_c0_seq1.p1				
comp24399_c0_seq1.p1				
comp24399_c0_seq3.p1	sp|Q6PDY2|AEDO_MOUSE_2-aminoethanethiol_dioxygenase_OS=Mus_musculus_GN=Ado_PE=1_SV=2	8.00E-27	[illegible]	[illegible]
comp24399_c0_seq4.p1				
comp2440_c0_seq1.p1	sp|A0E358|CATL2_PARTE_Cathepsin_L_2_OS=Paramecium_tetraurelia_GN=GSPATT00022898001_PE=3_SV=2	9.00E-23	[illegible]	[illegible]
comp24400_c0_seq2.p1	sp|O76734|TUP1_DICDI_General_transcriptional_corepressor_tupA_OS=Dictyostelium_discoideum_GN=tupA_PE=2_SV=1	2.00E-70	[illegible]	[illegible]
comp24403_c0_seq1.p1	sp|Q88KY8|STHA_PSEPK_Soluble_pyridine_nucleotide_transhydrogenase_OS=Pseudomonas_putida_(strain_KT2440)_GN=sthA_PE=3_SV=3	7.00E-43	[illegible]	[illegible]
comp24404_c0_seq1.p1	sp|Q6P9R1|DDX51_MOUSE_ATP-dependent_RNA_helicase_DDX51_OS=Mus_musculus_GN=Ddx51_PE=2_SV=1	2.00E-38	[illegible]	[illegible]
comp24404_c1_seq1.p1				
comp24406_c0_seq2.p1				
comp24408_c0_seq1.p1				
comp24408_c0_seq1.p2				
comp24408_c0_seq2.p2	sp|Q4R6Y5|ZNRF4_MACFA_Zinc/RING_finger_protein_4_OS=Macaca_fascicularis_GN=ZNRF4_PE=2_SV=1	2.00E-12	[illegible]	[illegible]
comp24408_c0_seq2.p3				
comp24411_c0_seq1.p1	sp|Q8I5R7|SYP_PLAF7_Proline--tRNA_ligase_OS=Plasmodium_falciparum_(isolate_3D7)_GN=proRS_PE=1_SV=1	0	[illegible]	[illegible]
comp24412_c0_seq1.p1				
comp24412_c0_seq2.p1				
comp24413_c1_seq1.p1	sp|Q0IIF2|EI2BA_BOVIN_Translation_initiation_factor_eIF-2B_subunit_alpha_OS=Bos_taurus_GN=EIF2B1_PE=2_SV=1	3.00E-78	[illegible]	[illegible]
comp24414_c0_seq1.p1				
comp24416_c0_seq3.p2				
comp24418_c0_seq3.p1	sp|O05389|YRBE_BACSU_Uncharacterized_oxidoreductase_yrbE_OS=Bacillus_subtilis_GN=yrbE_PE=3_SV=2	1.00E-82	[illegible]	[illegible]
comp24421_c0_seq2.p1	sp|Q9CZB9|TM128_MOUSE_Transmembrane_protein_128_OS=Mus_musculus_GN=Tmem128_PE=2_SV=2	5.00E-14	[illegible]	[illegible]
comp24421_c0_seq3.p1				
comp24422_c0_seq2.p1				
comp24422_c0_seq2.p2	sp|Q9SL05|PGR5_ARATH_Protein_PROTON_GRADIENT_REGULATION_5,_chloroplastic_OS=Arabidopsis_thaliana_GN=PGR5_PE=1_SV=1	3.00E-17	[illegible]	[illegible]
comp24423_c0_seq1.p1				
comp24423_c0_seq2.p1				
comp24425_c0_seq1.p1				
comp24429_c0_seq2.p1	sp|Q09571|YRD1_CAEEL_Uncharacterized_protein_K02A2.1_OS=Caenorhabditis_elegans_GN=K02A2.1_PE=2_SV=2	3.00E-17	[illegible]	[illegible]
comp24429_c0_seq2.p2	sp|Q54FR4|PX24D_DICDI_PXMP2/4_family_protein_4_OS=Dictyostelium_discoideum_GN=DDB_G0290631_PE=3_SV=1	7.00E-24	[illegible]	[illegible]
comp24429_c0_seq3.p1	sp|Q54FR4|PX24D_DICDI_PXMP2/4_family_protein_4_OS=Dictyostelium_discoideum_GN=DDB_G0290631_PE=3_SV=1	7.00E-24	[illegible]	[illegible]
comp24429_c0_seq3.p2				
comp24430_c0_seq1.p1				
comp24431_c0_seq2.p1	sp|Q8MZC4|CRLS1_DROME_Probable_cardiolipin_synthase_OS=Drosophila_melanogaster_GN=CLS_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp24431_c0_seq4.p1	sp|Q8MZC4|CRLS1_DROME_Probable_cardiolipin_synthase_OS=Drosophila_melanogaster_GN=CLS_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp24432_c0_seq3.p1				
comp24435_c0_seq1.p2	sp|Q9BLG3|AMT2_DICDI_Ammonium_transporter_2_OS=Dictyostelium_discoideum_GN=amtB_PE=1_SV=1	2.00E-14	[illegible]	[illegible]
comp24436_c0_seq1.p1				
comp24436_c1_seq1.p1				
comp24436_c1_seq2.p1	sp|Q9BZ29|DOCK9_HUMAN_Dedicator_of_cytokinesis_protein_9_OS=Homo_sapiens_GN=DOCK9_PE=1_SV=2	3.00E-23	[illegible]	[illegible]
comp24437_c0_seq1.p1				
comp24437_c0_seq1.p2				
comp24437_c0_seq2.p1				
comp24439_c0_seq1.p1	sp|B1XQF6|DNAJ_SYNP2_Chaperone_protein_DnaJ_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=dnaJ_PE=3_SV=1	1.00E-117	[illegible]	[illegible]
comp24440_c0_seq1.p1				
comp24440_c0_seq2.p1				
comp24442_c1_seq2.p1	sp|P23903|E13B_BACCI_Glucan_endo-1,3-beta-glucosidase_A1_OS=Bacillus_circulans_GN=glcA_PE=1_SV=1	2.00E-48	[illegible]	[illegible]
comp24443_c1_seq1.p1				
comp24446_c0_seq1.p1				
comp24446_c0_seq2.p1				
comp24447_c0_seq1.p1				
comp24448_c0_seq2.p1	sp|Q9WZ31|CORA_THEMA_Magnesium_transport_protein_CorA_OS=Thermotoga_maritima_GN=corA_PE=1_SV=1	3.00E-26	[illegible]	[illegible]
comp24450_c0_seq1.p1				
comp24451_c0_seq1.p1	sp|P23919|KTHY_HUMAN_Thymidylate_kinase_OS=Homo_sapiens_GN=DTYMK_PE=1_SV=4	3.00E-64	[illegible]	[illegible]
comp24452_c0_seq1.p1	sp|Q98DM9|RSMI_RHILO_Ribosomal_RNA_small_subunit_methyltransferase_I_OS=Rhizobium_loti_(strain_MAFF303099)_GN=rsmI_PE=3_SV=1	3.00E-39	[illegible]	[illegible]
comp24453_c0_seq1.p1	sp|Q9HBU6|EKI1_HUMAN_Ethanolamine_kinase_1_OS=Homo_sapiens_GN=ETNK1_PE=1_SV=1	9.00E-45	[illegible]	[illegible]
comp24454_c0_seq1.p1	sp|Q5ZKK3|APC5_CHICK_Anaphase-promoting_complex_subunit_5_OS=Gallus_gallus_GN=ANAPC5_PE=2_SV=1	1.00E-13	[illegible]	[illegible]
comp24456_c0_seq3.p1	sp|Q1MTP1|THP3_SCHPO_THP3_homolog_C2A9.11c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC2A9.11c_PE=3_SV=1	6.00E-48	[illegible]	[illegible]
comp24456_c0_seq4.p1	sp|Q1MTP1|THP3_SCHPO_THP3_homolog_C2A9.11c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC2A9.11c_PE=3_SV=1	5.00E-56	[illegible]	[illegible]
comp24457_c0_seq1.p1				
comp24458_c0_seq1.p1	sp|P97612|FAAH1_RAT_Fatty-acid_amide_hydrolase_1_OS=Rattus_norvegicus_GN=Faah_PE=1_SV=1	3.00E-77	[illegible]	[illegible]
comp24459_c0_seq1.p1				
comp24460_c0_seq2.p1				
comp24460_c0_seq3.p1	sp|Q9Y7X4|YGRG_SCHPO_Uncharacterized_membrane_protein_C365.16_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC365.16_PE=2_SV=1	4.00E-18	[illegible]	[illegible]
comp24461_c0_seq1.p1				
comp24462_c0_seq2.p1				
comp24463_c0_seq1.p1				
comp24464_c0_seq2.p1				
comp24465_c0_seq1.p2				
comp24466_c0_seq1.p1	sp|Q9BXW7|CECR5_HUMAN_Cat_eye_syndrome_critical_region_protein_5_OS=Homo_sapiens_GN=CECR5_PE=1_SV=1	1.00E-34	GO:0005739	[illegible]
comp24466_c1_seq1.p1	sp|P42327|ADH2_GEOSE_Alcohol_dehydrogenase_OS=Geobacillus_stearothermophilus_GN=adh_PE=1_SV=1	4.00E-25	[illegible]	[illegible]
comp24468_c0_seq1.p1	sp|A8NEP3|TRP_COPC7_Tryptophan_synthase_OS=Coprinopsis_cinerea_(strain_Okayama-7_/_130_/_ATCC_MYA-4618_/_FGSC_9003)_GN=TRP-1_PE=3_SV=2	0	[illegible]	[illegible]
comp24469_c0_seq2.p1	sp|Q54J73|PAP_DICDI_Poly(A)_polymerase_OS=Dictyostelium_discoideum_GN=papA_PE=3_SV=1	4.00E-110	[illegible]	[illegible]
comp24470_c0_seq1.p1	sp|A7SDW5|EIF3L_NEMVE_Eukaryotic_translation_initiation_factor_3_subunit_L_OS=Nematostella_vectensis_GN=v1g169424_PE=3_SV=1	2.00E-86	[illegible]	[illegible]
comp24474_c0_seq1.p1	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	5.00E-15	[illegible]	[illegible]
comp24479_c0_seq1.p1	sp|Q652B0|HFB2C_ORYSJ_Heat_stress_transcription_factor_B-2c_OS=Oryza_sativa_subsp._japonica_GN=HSFB2C_PE=2_SV=1	6.00E-15	[illegible]	[illegible]
comp24480_c0_seq1.p1				
comp24481_c0_seq1.p1	sp|Q00614|CACP_CANTR_Carnitine_O-acetyltransferase,_mitochondrial_OS=Candida_tropicalis_GN=CAT2_PE=3_SV=1	9.00E-52	[illegible]	[illegible]
comp24481_c0_seq1.p2	sp|Q00614|CACP_CANTR_Carnitine_O-acetyltransferase,_mitochondrial_OS=Candida_tropicalis_GN=CAT2_PE=3_SV=1	9.00E-36	[illegible]	[illegible]
comp24481_c0_seq2.p1	sp|Q00614|CACP_CANTR_Carnitine_O-acetyltransferase,_mitochondrial_OS=Candida_tropicalis_GN=CAT2_PE=3_SV=1	3.00E-71	[illegible]	[illegible]
comp24481_c0_seq2.p3	sp|Q00614|CACP_CANTR_Carnitine_O-acetyltransferase,_mitochondrial_OS=Candida_tropicalis_GN=CAT2_PE=3_SV=1	5.00E-17	[illegible]	[illegible]
comp24481_c0_seq4.p1	sp|Q00614|CACP_CANTR_Carnitine_O-acetyltransferase,_mitochondrial_OS=Candida_tropicalis_GN=CAT2_PE=3_SV=1	2.00E-102	[illegible]	[illegible]
comp24481_c0_seq5.p1	sp|Q00614|CACP_CANTR_Carnitine_O-acetyltransferase,_mitochondrial_OS=Candida_tropicalis_GN=CAT2_PE=3_SV=1	9.00E-52	[illegible]	[illegible]
comp24481_c0_seq5.p3	sp|Q00614|CACP_CANTR_Carnitine_O-acetyltransferase,_mitochondrial_OS=Candida_tropicalis_GN=CAT2_PE=3_SV=1	5.00E-17	[illegible]	[illegible]
comp24482_c0_seq1.p1	sp|Q54BM3|MCFG_DICDI_Mitochondrial_substrate_carrier_family_protein_G_OS=Dictyostelium_discoideum_GN=mcfG_PE=2_SV=1	2.00E-65	[illegible]	[illegible]
comp24483_c0_seq1.p1				
comp24484_c0_seq1.p1				
comp24485_c0_seq1.p1	sp|Q9CQU1|MFAP1_MOUSE_Microfibrillar-associated_protein_1_OS=Mus_musculus_GN=Mfap1_PE=1_SV=1	1.00E-42	[illegible]	[illegible]
comp24486_c0_seq6.p1	sp|Q8RY89|PI5K8_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_8_OS=Arabidopsis_thaliana_GN=PIP5K8_PE=2_SV=1	1.00E-34	[illegible]	[illegible]
comp24488_c0_seq3.p1	sp|A7HWQ8|EFG_PARL1_Elongation_factor_G_OS=Parvibaculum_lavamentivorans_(strain_DS-1_/_DSM_13023_/_NCIMB_13966)_GN=fusA_PE=3_SV=1	0	[illegible]	[illegible]
comp24490_c0_seq1.p1	sp|Q8N1B4|VPS52_HUMAN_Vacuolar_protein_sorting-associated_protein_52_homolog_OS=Homo_sapiens_GN=VPS52_PE=1_SV=1	3.00E-129	[illegible]	[illegible]
comp24490_c0_seq2.p1	sp|Q8C754|VPS52_MOUSE_Vacuolar_protein_sorting-associated_protein_52_homolog_OS=Mus_musculus_GN=Vps52_PE=2_SV=1	9.00E-22	[illegible]	[illegible]
comp24491_c0_seq1.p1				
comp24495_c0_seq1.p1	sp|Q80WB5|NTAQ1_MOUSE_Protein_N-terminal_glutamine_amidohydrolase_OS=Mus_musculus_GN=Wdyhv1_PE=1_SV=1	7.00E-35	[illegible]	[illegible]
comp24496_c0_seq2.p3				
comp24497_c0_seq2.p1	sp|P98200|AT8A2_MOUSE_Probable_phospholipid-transporting_ATPase_IB_OS=Mus_musculus_GN=Atp8a2_PE=1_SV=1	4.00E-141	[illegible]	[illegible]
comp24498_c0_seq1.p1				
comp24498_c0_seq2.p1				
comp24498_c0_seq2.p2				
comp24499_c0_seq1.p1	sp|Q00218|AROG_ARATH_Phospho-2-dehydro-3-deoxyheptonate_aldolase_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=DHS2_PE=2_SV=2	2.00E-175	[illegible]	[illegible]
comp24499_c1_seq1.p1	sp|Q54BM8|U652_DICDI_UPF0652_protein_OS=Dictyostelium_discoideum_GN=DDB_G0293552_PE=3_SV=1	4.00E-101	[illegible]	[illegible]
comp24500_c0_seq1.p1				
comp24502_c0_seq2.p1				
comp24503_c0_seq2.p1				
comp24503_c0_seq3.p1				
comp24504_c0_seq1.p1	sp|Q91YR5|MET13_MOUSE_Methyltransferase-like_protein_13_OS=Mus_musculus_GN=Mettl13_PE=1_SV=1	1.00E-28	[illegible]	[illegible]
comp24504_c0_seq2.p1	sp|Q91YR5|MET13_MOUSE_Methyltransferase-like_protein_13_OS=Mus_musculus_GN=Mettl13_PE=1_SV=1	2.00E-28	[illegible]	[illegible]
comp24504_c0_seq3.p1	sp|Q91YR5|MET13_MOUSE_Methyltransferase-like_protein_13_OS=Mus_musculus_GN=Mettl13_PE=1_SV=1	8.00E-29	[illegible]	[illegible]
comp24505_c1_seq1.p1				
comp24505_c1_seq2.p1	sp|Q8S4R4|CRTSO_SOLLC_Prolycopene_isomerase,_chloroplastic_OS=Solanum_lycopersicum_GN=CRTISO_PE=1_SV=1	9.00E-48	[illegible]	[illegible]
comp24505_c1_seq3.p1	sp|Q9M9Y8|CRTSO_ARATH_Prolycopene_isomerase,_chloroplastic_OS=Arabidopsis_thaliana_GN=CRTISO_PE=2_SV=2	6.00E-42	[illegible]	[illegible]
comp24506_c0_seq4.p1				
comp24507_c0_seq3.p1				
comp24507_c0_seq3.p2				
comp24508_c0_seq2.p1				
comp24508_c0_seq4.p1				
comp24509_c0_seq1.p1	sp|P56184|KPRS_HELPY_Ribose-phosphate_pyrophosphokinase_OS=Helicobacter_pylori_(strain_ATCC_700392_/_26695)_GN=prs_PE=3_SV=1	9.00E-93	[illegible]	[illegible]
comp24510_c0_seq2.p1				
comp24512_c0_seq1.p1				
comp24512_c1_seq2.p1				
comp24513_c0_seq2.p1	sp|Q4A1L3|BECN1_XENTR_Beclin-1_OS=Xenopus_tropicalis_GN=becn1_PE=2_SV=1	5.00E-30	[illegible]	[illegible]
comp24513_c0_seq3.p1	sp|Q6GP52|BECN1_XENLA_Beclin-1_OS=Xenopus_laevis_GN=becn1_PE=2_SV=1	2.00E-19	[illegible]	[illegible]
comp24515_c0_seq1.p1	sp|Q8I8U2|AP1G_DICDI_AP-1_complex_subunit_gamma_OS=Dictyostelium_discoideum_GN=ap1g1_PE=1_SV=1	6.00E-125	[illegible]	[illegible]
comp24515_c0_seq1.p4	sp|Q84K16|AP1G1_ARATH_AP-1_complex_subunit_gamma-1_OS=Arabidopsis_thaliana_GN=GAMMA-ADR_PE=1_SV=1	6.00E-22	[illegible]	[illegible]
comp24517_c0_seq2.p1				
comp24517_c0_seq2.p2				
comp24519_c0_seq1.p1				
comp24520_c0_seq1.p1				
comp24523_c0_seq1.p1	sp|Q1RMR5|TILB_BOVIN_Protein_TILB_homolog_OS=Bos_taurus_GN=LRRC6_PE=2_SV=1	1.00E-57	[illegible]	[illegible]
comp24524_c0_seq1.p1	sp|A6X554|LOVHK_OCHA4_Blue-light-activated_histidine_kinase_OS=Ochrobactrum_anthropi_(strain_ATCC_49188_/_DSM_6882_/_NCTC_12168)_GN=Oant_3652_PE=3_SV=1	8.00E-14	[illegible]	[illegible]
comp24525_c0_seq1.p1	sp|Q54W90|SEY1_DICDI_Protein_SEY1_homolog_OS=Dictyostelium_discoideum_GN=DDB_0206311_PE=3_SV=1	3.00E-22	[illegible]	[illegible]
comp24527_c0_seq1.p1	sp|P43351|RAD52_HUMAN_DNA_repair_protein_RAD52_homolog_OS=Homo_sapiens_GN=RAD52_PE=1_SV=1	5.00E-28	[illegible]	[illegible]
comp2453_c0_seq1.p1	sp|Q46821|YGFU_ECOLI_Putative_purine_permease_ygfU_OS=Escherichia_coli_(strain_K12)_GN=ygfU_PE=1_SV=2	2.00E-83	[illegible]	[illegible]
comp24530_c0_seq1.p1	sp|Q67YC9|Y4141_ARATH_Uncharacterized_protein_At4g14100_OS=Arabidopsis_thaliana_GN=At4g14100_PE=2_SV=1	4.00E-31	[illegible]	[illegible]
comp24530_c0_seq2.p1	sp|Q67YC9|Y4141_ARATH_Uncharacterized_protein_At4g14100_OS=Arabidopsis_thaliana_GN=At4g14100_PE=2_SV=1	5.00E-23	[illegible]	[illegible]
comp24530_c0_seq3.p1	sp|Q67YC9|Y4141_ARATH_Uncharacterized_protein_At4g14100_OS=Arabidopsis_thaliana_GN=At4g14100_PE=2_SV=1	3.00E-23	[illegible]	[illegible]
comp24532_c0_seq1.p1	sp|P46864|ATK2_ARATH_Kinesin-2_OS=Arabidopsis_thaliana_GN=ATK2_PE=2_SV=1	1.00E-69	[illegible]	[illegible]
comp24533_c0_seq1.p1				
comp24533_c0_seq2.p1	sp|Q07G10|ALKB8_XENTR_Alkylated_DNA_repair_protein_alkB_homolog_8_OS=Xenopus_tropicalis_GN=alkbh8_PE=2_SV=2	4.00E-40	[illegible]	[illegible]
comp24533_c0_seq3.p1	sp|Q07G10|ALKB8_XENTR_Alkylated_DNA_repair_protein_alkB_homolog_8_OS=Xenopus_tropicalis_GN=alkbh8_PE=2_SV=2	1.00E-45	[illegible]	[illegible]
comp24533_c0_seq5.p1				
comp24533_c0_seq5.p2	sp|Q07G10|ALKB8_XENTR_Alkylated_DNA_repair_protein_alkB_homolog_8_OS=Xenopus_tropicalis_GN=alkbh8_PE=2_SV=2	4.00E-36	[illegible]	[illegible]
comp24535_c0_seq1.p1	sp|Q90631|KTN1_CHICK_Kinectin_OS=Gallus_gallus_GN=KTN1_PE=1_SV=1	1.00E-11	[illegible]	[illegible]
comp24536_c0_seq1.p1	sp|P90727|U2AF2_CAEBR_Splicing_factor_U2AF_65_kDa_subunit_OS=Caenorhabditis_briggsae_GN=uaf-1_PE=3_SV=2	5.00E-21	[illegible]	[illegible]
comp24536_c0_seq2.p1	sp|P90978|U2AF2_CAEEL_Splicing_factor_U2AF_65_kDa_subunit_OS=Caenorhabditis_elegans_GN=uaf-1_PE=2_SV=2	1.00E-11	[illegible]	[illegible]
comp24536_c0_seq2.p2				
comp24538_c0_seq1.p1				
comp24538_c0_seq2.p1				
comp24539_c0_seq1.p1				
comp24539_c0_seq2.p1				
comp24541_c0_seq1.p1	sp|Q8L4M1|DWA1_ARATH_WD_repeat-containing_protein_DWA1_OS=Arabidopsis_thaliana_GN=DWA1_PE=1_SV=1	2.00E-18	[illegible]	[illegible]
comp24541_c0_seq2.p1	sp|Q8L4M1|DWA1_ARATH_WD_repeat-containing_protein_DWA1_OS=Arabidopsis_thaliana_GN=DWA1_PE=1_SV=1	1.00E-14	[illegible]	[illegible]
comp24544_c0_seq1.p1				
comp24546_c0_seq1.p1				
comp24549_c0_seq1.p1				
comp24549_c0_seq2.p1				
comp24549_c0_seq3.p1				
comp24550_c0_seq1.p1				
comp24553_c0_seq2.p1				
comp24553_c0_seq3.p1				
comp24554_c0_seq2.p1				
comp24554_c0_seq3.p1				
comp24555_c0_seq1.p1				
comp24555_c0_seq2.p1				
comp24556_c0_seq2.p1				
comp24557_c0_seq1.p1	sp|Q54BF6|MCFN_DICDI_Mitochondrial_substrate_carrier_family_protein_N_OS=Dictyostelium_discoideum_GN=mcfN_PE=1_SV=2	9.00E-17	[illegible]	[illegible]
comp24557_c0_seq2.p1	sp|Q54BF6|MCFN_DICDI_Mitochondrial_substrate_carrier_family_protein_N_OS=Dictyostelium_discoideum_GN=mcfN_PE=1_SV=2	3.00E-61	[illegible]	[illegible]
comp24559_c0_seq1.p1				
comp24559_c0_seq3.p1	sp|A0JMK5|MTMR2_DANRE_Myotubularin-related_protein_2_OS=Danio_rerio_GN=mtmr2_PE=2_SV=2	3.00E-106	[illegible]	[illegible]
comp24560_c0_seq1.p1	sp|O94684|TFB3_SCHPO_RNA_polymerase_II_transcription_factor_B_subunit_3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=pmh1_PE=1_SV=1	1.00E-19	[illegible]	[illegible]
comp24561_c0_seq1.p1				
comp24562_c0_seq1.p1	sp|Q8BGA9|OXA1L_MOUSE_Mitochondrial_inner_membrane_protein_OXA1L_OS=Mus_musculus_GN=Oxa1l_PE=2_SV=1	3.00E-30	[illegible]	[illegible]
comp24563_c0_seq1.p1	sp|Q7ZXZ2|UTP15_XENLA_U3_small_nucleolar_RNA-associated_protein_15_homolog_OS=Xenopus_laevis_GN=utp15_PE=2_SV=1	8.00E-91	[illegible]	[illegible]
comp24563_c0_seq2.p1	sp|Q7ZXZ2|UTP15_XENLA_U3_small_nucleolar_RNA-associated_protein_15_homolog_OS=Xenopus_laevis_GN=utp15_PE=2_SV=1	4.00E-34	[illegible]	[illegible]
comp24564_c0_seq1.p1	sp|P0AF52|YJCD_ECOLI_Putative_permease_yjcD_OS=Escherichia_coli_(strain_K12)_GN=yjcD_PE=1_SV=1	1.00E-93	[illegible]	[illegible]
comp24565_c0_seq1.p1				
comp24565_c0_seq4.p1				
comp24567_c0_seq1.p1				
comp24571_c0_seq1.p1	sp|Q0E0Y3|PUS7_ORYSJ_RNA_pseudouridine_synthase_7_OS=Oryza_sativa_subsp._japonica_GN=Os02g0512300_PE=2_SV=2	7.00E-48	[illegible]	[illegible]
comp24571_c0_seq1.p2	sp|Q8W206|CSN6A_ARATH_COP9_signalosome_complex_subunit_6a_OS=Arabidopsis_thaliana_GN=CSN6A_PE=1_SV=2	4.00E-57	[illegible]	[illegible]
comp24571_c0_seq2.p1	sp|Q0E0Y3|PUS7_ORYSJ_RNA_pseudouridine_synthase_7_OS=Oryza_sativa_subsp._japonica_GN=Os02g0512300_PE=2_SV=2	6.00E-48	[illegible]	[illegible]
comp24571_c0_seq2.p2	sp|Q8W206|CSN6A_ARATH_COP9_signalosome_complex_subunit_6a_OS=Arabidopsis_thaliana_GN=CSN6A_PE=1_SV=2	4.00E-57	[illegible]	[illegible]
comp24572_c0_seq1.p1	sp|Q84ZC0|VATH_ORYSJ_Probable_V-type_proton_ATPase_subunit_H_OS=Oryza_sativa_subsp._japonica_GN=Os07g0549700_PE=2_SV=1	2.00E-51	[illegible]	[illegible]
comp24572_c0_seq2.p2				

comp24573_c0_seq2.p1	sp|P42058|ALTA7_ALTAL_Minor_allergen_Alt_a_7_OS=Alternaria_alternata_GN=ALTA7_PE=1_SV=1	7.00E-52	[illegible]	[illegible]
comp24577_c0_seq1.p1	sp|Q949S9|SPF27_ARATH_Pre-mRNA-splicing_factor_SPF27_homolog_OS=Arabidopsis_thaliana_GN=MOS4_PE=1_SV=1	4.00E-29	[illegible]	[illegible]
comp24577_c0_seq2.p1	sp|Q949S9|SPF27_ARATH_Pre-mRNA-splicing_factor_SPF27_homolog_OS=Arabidopsis_thaliana_GN=MOS4_PE=1_SV=1	2.00E-20	[illegible]	[illegible]
comp24578_c0_seq1.p1				
comp24579_c0_seq1.p1	sp|A7HSX5|PHS_PARL1_Putative_pterin-4-alpha-carbinolamine_dehydratase_OS=Parvibaculum_lavamentivorans_(strain_DS-1_/_DSM_13023_/_NCIMB_13966)_GN=Plav_1388_PE=3_SV=1	2.00E-24	[illegible]	[illegible]
comp24579_c0_seq2.p1	sp|A7HSX5|PHS_PARL1_Putative_pterin-4-alpha-carbinolamine_dehydratase_OS=Parvibaculum_lavamentivorans_(strain_DS-1_/_DSM_13023_/_NCIMB_13966)_GN=Plav_1388_PE=3_SV=1	9.00E-22	[illegible]	[illegible]
comp24580_c0_seq1.p1				
comp24582_c1_seq1.p1	sp|Q5R4H6|NRDC_PONAB_Nardilysin_OS=Pongo_abelii_GN=NRD1_PE=2_SV=1	2.00E-89	[illegible]	[illegible]
comp24583_c0_seq1.p1	sp|Q8ZBY6|FADE_YERPE_Acyl-coenzyme_A_dehydrogenase_OS=Yersinia_pestis_GN=fadE_PE=3_SV=1	3.00E-179	[illegible]	[illegible]
comp24584_c0_seq1.p1	sp|Q9FVR6|Y1222_ARATH_Uncharacterized_protein_At1g32220,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g32220_PE=1_SV=1	2.00E-29	[illegible]	[illegible]
comp24587_c0_seq1.p1				
comp24587_c0_seq2.p1				
comp24589_c0_seq1.p1	sp|Q5XPI4|RN123_HUMAN_E3_ubiquitin-protein_ligase_RNF123_OS=Homo_sapiens_GN=RNF123_PE=1_SV=1	1.00E-20	[illegible]	[illegible]
comp24590_c1_seq1.p1	sp|O76054|S14L2_HUMAN_SEC14-like_protein_2_OS=Homo_sapiens_GN=SEC14L2_PE=1_SV=1	1.00E-14	[illegible]	[illegible]
comp24590_c1_seq1.p5				
comp24591_c0_seq1.p1	sp|Q7XUH5|POED1_ORYSJ_Probable_polyprenol_reductase_1_OS=Oryza_sativa_subsp._japonica_GN=Os04g0576800_PE=2_SV=2	1.00E-28	[illegible]	[illegible]
comp24591_c0_seq1.p4				
comp24591_c0_seq2.p1				
comp24591_c0_seq2.p2	sp|Q7XUH5|POED1_ORYSJ_Probable_polyprenol_reductase_1_OS=Oryza_sativa_subsp._japonica_GN=Os04g0576800_PE=2_SV=2	1.00E-28	[illegible]	[illegible]
comp24592_c0_seq2.p1	sp|Q5IS35|TPC_MACFA_Mitochondrial_thiamine_pyrophosphate_carrier_OS=Macaca_fascicularis_GN=SLC25A19_PE=2_SV=1	1.00E-25	[illegible]	[illegible]
comp24594_c0_seq1.p1	sp|Q55535|Y328_SYNY3_Putative_low_molecular_weight_protein-tyrosine-phosphatase_slr0328_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0328_PE=3_SV=1	1.00E-17	[illegible]	[illegible]
comp24594_c0_seq3.p1	sp|Q55535|Y328_SYNY3_Putative_low_molecular_weight_protein-tyrosine-phosphatase_slr0328_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0328_PE=3_SV=1	4.00E-33	[illegible]	[illegible]
comp24595_c0_seq2.p1				
comp24597_c1_seq1.p1	sp|Q8WV93|LACE1_HUMAN_Lactation_elevated_protein_1_OS=Homo_sapiens_GN=LACE1_PE=2_SV=2	2.00E-71	[illegible]	[illegible]
comp24597_c1_seq2.p1	sp|Q8WV93|LACE1_HUMAN_Lactation_elevated_protein_1_OS=Homo_sapiens_GN=LACE1_PE=2_SV=2	5.00E-72	[illegible]	[illegible]
comp24598_c0_seq1.p1				
comp24598_c0_seq1.p3				
comp24598_c0_seq2.p1				
comp24598_c0_seq2.p3				
comp24599_c0_seq1.p1				
comp24600_c0_seq1.p1				
comp24602_c0_seq3.p1				
comp24605_c0_seq1.p1	sp|Q5BKI6|ANKR1_XENTR_Ankyrin_repeat_domain-containing_protein_1_OS=Xenopus_tropicalis_GN=ankrd1_PE=2_SV=1	3.00E-21	[illegible]	[illegible]
comp24606_c0_seq1.p1	sp|Q9S7Q2|PP124_ARATH_Pentatricopeptide_repeat-containing_protein_At1g74850,_chloroplastic_OS=Arabidopsis_thaliana_GN=PTAC2_PE=2_SV=1	7.00E-12	[illegible]	[illegible]
comp24606_c0_seq2.p1				
comp24607_c0_seq1.p1				
comp24608_c0_seq1.p1	sp|Q9SRQ3|PE191_ARATH_Peroxisome_biogenesis_protein_19-1_OS=Arabidopsis_thaliana_GN=PEX19-1_PE=1_SV=1	1.00E-25	[illegible]	[illegible]
comp24609_c0_seq1.p2				
comp24610_c0_seq3.p1	sp|Q9S7I0|TADA_ARATH_tRNA-specific_adenosine_deaminase,_chloroplastic_OS=Arabidopsis_thaliana_GN=TADA_PE=1_SV=1	2.00E-31	[illegible]	[illegible]
comp24613_c0_seq2.p1				
comp24615_c0_seq1.p1				
comp24615_c0_seq1.p2				
comp24615_c0_seq2.p1				
comp24616_c0_seq1.p1				
comp24618_c0_seq2.p1	sp|Q9DA39|LFG4_MOUSE_Protein_lifeguard_4_OS=Mus_musculus_GN=Tmbim4_PE=2_SV=1	6.00E-18	[illegible]	[illegible]
comp24618_c0_seq2.p2				
comp24619_c0_seq1.p1	sp|O74803|RHP23_SCHPO_UV_excision_repair_protein_rhp23_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rhp23_PE=1_SV=1	2.00E-26	[illegible]	[illegible]
comp24621_c0_seq1.p1	sp|Q99L04|DHRS1_MOUSE_Dehydrogenase/reductase_SDR_family_member_1_OS=Mus_musculus_GN=Dhrs1_PE=2_SV=1	5.00E-55	[illegible]	[illegible]
comp24623_c0_seq1.p1				
comp24624_c0_seq1.p1	sp|P84239|H3_URECA_Histone_H3_OS=Urechis_caupo_PE=1_SV=2	2.00E-33	[illegible]	[illegible]
comp24624_c0_seq1.p3				
comp24625_c0_seq1.p1	sp|Q9MAB3|NOP5B_ARATH_Probable_nucleolar_protein_5-2_OS=Arabidopsis_thaliana_GN=NOP5-2_PE=2_SV=1	3.00E-169	[illegible]	[illegible]
comp24626_c0_seq1.p1	sp|Q54T76|DUSP4_DICDI_Probable_dual_specificity_protein_phosphatase_DDB_G0281963_OS=Dictyostelium_discoideum_GN=DDB_G0281963_PE=3_SV=1	1.00E-18	[illegible]	[illegible]
comp24626_c0_seq3.p1	sp|Q9UNI6|DUS12_HUMAN_Dual_specificity_protein_phosphatase_12_OS=Homo_sapiens_GN=DUSP12_PE=1_SV=1	3.00E-14	[illegible]	[illegible]
comp24626_c0_seq3.p2				
comp24627_c0_seq1.p1	sp|P61872|LIP_RHIOR_Lipase_OS=Rhizopus_oryzae_PE=1_SV=1	6.00E-20	[illegible]	[illegible]
comp24627_c0_seq2.p1				
comp24628_c0_seq1.p1	sp|Q9UH99|SUN2_HUMAN_SUN_domain-containing_protein_2_OS=Homo_sapiens_GN=SUN2_PE=1_SV=3	5.00E-21	[illegible]	[illegible]
comp24628_c0_seq2.p1				
comp24628_c0_seq3.p1	sp|Q5SS91|SUN3_MOUSE_SUN_domain-containing_protein_3_OS=Mus_musculus_GN=Sun3_PE=2_SV=1	2.00E-22	[illegible]	[illegible]
comp24629_c0_seq1.p1	sp|Q13823|NOG2_HUMAN_Nucleolar_GTP-binding_protein_2_OS=Homo_sapiens_GN=GNL2_PE=1_SV=1	9.00E-158	[illegible]	[illegible]
comp24632_c0_seq1.p1				
comp24635_c0_seq1.p1				
comp24637_c0_seq1.p1				
comp24637_c0_seq2.p1	sp|P93740|NUD23_ARATH_Nudix_hydrolase_23,_chloroplastic_OS=Arabidopsis_thaliana_GN=NUDT23_PE=1_SV=2	1.00E-15	[illegible]	[illegible]
comp24638_c0_seq1.p1				
comp24638_c0_seq1.p2				
comp24638_c0_seq1.p3	sp|Q14318|FKBP8_HUMAN_Peptidyl-prolyl_cis-trans_isomerase_FKBP8_OS=Homo_sapiens_GN=FKBP8_PE=1_SV=2	6.00E-29	[illegible]	[illegible]
comp24638_c0_seq2.p1				
comp24638_c0_seq2.p2	sp|Q14318|FKBP8_HUMAN_Peptidyl-prolyl_cis-trans_isomerase_FKBP8_OS=Homo_sapiens_GN=FKBP8_PE=1_SV=2	6.00E-29	[illegible]	[illegible]
comp24641_c0_seq1.p1	sp|Q91309|F26_LITCT_6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase_OS=Lithobates_catesbeiana_PE=2_SV=1	3.00E-89	[illegible]	[illegible]
comp24642_c0_seq2.p1	sp|O36015|YEK3_SCHPO_Putative_ribosomal_RNA_methyltransferase_C4F10.03c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC4F10.03c_PE=2_SV=1	3.00E-80	[illegible]	[illegible]
comp24644_c0_seq2.p1				
comp24646_c0_seq1.p1				
comp24646_c0_seq3.p1				
comp24648_c0_seq1.p1	sp|Q2QYY8|PHT1A_ORYSJ_Phototropin-1A_OS=Oryza_sativa_subsp._japonica_GN=PHOT1A_PE=1_SV=2	5.00E-26	[illegible]	[illegible]
comp24649_c0_seq1.p1				
comp24650_c0_seq1.p1	sp|B9DFG3|ISE2_ARATH_DEAD-box_ATP-dependent_RNA_helicase_ISE2,_chloroplastic_OS=Arabidopsis_thaliana_GN=ISE2_PE=1_SV=2	2.00E-57	[illegible]	[illegible]
comp24651_c0_seq1.p1	sp|Q8L633|RNZC_ARATH_Ribonuclease_Z,_chloroplastic_OS=Arabidopsis_thaliana_GN=CPZ_PE=2_SV=1	5.00E-24	[illegible]	[illegible]
comp24651_c0_seq3.p1				
comp24652_c0_seq1.p1	sp|P07102|PPA_ECOLI_Periplasmic_AppA_protein_OS=Escherichia_coli_(strain_K12)_GN=appA_PE=1_SV=2	6.00E-24	[illegible]	[illegible]
comp24653_c0_seq1.p1				
comp24655_c0_seq1.p1	sp|Q3SZL5|PIGS_BOVIN_GPI_transamidase_component_PIG-S_OS=Bos_taurus_GN=PIGS_PE=2_SV=3	2.00E-11	[illegible]	[illegible]
comp24656_c0_seq1.p1	sp|Q55DP8|ACY1_DICDI_Aminoacylase-1_OS=Dictyostelium_discoideum_GN=acy1_PE=2_SV=1	6.00E-123	[illegible]	[illegible]
comp24656_c0_seq1.p2				
comp24656_c0_seq2.p1	sp|Q55DP8|ACY1_DICDI_Aminoacylase-1_OS=Dictyostelium_discoideum_GN=acy1_PE=2_SV=1	1.00E-90	[illegible]	[illegible]
comp24656_c0_seq2.p2				
comp24656_c0_seq2.p6	sp|Q99JW2|ACY1_MOUSE_Aminoacylase-1_OS=Mus_musculus_GN=Acy1_PE=1_SV=1	3.00E-26	[illegible]	[illegible]
comp24657_c0_seq1.p1	sp|O09101|PIGF_MOUSE_Phosphatidylinositol-glycan_biosynthesis_class_F_protein_OS=Mus_musculus_GN=Pigf_PE=1_SV=1	9.00E-16	[illegible]	[illegible]
comp24657_c0_seq2.p1	sp|O09101|PIGF_MOUSE_Phosphatidylinositol-glycan_biosynthesis_class_F_protein_OS=Mus_musculus_GN=Pigf_PE=1_SV=1	1.00E-15	[illegible]	[illegible]
comp24658_c1_seq2.p1	sp|Q29460|PA1B3_BOVIN_Platelet-activating_factor_acetylhydrolase_IB_subunit_gamma_OS=Bos_taurus_GN=PAFAH1B3_PE=1_SV=1	4.00E-23	[illegible]	[illegible]
comp24658_c1_seq3.p1				
comp24658_c1_seq3.p3	sp|Q5ZMS2|PA1B2_CHICK_Platelet-activating_factor_acetylhydrolase_IB_subunit_beta_OS=Gallus_gallus_GN=PAFAH1B2_PE=2_SV=1	3.00E-17	[illegible]	[illegible]
comp24659_c0_seq1.p2				
comp24660_c0_seq3.p1				
comp24662_c0_seq2.p1				
comp24663_c0_seq1.p1	sp|B9L101|OBG_THERP_GTPase_obg_OS=Thermomicrobium_roseum_(strain_ATCC_27502_/_DSM_5159_/_P-2)_GN=obg_PE=3_SV=1	4.00E-69	[illegible]	[illegible]
comp24663_c0_seq1.p3				
comp24663_c0_seq2.p1	sp|B9L101|OBG_THERP_GTPase_obg_OS=Thermomicrobium_roseum_(strain_ATCC_27502_/_DSM_5159_/_P-2)_GN=obg_PE=3_SV=1	1.00E-78	[illegible]	[illegible]
comp24664_c0_seq1.p1				
comp24664_c0_seq3.p1	sp|Q90972|RNF13_CHICK_E3_ubiquitin-protein_ligase_RNF13_OS=Gallus_gallus_GN=RNF13_PE=1_SV=1	4.00E-23	[illegible]	[illegible]
comp24665_c0_seq1.p1				
comp24666_c0_seq1.p1				
comp24666_c0_seq2.p1				
comp24666_c0_seq4.p1				
comp24667_c0_seq1.p1				
comp24668_c0_seq1.p1	sp|Q9M8Y0|SEC_ARATH_Probable_UDP-N-acetylglucosamine--peptide_N-acetylglucosaminyltransferase_SEC_OS=Arabidopsis_thaliana_GN=SEC_PE=2_SV=1	2.00E-12	[illegible]	[illegible]
comp24669_c1_seq1.p1	sp|P57740|NU107_HUMAN_Nuclear_pore_complex_protein_Nup107_OS=Homo_sapiens_GN=NUP107_PE=1_SV=1	7.00E-25	[illegible]	[illegible]
comp24670_c0_seq1.p1	sp|A3KP37|CT007_DANRE_Probable_methyltransferase_C20orf7_homolog,_mitochondrial_OS=Danio_rerio_GN=zgc:162919_PE=2_SV=1	5.00E-74	[illegible]	[illegible]
comp24672_c0_seq1.p3				
comp24673_c0_seq3.p1				
comp24673_c0_seq5.p1				
comp24673_c0_seq5.p2				
comp24673_c0_seq7.p1				
comp24674_c0_seq1.p1				
comp24675_c0_seq4.p1	sp|Q9C9H7|RLP12_ARATH_Receptor-like_protein_12_OS=Arabidopsis_thaliana_GN=RLP12_PE=2_SV=2	2.00E-15	[illegible]	[illegible]
comp24678_c0_seq2.p1	sp|O60016|CLR4_SCHPO_Histone-lysine_N-methyltransferase,_H3_lysine-9_specific_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=clr4_PE=1_SV=2	3.00E-18	[illegible]	[illegible]
comp24679_c0_seq1.p1	sp|P29766|RL8_SOLLC_60S_ribosomal_protein_L8_OS=Solanum_lycopersicum_GN=RPL8_PE=2_SV=1	3.00E-59	[illegible]	[illegible]
comp24681_c0_seq1.p1				
comp24683_c0_seq1.p2				
comp24684_c0_seq1.p1	sp|P0CF52|KDM7B_DANRE_Lysine-specific_demethylase_7B_OS=Danio_rerio_GN=jhdm1db_PE=2_SV=1	5.00E-78	[illegible]	[illegible]
comp24685_c0_seq1.p1	sp|Q2JV68|CLPP2_SYNJA_ATP-dependent_Clp_protease_proteolytic_subunit_2_OS=Synechococcus_sp._(strain_JA-3-3Ab)_GN=clpP2_PE=3_SV=1	1.00E-81	[illegible]	[illegible]
comp24686_c0_seq1.p1	sp|A4WX36|PUR5_RHOS5_Phosphoribosylformylglycinamidine_cyclo-ligase_OS=Rhodobacter_sphaeroides_(strain_ATCC_17025_/_ATH_2.4.3)_GN=purM_PE=3_SV=1	2.00E-104	[illegible]	[illegible]
comp24687_c0_seq1.p1	sp|Q6AY40|JMJD8_RAT_JmjC_domain-containing_protein_8_OS=Rattus_norvegicus_GN=Jmjd8_PE=2_SV=2	6.00E-25	GO:0070062	[illegible]
comp24688_c0_seq3.p1	sp|Q9GP32|ALF_ECHMU_Fructose-bisphosphate_aldolase_OS=Echinococcus_multilocularis_GN=FBPA_PE=2_SV=1	1.00E-90	[illegible]	[illegible]
comp24689_c0_seq1.p1				
comp24690_c0_seq2.p1	sp|P33731|SRP72_CANFA_Signal_recognition_particle_72_kDa_protein_OS=Canis_familiaris_GN=SRP72_PE=1_SV=3	1.00E-34	[illegible]	[illegible]
comp24692_c0_seq1.p1				
comp24693_c0_seq1.p1				
comp24694_c1_seq1.p1	sp|P59941|SIRT6_MOUSE_NAD-dependent_deacetylase_sirtuin-6_OS=Mus_musculus_GN=Sirt6_PE=1_SV=1	9.00E-63	[illegible]	[illegible]
comp24694_c1_seq1.p2				
comp24694_c1_seq3.p1	sp|Q8N6T7|SIRT6_HUMAN_NAD-dependent_deacetylase_sirtuin-6_OS=Homo_sapiens_GN=SIRT6_PE=1_SV=2	7.00E-61	[illegible]	[illegible]
comp24694_c1_seq4.p1	sp|Q8N6T7|SIRT6_HUMAN_NAD-dependent_deacetylase_sirtuin-6_OS=Homo_sapiens_GN=SIRT6_PE=1_SV=2	8.00E-61	[illegible]	[illegible]
comp24695_c0_seq1.p1				
comp24696_c0_seq1.p1				
comp24697_c0_seq1.p1				
comp24698_c0_seq1.p2				
comp24698_c0_seq2.p2				
comp24698_c0_seq3.p1				
comp24699_c0_seq1.p1				
comp24700_c0_seq1.p1	sp|Q9SZJ5|GLYM_ARATH_Serine_hydroxymethyltransferase,_mitochondrial_OS=Arabidopsis_thaliana_GN=SHM1_PE=1_SV=1	0	[illegible]	[illegible]
comp24700_c0_seq2.p1	sp|P50433|GLYM_SOLTU_Serine_hydroxymethyltransferase,_mitochondrial_OS=Solanum_tuberosum_PE=2_SV=1	0	[illegible]	[illegible]
comp24700_c0_seq2.p2				
comp24702_c0_seq1.p1	sp|Q9SSU8|PSY_DAUCA_Phytoene_synthase,_chloroplastic_OS=Daucus_carota_GN=PSY_PE=2_SV=1	8.00E-92	[illegible]	[illegible]
comp24704_c1_seq2.p1	sp|O70496|CLCN7_MOUSE_H(+)/Cl(-)_exchange_transporter_7_OS=Mus_musculus_GN=Clcn7_PE=1_SV=1	7.00E-112	[illegible]	[illegible]
comp24704_c1_seq2.p2				
comp24705_c1_seq1.p1				
comp24706_c0_seq2.p1				
comp24706_c0_seq2.p2				
comp24708_c0_seq2.p1				
comp24709_c0_seq2.p1	sp|P14834|HSP70_LEIMA_Heat_shock_70_kDa_protein_(Fragment)_OS=Leishmania_major_GN=HSP70_PE=3_SV=1	2.00E-79	[illegible]	[illegible]
comp24710_c0_seq2.p1				
comp24711_c0_seq1.p1				
comp24712_c0_seq2.p1				
comp24716_c0_seq1.p1	sp|Q8N8Q3|ENDOV_HUMAN_Endonuclease_V_OS=Homo_sapiens_GN=ENDOV_PE=2_SV=1	6.00E-17	[illegible]	[illegible]
comp24717_c0_seq1.p1	sp|Q9H2U1|DHX36_HUMAN_Probable_ATP-dependent_RNA_helicase_DHX36_OS=Homo_sapiens_GN=DHX36_PE=1_SV=2	6.00E-81	[illegible]	[illegible]
comp24718_c0_seq1.p1				
comp24720_c0_seq1.p1	sp|Q8N766|K0090_HUMAN_Uncharacterized_protein_KIAA0090_OS=Homo_sapiens_GN=KIAA0090_PE=1_SV=1	2.00E-63	[illegible]	[illegible]
comp24720_c1_seq1.p1				
comp24722_c0_seq1.p1				
comp24724_c0_seq1.p1	sp|Q66L58|VAC14_DANRE_Protein_VAC14_homolog_OS=Danio_rerio_GN=vac14_PE=2_SV=1	3.00E-147	[illegible]	[illegible]
comp24725_c0_seq1.p1	sp|Q5U4X5|NDC80_XENTR_Kinetochore_protein_NDC80_homolog_OS=Xenopus_tropicalis_GN=ndc80_PE=2_SV=1	1.00E-37	[illegible]	[illegible]
comp24726_c0_seq1.p1				
comp24726_c0_seq2.p1				
comp24727_c0_seq1.p1				
comp24728_c0_seq1.p1	sp|Q869L4|FNKA_DICDI_Probable_serine/threonine-protein_kinase_fnkA_OS=Dictyostelium_discoideum_GN=fnkA_PE=3_SV=1	2.00E-18	[illegible]	[illegible]
comp24728_c0_seq3.p1	sp|Q6TBX7|LUT1_ARATH_Carotene_epsilon-monooxygenase,_chloroplastic_OS=Arabidopsis_thaliana_GN=CYP97C1_PE=1_SV=1	2.00E-19	[illegible]	[illegible]
comp24729_c0_seq1.p1	sp|Q9H553|ALG2_HUMAN_Alpha-1,3/1,6-mannosyltransferase_ALG2_OS=Homo_sapiens_GN=ALG2_PE=2_SV=1	7.00E-104	[illegible]	[illegible]
comp24730_c0_seq1.p1	sp|A9EYY7|SYL_SORC5_Leucine--tRNA_ligase_OS=Sorangium_cellulosum_(strain_So_ce56)_GN=leuS_PE=3_SV=1	0	[illegible]	[illegible]
comp24731_c0_seq1.p1	sp|Q8L7S3|C3H24_ARATH_Zinc_finger_CCCH_domain-containing_protein_24_OS=Arabidopsis_thaliana_GN=At2g28450_PE=2_SV=1	6.00E-59	[illegible]	[illegible]
comp24732_c0_seq1.p1	sp|A4VGS1|PYRE_PSEU5_Orotate_phosphoribosyltransferase_OS=Pseudomonas_stutzeri_(strain_A1501)_GN=pyrE_PE=3_SV=1	1.00E-71	[illegible]	[illegible]
comp24732_c0_seq2.p1	sp|A9B3C5|PYRF_HERA2_Orotidine_5'-phosphate_decarboxylase_OS=Herpetosiphon_aurantiacus_(strain_ATCC_23779_/_DSM_785)_GN=pyrF_PE=3_SV=1	3.00E-49	[illegible]	[illegible]
comp24734_c0_seq1.p1	sp|Q5XIC0|ECI2_RAT_Enoyl-CoA_delta_isomerase_2,_mitochondrial_OS=Rattus_norvegicus_GN=Eci2_PE=1_SV=1	6.00E-20	[illegible]	[illegible]
comp24735_c0_seq1.p1				
comp24737_c0_seq1.p1				
comp24737_c0_seq2.p1				
comp24737_c0_seq3.p1				
comp24738_c0_seq3.p1				
comp24739_c0_seq2.p1	sp|Q9NW38|FANCL_HUMAN_E3_ubiquitin-protein_ligase_FANCL_OS=Homo_sapiens_GN=FANCL_PE=1_SV=2	5.00E-86	[illegible]	[illegible]
comp24739_c0_seq5.p1	sp|Q9NW38|FANCL_HUMAN_E3_ubiquitin-protein_ligase_FANCL_OS=Homo_sapiens_GN=FANCL_PE=1_SV=2	8.00E-77	[illegible]	[illegible]
comp24740_c0_seq1.p1				
comp24741_c0_seq2.p1				
comp24741_c0_seq2.p2	sp|Q6GQE1|T184C_XENLA_Transmembrane_protein_184C_OS=Xenopus_laevis_GN=tmem184c_PE=2_SV=1	2.00E-62	[illegible]	[illegible]
comp24741_c0_seq7.p1				
comp24741_c0_seq7.p2	sp|Q6GQE1|T184C_XENLA_Transmembrane_protein_184C_OS=Xenopus_laevis_GN=tmem184c_PE=2_SV=1	2.00E-62	[illegible]	[illegible]
comp24742_c0_seq1.p1				
comp24743_c0_seq1.p1	sp|O04397|FENR2_TOBAC_Ferredoxin--NADP_reductase,_root-type_isozyme,_chloroplastic_OS=Nicotiana_tabacum_PE=2_SV=1	3.00E-137	[illegible]	[illegible]
comp24744_c0_seq1.p2				
comp24745_c0_seq1.p1	sp|Q6P7Q4|LGUL_RAT_Lactoylglutathione_lyase_OS=Rattus_norvegicus_GN=Glo1_PE=1_SV=3	2.00E-73	[illegible]	[illegible]
comp24745_c0_seq1.p3				
comp24745_c0_seq2.p1	sp|Q6P7Q4|LGUL_RAT_Lactoylglutathione_lyase_OS=Rattus_norvegicus_GN=Glo1_PE=1_SV=3	1.00E-64	[illegible]	[illegible]
comp24747_c0_seq2.p1				
comp24748_c0_seq1.p1	sp|Q5ZMR3|PCMD1_CHICK_Protein-L-isoaspartate_O-methyltransferase_domain-containing_protein_1_OS=Gallus_gallus_GN=PCMTD1_PE=2_SV=1	1.00E-37	[illegible]	[illegible]
comp24749_c0_seq1.p1	sp|Q924M7|MPI_MOUSE_Mannose-6-phosphate_isomerase_OS=Mus_musculus_GN=Mpi_PE=2_SV=1	1.00E-45	[illegible]	[illegible]
comp24749_c0_seq1.p6				
comp24750_c0_seq1.p1				
comp24752_c0_seq2.p1				
comp24754_c0_seq1.p1				
comp24755_c0_seq2.p1	sp|P52232|THIO1_SYNY3_Thioredoxin-like_protein_slr0233_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0233_PE=3_SV=1	7.00E-31	[illegible]	[illegible]
comp24757_c0_seq1.p1				
comp24759_c0_seq1.p1	sp|Q7TPN3|PIGV_MOUSE_GPI_mannosyltransferase_2_OS=Mus_musculus_GN=Pigv_PE=2_SV=2	3.00E-30	[illegible]	[illegible]
comp24759_c0_seq1.p2	sp|Q08C69|RUSD1_DANRE_RNA_pseudouridylate_synthase_domain-containing_protein_1_OS=Danio_rerio_GN=rpusd1_PE=2_SV=1	8.00E-15	[illegible]	[illegible]
comp24759_c0_seq1.p4	sp|Q8VCZ8|RUSD1_MOUSE_RNA_pseudouridylate_synthase_domain-containing_protein_1_OS=Mus_musculus_GN=Rpusd1_PE=2_SV=1	6.00E-17	[illegible]	[illegible]
comp24760_c0_seq1.p1				
comp24761_c0_seq2.p1				
comp24762_c0_seq1.p1	sp|Q6T3U3|NPCL1_RAT_Niemann-Pick_C1-like_protein_1_OS=Rattus_norvegicus_GN=Npc1l1_PE=1_SV=1	2.00E-21	[illegible]	[illegible]
comp24763_c0_seq1.p1				
comp24764_c0_seq1.p1	sp|P51181|KPYK_BACLI_Pyruvate_kinase_OS=Bacillus_licheniformis_GN=pyk_PE=3_SV=1	1.00E-123	[illegible]	[illegible]
comp24766_c0_seq1.p1	sp|P72702|Y245_SYNY3_Uncharacterized_protein_slr0245_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0245_PE=3_SV=1	2.00E-54	[illegible]	[illegible]
comp24766_c0_seq2.p1	sp|P72702|Y245_SYNY3_Uncharacterized_protein_slr0245_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0245_PE=3_SV=1	1.00E-59	[illegible]	[illegible]
comp24767_c0_seq1.p1	sp|Q39017|DGK1_ARATH_Diacylglycerol_kinase_1_OS=Arabidopsis_thaliana_GN=DGK1_PE=1_SV=2	9.00E-49	[illegible]	[illegible]
comp24769_c0_seq1.p1	sp|Q9Y6W3|CAN7_HUMAN_Calpain-7_OS=Homo_sapiens_GN=CAPN7_PE=1_SV=1	7.00E-159	[illegible]	[illegible]
comp24770_c0_seq1.p1				
comp24773_c0_seq2.p1				
comp24773_c0_seq3.p1				
comp24776_c0_seq2.p1				
comp24777_c0_seq1.p1				
comp24777_c0_seq2.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	7.00E-36		
comp24778_c0_seq1.p1	sp|Q9D9I4|TBC20_MOUSE_TBC1_domain_family_member_20_OS=Mus_musculus_GN=Tbc1d20_PE=2_SV=1	4.00E-39	[illegible]	[illegible]
comp24778_c0_seq4.p1	sp|Q9D9I4|TBC20_MOUSE_TBC1_domain_family_member_20_OS=Mus_musculus_GN=Tbc1d20_PE=2_SV=1	4.00E-39	[illegible]	[illegible]
comp24779_c0_seq1.p1	sp|Q8VQZ3|Y6689_MYXXD_UPF0272_protein_MXAN_6689_OS=Myxococcus_xanthus_(strain_DK_1622)_GN=MXAN_6689_PE=3_SV=1	3.00E-75		
comp24781_c0_seq1.p1				
comp24784_c0_seq1.p1	sp|P48580|PP2A1_NEUCR_Serine/threonine-protein_phosphatase_PP2A_catalytic_subunit_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=ppb-1_PE=3_SV=3	2.00E-171	[illegible]	[illegible]
comp24784_c0_seq1.p5				
comp24784_c0_seq2.p1	sp|P48580|PP2A1_NEUCR_Serine/threonine-protein_phosphatase_PP2A_catalytic_subunit_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=ppb-1_PE=3_SV=3	0	[illegible]	[illegible]
comp24785_c0_seq1.p1				
comp24786_c0_seq1.p2	sp|Q9ZTN2|ERD2_PETHY_ER_lumen_protein_retaining_receptor_OS=Petunia_hybrida_GN=ERD2_PE=2_SV=1	2.00E-57	[illegible]	[illegible]
comp24788_c0_seq1.p1	sp|Q90ZA1|PARN_XENLA_Poly(A)-specific_ribonuclease_PARN_OS=Xenopus_laevis_GN=parn_PE=1_SV=1	1.00E-53	[illegible]	[illegible]
comp24788_c0_seq1.p2				
comp24790_c0_seq1.p1	sp|Q86IZ9|DDX52_DICDI_Probable_ATP-dependent_RNA_helicase_ddx52_OS=Dictyostelium_discoideum_GN=ddx52_PE=3_SV=1	2.00E-128	[illegible]	[illegible]
comp24790_c0_seq1.p2	sp|Q14AK4|ZDH11_MOUSE_Probable_palmitoyltransferase_ZDHHC11_OS=Mus_musculus_GN=Zdhhc11_PE=2_SV=2	2.00E-26	[illegible]	[illegible]
comp24791_c0_seq1.p1				
comp24791_c0_seq2.p1	sp|Q502K3|ANR52_DANRE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_C_OS=Danio_rerio_GN=ankrd52_PE=2_SV=1	2.00E-11	[illegible]	[illegible]
comp24792_c0_seq1.p1				
comp24792_c0_seq2.p1				
comp24793_c0_seq1.p1	sp|Q91YR5|MET13_MOUSE_Methyltransferase-like_protein_13_OS=Mus_musculus_GN=Mettl13_PE=1_SV=1	1.00E-29	[illegible]	[illegible]
comp24793_c0_seq2.p1				
comp24793_c0_seq2.p2				
comp24794_c0_seq1.p1				
comp24794_c0_seq3.p1				
comp24797_c0_seq1.p3	sp|Q8VE42|ANR49_MOUSE_Ankyrin_repeat_domain-containing_protein_49_OS=Mus_musculus_GN=Ankrd49_PE=1_SV=1	3.00E-14	[illegible]	[illegible]
comp24798_c0_seq2.p1				
comp24798_c0_seq2.p2	sp|Q505D1|ANR28_MOUSE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_A_OS=Mus_musculus_GN=Ankrd28_PE=1_SV=1	3.00E-17	[illegible]	[illegible]
comp24800_c0_seq2.p1	sp|Q5N749|MOR1_ORYSJ_Protein_MOR1_OS=Oryza_sativa_subsp._japonica_GN=MOR1_PE=2_SV=1	2.00E-44	[illegible]	[illegible]
comp24800_c0_seq3.p1	sp|Q94FN2|MOR1_ARATH_Protein_MOR1_OS=Arabidopsis_thaliana_GN=MOR1_PE=1_SV=1	5.00E-36	[illegible]	[illegible]
comp24802_c0_seq1.p1				
comp24805_c0_seq1.p1	sp|Q55156|Y064_SYNY3_Putative_RNA_methyltransferase_slr0064_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0064_PE=3_SV=1	2.00E-53	[illegible]	[illegible]
comp24806_c0_seq3.p1				
comp24806_c0_seq4.p1				
comp24808_c0_seq1.p1	sp|O94590|SEC1_SCHPO_Protein_transport_protein_sec1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=sec1_PE=2_SV=1	3.00E-28	[illegible]	[illegible]
comp24808_c0_seq2.p1	sp|Q07327|ROP_DROME_Protein_ROP_OS=Drosophila_melanogaster_GN=Rop_PE=2_SV=2	8.00E-28	[illegible]	[illegible]
comp24809_c0_seq1.p1				
comp24810_c0_seq3.p1				
comp24810_c0_seq4.p1				
comp24811_c0_seq1.p1	sp|P97756|KKCC1_RAT_Calcium/calmodulin-dependent_protein_kinase_kinase_1_OS=Rattus_norvegicus_GN=Camkk1_PE=1_SV=1	1.00E-36	[illegible]	[illegible]
comp24812_c0_seq1.p1				
comp24813_c0_seq1.p1				
comp24813_c0_seq1.p2	sp|Q9SKI2|VPS2A_ARATH_Vacuolar_protein_sorting-associated_protein_2_homolog_1_OS=Arabidopsis_thaliana_GN=VPS2.1_PE=1_SV=2	2.00E-65	[illegible]	[illegible]
comp24813_c0_seq2.p1				
comp24815_c0_seq2.p1				
comp24815_c0_seq2.p4				
comp24816_c0_seq1.p1	sp|Q5RBU8|ROA2_PONAB_Heterogeneous_nuclear_ribonucleoproteins_A2/B1_OS=Pongo_abelii_GN=HNRNPA2B1_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp24817_c0_seq1.p1	sp|Q9VXB0|NECAP_DROME_NECAP-like_protein_CG9132_OS=Drosophila_melanogaster_GN=CG9132_PE=2_SV=1	4.00E-26	[illegible]	[illegible]
comp24818_c0_seq2.p1	sp|P34657|YOTB_CAEEL_Uncharacterized_protein_ZK632.12_OS=Caenorhabditis_elegans_GN=ZK632.12_PE=1_SV=2	2.00E-11	[illegible]	[illegible]
comp24819_c0_seq1.p1				
comp24819_c0_seq3.p1				
comp24821_c0_seq2.p1	sp|Q01284|2NPD_NEUCR_Nitronate_monooxygenase_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=ncd-2_PE=1_SV=1	3.00E-18	[illegible]	[illegible]
comp24821_c0_seq3.p1				
comp24822_c0_seq1.p1				
comp24824_c0_seq1.p1				
comp24826_c0_seq1.p1				
comp24827_c0_seq2.p1				
comp24828_c0_seq1.p1	sp|P72991|FTSH3_SYNY3_ATP-dependent_zinc_metalloprotease_FtsH_3_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=ftsH3_PE=1_SV=1	0	[illegible]	[illegible]
comp24829_c0_seq1.p1				
comp24829_c0_seq2.p1				
comp24830_c0_seq2.p1				
comp24831_c0_seq1.p1	sp|Q3MH14|FABZ_ANAVT_(3R)-hydroxymyristoyl-[acyl-carrier-protein]_dehydratase_OS=Anabaena_variabilis_(strain_ATCC_29413_/_PCC_7937)_GN=fabZ_PE=3_SV=2	3.00E-43	[illegible]	[illegible]
comp24831_c0_seq2.p1	sp|A5GV11|FABZ_SYNR3_(3R)-hydroxymyristoyl-[acyl-carrier-protein]_dehydratase_OS=Synechococcus_sp._(strain_RCC307)_GN=fabZ_PE=3_SV=1	2.00E-31	[illegible]	[illegible]
comp24832_c0_seq1.p2				
comp24836_c0_seq1.p2				
comp24836_c0_seq2.p1	sp|Q9Y5A7|NUB1_HUMAN_NEDD8_ultimate_buster_1_OS=Homo_sapiens_GN=NUB1_PE=1_SV=2	6.00E-14	[illegible]	[illegible]
comp24840_c0_seq1.p1	sp|Q54I48|CTL2_DICDI_Choline_transporter-like_protein_2_OS=Dictyostelium_discoideum_GN=slc44a2_PE=3_SV=1	2.00E-61	[illegible]	[illegible]
comp24840_c0_seq1.p2	sp|Q4V8C8|CDC73_RAT_Parafibromin_OS=Rattus_norvegicus_GN=Cdc73_PE=2_SV=1	6.00E-38	[illegible]	[illegible]
comp24841_c0_seq1.p1				
comp24841_c1_seq1.p1				
comp24843_c0_seq1.p1	sp|Q53H47|SETMR_HUMAN_Histone-lysine_N-methyltransferase_SETMAR_OS=Homo_sapiens_GN=SETMAR_PE=1_SV=1	5.00E-27	[illegible]	[illegible]
comp24843_c0_seq2.p1	sp|Q0VD24|SETMR_BOVIN_Histone-lysine_N-methyltransferase_SETMAR_OS=Bos_taurus_GN=SETMAR_PE=2_SV=1	4.00E-32	[illegible]	[illegible]
comp24844_c0_seq3.p1				
comp24845_c0_seq1.p1	sp|Q7NL66|PEBA_GLOVI_15,16-dihydrobiliverdin:ferredoxin_oxidoreductase_OS=Gloeobacter_violaceus_(strain_PCC_7421)_GN=pebA_PE=3_SV=2	2.00E-25	[illegible]	[illegible]
comp24845_c0_seq1.p2				
comp24846_c0_seq1.p1				
comp24846_c1_seq1.p1				
comp24848_c0_seq1.p2	sp|Q3Z5B4|GMHA_SHISS_Phosphoheptose_isomerase_OS=Shigella_sonnei_(strain_Ss046)_GN=gmhA_PE=3_SV=1	1.00E-89	[illegible]	[illegible]
comp24849_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	1.00E-25		
comp24851_c0_seq1.p1				
comp24855_c0_seq1.p1	sp|A6U864|RL22_SINMW_50S_ribosomal_protein_L22_OS=Sinorhizobium_medicae_(strain_WSM419)_GN=rplV_PE=3_SV=1	1.00E-15	[illegible]	[illegible]
comp24856_c0_seq1.p1	sp|P23903|E13B_BACCI_Glucan_endo-1,3-beta-glucosidase_A1_OS=Bacillus_circulans_GN=glcA_PE=1_SV=1	2.00E-18	[illegible]	[illegible]
comp24856_c0_seq3.p1	sp|P23903|E13B_BACCI_Glucan_endo-1,3-beta-glucosidase_A1_OS=Bacillus_circulans_GN=glcA_PE=1_SV=1	3.00E-17	[illegible]	[illegible]
comp24857_c0_seq2.p1	sp|Q9R099|TBL2_MOUSE_Transducin_beta-like_protein_2_OS=Mus_musculus_GN=Tbl2_PE=2_SV=2	4.00E-41	[illegible]	[illegible]
comp24858_c0_seq1.p1	sp|Q7SCY7|SYM1_NEUCR_Protein_sym-1_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=sym-1_PE=3_SV=2	5.00E-23	[illegible]	[illegible]
comp2486_c0_seq1.p1				
comp24860_c1_seq1.p2				
comp24861_c0_seq1.p1	sp|Q8BGA9|OXA1L_MOUSE_Mitochondrial_inner_membrane_protein_OXA1L_OS=Mus_musculus_GN=Oxa1l_PE=2_SV=1	4.00E-36	[illegible]	[illegible]
comp24862_c0_seq1.p1	sp|Q8GY91|APX6_ARATH_Putative_L-ascorbate_peroxidase_6_OS=Arabidopsis_thaliana_GN=APX6_PE=2_SV=1	1.00E-19	[illegible]	[illegible]
comp24864_c0_seq1.p1				
comp24866_c0_seq1.p1	sp|Q05197|PMTA_RHOSH_Phosphatidylethanolamine_N-methyltransferase_OS=Rhodobacter_sphaeroides_GN=pmtA_PE=4_SV=1	5.00E-27	[illegible]	[illegible]
comp24867_c0_seq3.p1	sp|Q8C436|MT21D_MOUSE_Methyltransferase-like_protein_21D_OS=Mus_musculus_GN=Mettl21d_PE=2_SV=2	6.00E-21	[illegible]	[illegible]
comp24868_c0_seq1.p1				
comp24868_c0_seq2.p3				
comp24871_c0_seq1.p1				
comp24873_c0_seq1.p1	sp|Q5U458|DJC11_MOUSE_DnaJ_homolog_subfamily_C_member_11_OS=Mus_musculus_GN=Dnajc11_PE=2_SV=2	9.00E-24	[illegible]	[illegible]
comp24873_c0_seq1.p4	sp|P34730|BMH2_YEAST_Protein_BMH2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=BMH2_PE=1_SV=3	1.00E-53	[illegible]	[illegible]
comp24873_c0_seq4.p1				
comp24874_c0_seq1.p1				
comp24874_c0_seq4.p1				
comp24875_c1_seq1.p1				
comp24875_c1_seq2.p1	sp|Q2KIB9|RPP29_BOVIN_Ribonuclease_P_protein_subunit_p29_OS=Bos_taurus_GN=POP4_PE=2_SV=1	6.00E-15	[illegible]	[illegible]
comp24880_c0_seq1.p1	sp|Q9LV93|AB5F_ARATH_ABC_transporter_F_family_member_5_OS=Arabidopsis_thaliana_GN=ABCF5_PE=2_SV=1	9.00E-151	[illegible]	[illegible]
comp24880_c0_seq1.p2	sp|P53383|MRP_SYNY3_Protein_mrp_homolog_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=mrp_PE=3_SV=1	2.00E-66	[illegible]	[illegible]

comp24881_c0_seq1.p2	sp|Q54XS6|UBE2C_DICDI_Probable_ubiquitin-conjugating_enzyme_E2_C_OS=Dictyostelium_discoideum_GN=ube2c_PE=3_SV=1	4.00E-62
comp24881_c0_seq2.p1	sp|Q9LJZ5|UBC19_ARATH_Ubiquitin-conjugating_enzyme_E2_19_OS=Arabidopsis_thaliana_GN=UBC19_PE=1_SV=1	3.00E-11
comp24883_c0_seq2.p1	sp|Q9GSB0|CRTP1_DICDI_Crt_homolog_1_OS=Dictyostelium_discoideum_GN=crtp1_PE=2_SV=1	8.00E-28
comp24884_c0_seq2.p2		
comp24885_c0_seq1.p1	sp|Q91VU6|DCA11_MOUSE_DDB1-_and_CUL4-associated_factor_11_OS=Mus_musculus_GN=Dcaf11_PE=1_SV=1	1.00E-84
comp24885_c0_seq2.p2		
comp24886_c0_seq1.p1	sp|Q6PAC3|DCA13_MOUSE_DDB1-_and_CUL4-associated_factor_13_OS=Mus_musculus_GN=Dcaf13_PE=2_SV=2	7.00E-165
comp24889_c0_seq1.p1	sp|Q9P4X3|UTP7_SCHPO_Probable_U3_small_nucleolar_RNA-associated_protein_7_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=utp7_PE=2_SV=1	2.00E-146
comp24890_c0_seq1.p1		
comp24890_c0_seq1.p2	sp|Q2UUT6|ATG9_ASPOR_Autophagy-related_protein_9_OS=Aspergillus_oryzae_(strain_ATCC_42149_/_RIB_40)_GN=atg9_PE=3_SV=1	4.00E-73
comp24890_c0_seq2.p1	sp|Q4P683|ATG9_USTMA_Autophagy-related_protein_9_OS=Ustilago_maydis_(strain_521_/_FGSC_9021)_GN=ATG9_PE=3_SV=1	2.00E-71
comp24891_c0_seq1.p1	sp|Q54XQ8|LUC7L_DICDI_Luc7-like_protein_OS=Dictyostelium_discoideum_GN=crop_PE=3_SV=1	8.00E-32
comp24892_c0_seq1.p1	sp|A6QNK1|G3ST1_BOVIN_Galactosylceramide_sulfotransferase_OS=Bos_taurus_GN=GAL3ST1_PE=2_SV=1	5.00E-13
comp24892_c0_seq1.p2		
comp24892_c0_seq3.p1	sp|A6QNK1|G3ST1_BOVIN_Galactosylceramide_sulfotransferase_OS=Bos_taurus_GN=GAL3ST1_PE=2_SV=1	5.00E-13
comp24892_c0_seq3.p2		
comp24896_c0_seq1.p1		
comp24896_c0_seq1.p2		
comp24896_c0_seq2.p1		
comp24897_c0_seq2.p1		
comp24899_c0_seq1.p1		
comp24900_c0_seq1.p1		
comp24900_c0_seq4.p1	sp|Q84J71|PP161_ARATH_Pentatricopeptide_repeat-containing_protein_At2g17670_OS=Arabidopsis_thaliana_GN=At2g17670_PE=2_SV=1	2.00E-11
comp24901_c0_seq3.p1	sp|Q9ZVJ2|AMERL_ARATH_Uncharacterized_protein_At2g38710_OS=Arabidopsis_thaliana_GN=At2g38710_PE=2_SV=1	4.00E-48
comp24902_c0_seq1.p1	sp|Q9FQ04|XRN4_ARATH_5'-3'_exoribonuclease_4_OS=Arabidopsis_thaliana_GN=XRN4_PE=2_SV=1	1.00E-124
comp24902_c0_seq1.p2		
comp24903_c0_seq1.p1		
comp24904_c0_seq1.p1	sp|Q91Y78|UCHL3_RAT_Ubiquitin_carboxyl-terminal_hydrolase_isozyme_L3_OS=Rattus_norvegicus_GN=Uchl3_PE=1_SV=1	2.00E-49
comp24904_c1_seq1.p1	sp|A0JC51|ZIC4_XENLA_Zinc_finger_protein_ZIC_4_OS=Xenopus_laevis_GN=zic4_PE=2_SV=1	2.00E-26
comp24906_c0_seq1.p1	sp|Q54NS8|AIFB_DICDI_Apoptosis-inducing_factor_homolog_B_OS=Dictyostelium_discoideum_GN=aifB_PE=3_SV=1	2.00E-37
comp24907_c0_seq1.p1	sp|Q5UP39|YR873_MIMIV_Putative_ankyrin_repeat_protein_R873_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R873_PE=4_SV=1	4.00E-21
comp24907_c0_seq2.p1	sp|Q5UP39|YR873_MIMIV_Putative_ankyrin_repeat_protein_R873_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R873_PE=4_SV=1	2.00E-23
comp24912_c0_seq1.p1		
comp24913_c0_seq1.p1		
comp24914_c0_seq1.p1		

comp25169_c0_seq1.p1	sp|Q0V4H8|FCJ1_PHANO_Formation_of_crista_junctions_protein_1_OS=Phaeosphaeria_nodorum_(strain_SN15_/_ATCC_MYA-4574_/_FGSC_10173)_GN=FCJ1_PE=3_SV=2	9.00E-20
comp25169_c0_seq2.p1		
comp25170_c0_seq2.p1	sp|O48721|HEM4_ARATH_Uroporphyrinogen-III_synthase,_chloroplastic_OS=Arabidopsis_thaliana_GN=UROS_PE=2_SV=2	1.00E-48
comp25171_c0_seq1.p1	sp|P35270|SPRE_HUMAN_Sepiapterin_reductase_OS=Homo_sapiens_GN=SPR_PE=1_SV=1	5.00E-32
comp25171_c0_seq1.p2	sp|Q9KUX9|DUSA_VIBCH_tRNA-dihydrouridine_synthase_A_OS=Vibrio_cholerae_GN=dusA_PE=3_SV=1	6.00E-60
comp25172_c0_seq1.p1	sp|A8GP89|RL20_RICAH_50S_ribosomal_protein_L20_OS=Rickettsia_akari_(strain_Hartford)_GN=rplT_PE=3_SV=1	2.00E-32
comp25172_c0_seq2.p1	sp|B3CRZ0|RL20_ORITI_50S_ribosomal_protein_L20_OS=Orientia_tsutsugamushi_(strain_Ikeda)_GN=rplT_PE=3_SV=1	5.00E-13
comp25173_c0_seq2.p1		
comp25173_c0_seq2.p2		
comp25175_c0_seq3.p1	sp|Q28E13|MFSD5_XENTR_Major_facilitator_superfamily_domain-containing_protein_5_OS=Xenopus_tropicalis_GN=mfsd5_PE=2_SV=1	4.00E-39
comp25176_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	3.00E-23
comp25178_c0_seq2.p1		
comp25180_c0_seq1.p1		
comp25181_c0_seq1.p1	sp|B1XM04|IF3_SYNP2_Translation_initiation_factor_IF-3_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=infC_PE=3_SV=1	2.00E-43
comp25183_c0_seq1.p1	sp|B8G643|PANC_CHLAD_Pantothenate_synthetase_OS=Chloroflexus_aggregans_(strain_MD-66_/_DSM_9485)_GN=panC_PE=3_SV=1	5.00E-48
comp25183_c0_seq2.p1	sp|B8G643|PANC_CHLAD_Pantothenate_synthetase_OS=Chloroflexus_aggregans_(strain_MD-66_/_DSM_9485)_GN=panC_PE=3_SV=1	3.00E-88
comp25184_c0_seq1.p1	sp|Q2KID6|PLRG1_BOVIN_Pleiotropic_regulator_1_OS=Bos_taurus_GN=PLRG1_PE=2_SV=1	3.00E-155
comp25187_c0_seq1.p1	sp|Q8BMJ2|SYLC_MOUSE_Leucine--tRNA_ligase,_cytoplasmic_OS=Mus_musculus_GN=Lars_PE=2_SV=2	0
comp25187_c0_seq2.p1		
comp25188_c0_seq1.p1	sp|P09099|XYLB_ECOLI_Xylulose_kinase_OS=Escherichia_coli_(strain_K12)_GN=xylB_PE=1_SV=1	6.00E-56
comp25189_c0_seq3.p1		
comp25191_c0_seq1.p1		
comp25193_c0_seq1.p1	sp|Q54L40|SAE2_DICDI_SUMO-activating_enzyme_subunit_2_OS=Dictyostelium_discoideum_GN=uba2_PE=3_SV=1	1.00E-119
comp25194_c0_seq1.p1	sp|Q9SR00|PP213_ARATH_Pentatricopeptide_repeat-containing_protein_At3g04760,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g04760_PE=2_SV=1	2.00E-35
comp25194_c0_seq1.p2	sp|Q9CAK8|ISPF_ARATH_2-C-methyl-D-erythritol_2,4-cyclodiphosphate_synthase,_chloroplastic_OS=Arabidopsis_thaliana_GN=ISPF_PE=1_SV=1	3.00E-61
comp25196_c0_seq1.p1	sp|Q8R753|KPRS_THETN_Ribose-phosphate_pyrophosphokinase_OS=Thermoanaerobacter_tengcongensis_(strain_DSM_15242_/_JCM_11007_/_NBRC_100824_/_MB4)_GN=prs_PE=3_SV=1	5.00E-51
comp25196_c0_seq2.p1		
comp25197_c0_seq1.p1		
comp25198_c0_seq1.p1		
comp252_c0_seq1.p1	sp|Q8LQJ8|FTSH5_ORYSJ_ATP-dependent_zinc_metalloprotease_FTSH_5,_mitochondrial_OS=Oryza_sativa_subsp._japonica_GN=FTSH5_PE=3_SV=1	1.00E-42
comp25201_c0_seq1.p1		
comp25204_c0_seq2.p1	sp|P0A0E9|RELA_STAAW_GTP_pyrophosphokinase_OS=Staphylococcus_aureus_(strain_MW2)_GN=relA_PE=3_SV=1	1.00E-37
comp25205_c0_seq1.p1		
comp25206_c0_seq1.p1	sp|Q9HW09|PANE_PSEAE_Probable_2-dehydropantoate_2-reductase_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=panE_PE=3_SV=1	3.00E-36
comp25206_c0_seq1.p2	sp|Q8ETW2|IF1_OCEIH_Translation_initiation_factor_IF-1_OS=Oceanobacillus_iheyensis_(strain_DSM_14371_/_JCM_11309_/_KCTC_3954_/_HTE831)_GN=infA_PE=3_SV=1	3.00E-26
comp25206_c0_seq3.p1	sp|Q9HW09|PANE_PSEAE_Probable_2-dehydropantoate_2-reductase_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=panE_PE=3_SV=1	3.00E-36
comp25206_c0_seq3.p2	sp|Q8ETW2|IF1_OCEIH_Translation_initiation_factor_IF-1_OS=Oceanobacillus_iheyensis_(strain_DSM_14371_/_JCM_11309_/_KCTC_3954_/_HTE831)_GN=infA_PE=3_SV=1	3.00E-26
comp25207_c0_seq1.p1	sp|Q9DCM0|ETHE1_MOUSE_Protein_ETHE1,_mitochondrial_OS=Mus_musculus_GN=Ethe1_PE=1_SV=2	6.00E-95
comp25208_c0_seq1.p1		
comp25208_c0_seq2.p1		
comp25208_c0_seq3.p1		
comp25208_c0_seq4.p1		
comp25209_c0_seq1.p1	sp|Q6P7N1|MAK16_XENTR_Protein_MAK16_homolog_OS=Xenopus_tropicalis_GN=mak16_PE=2_SV=1	2.00E-72
comp25209_c0_seq2.p2		
comp25210_c0_seq1.p1	sp|Q9M0Z3|KEA3_ARATH_K(+)_efflux_antiporter_3,_chloroplastic_OS=Arabidopsis_thaliana_GN=KEA3_PE=1_SV=2	3.00E-139
comp25211_c0_seq1.p1		
comp25213_c0_seq1.p1		
comp25214_c0_seq1.p1	sp|O07631|TYPA_BACSU_GTP-binding_protein_TypA/BipA_homolog_OS=Bacillus_subtilis_GN=typA_PE=3_SV=1	2.00E-155
comp25215_c0_seq1.p1		
comp25215_c0_seq2.p1		
comp25216_c0_seq1.p1		
comp25217_c0_seq1.p1	sp|Q9SFU0|SC24A_ARATH_Protein_transport_protein_Sec24-like_At3g07100_OS=Arabidopsis_thaliana_GN=At3g07100_PE=1_SV=2	7.00E-112
comp25217_c0_seq3.p1	sp|Q9SFU0|SC24A_ARATH_Protein_transport_protein_Sec24-like_At3g07100_OS=Arabidopsis_thaliana_GN=At3g07100_PE=1_SV=2	1.00E-27
comp25218_c0_seq1.p1		
comp25220_c0_seq1.p1	sp|B9A1H3|TRXR1_EMIHU_Thioredoxin_reductase_SEP1_OS=Emiliania_huxleyi_GN=SEP1_PE=1_SV=1	1.00E-176
comp25225_c0_seq1.p1	sp|O50606|FPG_THET8_Formamidopyrimidine-DNA_glycosylase_OS=Thermus_thermophilus_(strain_HB8_/_ATCC_27634_/_DSM_579)_GN=mutM_PE=1_SV=3	3.00E-21
comp25226_c0_seq1.p1	sp|Q7XWS7|FH12_ORYSJ_Formin-like_protein_12_OS=Oryza_sativa_subsp._japonica_GN=FH12_PE=3_SV=3	4.00E-20
comp25226_c0_seq2.p1		
comp25229_c0_seq1.p1	sp|Q93WI0|STR12_ARATH_Rhodanese-like/PpiC_domain-containing_protein_12_OS=Arabidopsis_thaliana_GN=At5g19370_PE=2_SV=1	2.00E-39
comp25231_c0_seq1.p1		
comp25231_c0_seq1.p2		
comp25232_c0_seq1.p1	sp|P45951|ARP_ARATH_Apurinic_endonuclease-redox_protein_OS=Arabidopsis_thaliana_GN=ARP_PE=2_SV=2	3.00E-54
comp25233_c0_seq1.p1		
comp25234_c0_seq2.p2		
comp25235_c1_seq1.p1	sp|P04825|AMPN_ECOLI_Aminopeptidase_N_OS=Escherichia_coli_(strain_K12)_GN=pepN_PE=1_SV=2	0
comp25236_c0_seq1.p2	sp|Q66HG8|RED_RAT_Protein_Red_OS=Rattus_norvegicus_GN=Ik_PE=1_SV=1	3.00E-11
comp25236_c0_seq2.p1		
comp25238_c0_seq1.p1	sp|Q9FPT1|UBP12_ARATH_Ubiquitin_carboxyl-terminal_hydrolase_12_OS=Arabidopsis_thaliana_GN=UBP12_PE=1_SV=2	4.00E-39
comp25239_c0_seq2.p1		
comp25239_c0_seq2.p2		
comp25241_c0_seq1.p1	sp|Q554J3|FKBP1_DICDI_FK506-binding_protein_1_OS=Dictyostelium_discoideum_GN=fkbp1_PE=3_SV=1	8.00E-29
comp25243_c0_seq1.p2		
comp25243_c0_seq2.p1		
comp25243_c0_seq3.p1		
comp25244_c0_seq1.p1	sp|A0LV27|IF2_ACIC1_Translation_initiation_factor_IF-2_OS=Acidothermus_cellulolyticus_(strain_ATCC_43068_/_11B)_GN=infB_PE=3_SV=1	1.00E-24
comp25245_c0_seq3.p1	sp|B1ZB18|RUTD_METPB_Putative_aminoacrylate_hydrolase_RutD_OS=Methylobacterium_populi_(strain_ATCC_BAA-705_/_NCIMB_13946_/_BJ001)_GN=rutD_PE=3_SV=1	4.00E-15
comp25246_c0_seq2.p1		
comp25247_c0_seq1.p1	sp|P29495|PFP_PROFR_Pyrophosphate--fructose_6-phosphate_1-phosphotransferase_OS=Propionibacterium_freudenreichii_subsp._shermanii_GN=pfp_PE=1_SV=2	1.00E-33
comp25249_c0_seq1.p1		
comp25249_c0_seq2.p3		
comp2525_c0_seq2.p1		
comp25250_c0_seq2.p1		
comp25250_c0_seq2.p2		
comp25252_c0_seq2.p1	sp|Q21890|YF64_CAEEL_Uncharacterized_protein_R102.4_OS=Caenorhabditis_elegans_GN=R102.4_PE=2_SV=3	3.00E-84
comp25252_c0_seq2.p3		
comp25253_c1_seq1.p1		
comp25254_c0_seq1.p1		
comp25256_c0_seq1.p1	sp|Q8LPJ4|AB2E_ARATH_ABC_transporter_E_family_member_2_OS=Arabidopsis_thaliana_GN=ABCE2_PE=2_SV=1	0
comp25256_c0_seq1.p5		
comp25256_c1_seq1.p1	sp|Q54LP3|DPM1_DICDI_Dolichol-phosphate_mannosyltransferase_OS=Dictyostelium_discoideum_GN=dpm1_PE=3_SV=1	5.00E-100
comp25257_c0_seq2.p1		
comp25260_c0_seq1.p3	sp|P35130|UBC2_MEDSA_Ubiquitin-conjugating_enzyme_E2_2_OS=Medicago_sativa_GN=UBC2_PE=2_SV=1	2.00E-70
comp25261_c0_seq1.p1		
comp25261_c0_seq2.p1		
comp25261_c0_seq3.p1		
comp25264_c0_seq1.p1		
comp25265_c0_seq1.p1	sp|Q6IQT4|CSN2_DANRE_COP9_signalosome_complex_subunit_2_OS=Danio_rerio_GN=cops2_PE=2_SV=1	4.00E-143
comp25266_c0_seq1.p1	sp|P40228|CSK2B_ARATH_Casein_kinase_II_subunit_beta_OS=Arabidopsis_thaliana_GN=CKB1_PE=1_SV=1	2.00E-81
comp25267_c0_seq2.p1		
comp25267_c0_seq2.p2	sp|Q5HZT9|DJC25_XENTR_DnaJ_homolog_subfamily_C_member_25_OS=Xenopus_tropicalis_GN=dnajc25_PE=2_SV=1	7.00E-26
comp25267_c0_seq2.p3		
comp25269_c0_seq1.p1		
comp25269_c0_seq2.p1		
comp25270_c0_seq1.p1		
comp25270_c0_seq1.p2		
comp25270_c0_seq3.p1	sp|Q9SIC9|PP178_ARATH_Pentatricopeptide_repeat-containing_protein_At2g31400,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g31400_PE=2_SV=1	8.00E-25
comp25271_c0_seq1.p1		
comp25271_c0_seq2.p1		
comp25272_c0_seq1.p2		
comp25272_c0_seq2.p1		
comp25272_c0_seq3.p3		
comp25272_c0_seq4.p1		
comp25273_c0_seq1.p1	sp|Q03066|RPSC_NOSS1_RNA_polymerase_sigma-C_factor_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=sigC_PE=3_SV=2	1.00E-18
comp25274_c0_seq1.p1	sp|Q9UHL4|DPP2_HUMAN_Dipeptidyl_peptidase_2_OS=Homo_sapiens_GN=DPP7_PE=1_SV=3	4.00E-45
comp25274_c1_seq1.p1	sp|Q7TMR0|PCP_MOUSE_Lysosomal_Pro-X_carboxypeptidase_OS=Mus_musculus_GN=Prcp_PE=2_SV=2	5.00E-39
comp25274_c1_seq2.p1	sp|Q7TMR0|PCP_MOUSE_Lysosomal_Pro-X_carboxypeptidase_OS=Mus_musculus_GN=Prcp_PE=2_SV=2	4.00E-32
comp25275_c0_seq2.p1	sp|Q1JP75|DCXR_BOVIN_L-xylulose_reductase_OS=Bos_taurus_GN=DCXR_PE=2_SV=1	3.00E-36
comp25276_c0_seq1.p1		
comp25276_c0_seq2.p1		
comp25277_c0_seq1.p2		
comp25279_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	2.00E-24
comp25281_c0_seq1.p1		
comp25281_c0_seq1.p3		
comp25281_c0_seq2.p1		
comp25284_c0_seq1.p1		
comp25284_c0_seq2.p1		
comp25285_c0_seq1.p1	sp|Q3YWM3|HSLO_SHISS_33_kDa_chaperonin_OS=Shigella_sonnei_(strain_Ss046)_GN=hslO_PE=3_SV=2	3.00E-114
comp25287_c0_seq1.p1	sp|Q96LW4|CC111_HUMAN_Coiled-coil_domain-containing_protein_111_OS=Homo_sapiens_GN=CCDC111_PE=1_SV=2	3.00E-41
comp25287_c0_seq2.p1		
comp25288_c0_seq1.p1	sp|Q3EAQ5|PTR36_ARATH_Probable_peptide/nitrate_transporter_At3g43790_OS=Arabidopsis_thaliana_GN=ZIFL2_PE=2_SV=2	6.00E-41
comp2529_c0_seq1.p1	sp|P77495|PRPE_ECOLI_Propionate--CoA_ligase_OS=Escherichia_coli_(strain_K12)_GN=prpE_PE=3_SV=1	8.00E-130
comp25293_c0_seq2.p1		
comp25295_c0_seq4.p3	sp|Q5BKI6|ANKR1_XENTR_Ankyrin_repeat_domain-containing_protein_1_OS=Xenopus_tropicalis_GN=ankrd1_PE=2_SV=1	3.00E-11
comp25296_c0_seq1.p1		
comp25296_c0_seq2.p2		
comp25298_c0_seq1.p1		
comp25298_c1_seq1.p2		
comp25298_c2_seq1.p1		
comp25301_c0_seq2.p1		
comp25301_c0_seq3.p2		
comp25303_c0_seq1.p2	sp|P36672|PTTBC_ECOLI_PTS_system_trehalose-specific_EIIBC_component_OS=Escherichia_coli_(strain_K12)_GN=treB_PE=1_SV=4	5.00E-80
comp25304_c0_seq1.p1		
comp25304_c0_seq2.p1		
comp25304_c0_seq3.p2		
comp25307_c0_seq1.p1		
comp25307_c0_seq1.p2		
comp25310_c0_seq1.p1		
comp25313_c0_seq1.p1	sp|O31570|YFHB_BACSU_Uncharacterized_isomerase_yfhB_OS=Bacillus_subtilis_GN=yfhB_PE=3_SV=1	2.00E-19
comp25316_c0_seq2.p1		
comp25316_c0_seq5.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	4.00E-20
comp25317_c0_seq3.p1	sp|P40228|CSK2B_ARATH_Casein_kinase_II_subunit_beta_OS=Arabidopsis_thaliana_GN=CKB1_PE=1_SV=1	1.00E-51
comp25317_c0_seq5.p1		
comp25319_c0_seq1.p1		
comp25326_c0_seq2.p1	sp|O48651|ERG1_PANGI_Squalene_monooxygenase_OS=Panax_ginseng_PE=2_SV=1	1.00E-91
comp25328_c0_seq1.p1	sp|Q5REC9|RAB8B_PONAB_Ras-related_protein_Rab-8B_OS=Pongo_abelii_GN=RAB8B_PE=2_SV=1	2.00E-59
comp25329_c0_seq1.p2		
comp25329_c0_seq2.p1		
comp25331_c0_seq1.p2		
comp25331_c0_seq3.p2		
comp25331_c0_seq4.p1		
comp25340_c0_seq1.p1		
comp25346_c0_seq2.p1		
comp25347_c0_seq1.p1		
comp25348_c0_seq1.p1	sp|Q5ZML3|SRSF1_CHICK_Serine/arginine-rich_splicing_factor_1_OS=Gallus_gallus_GN=SRSF1_PE=1_SV=3	4.00E-37
comp25348_c0_seq1.p3		
comp25348_c0_seq2.p1	sp|Q5ZML3|SRSF1_CHICK_Serine/arginine-rich_splicing_factor_1_OS=Gallus_gallus_GN=SRSF1_PE=1_SV=3	3.00E-36
comp25348_c0_seq2.p2		
comp25348_c0_seq3.p1	sp|Q5ZML3|SRSF1_CHICK_Serine/arginine-rich_splicing_factor_1_OS=Gallus_gallus_GN=SRSF1_PE=1_SV=3	4.00E-37
comp25348_c0_seq4.p1	sp|Q5ZML3|SRSF1_CHICK_Serine/arginine-rich_splicing_factor_1_OS=Gallus_gallus_GN=SRSF1_PE=1_SV=3	3.00E-36
comp25354_c0_seq1.p1	sp|P26369|U2AF2_MOUSE_Splicing_factor_U2AF_65_kDa_subunit_OS=Mus_musculus_GN=U2af2_PE=1_SV=3	8.00E-14
comp25354_c0_seq1.p3	sp|P26368|U2AF2_HUMAN_Splicing_factor_U2AF_65_kDa_subunit_OS=Homo_sapiens_GN=U2AF2_PE=1_SV=4	1.00E-12
comp25354_c0_seq1.p8		
comp25354_c0_seq2.p1	sp|P26369|U2AF2_MOUSE_Splicing_factor_U2AF_65_kDa_subunit_OS=Mus_musculus_GN=U2af2_PE=1_SV=3	8.00E-14
comp25354_c0_seq2.p3	sp|P26368|U2AF2_HUMAN_Splicing_factor_U2AF_65_kDa_subunit_OS=Homo_sapiens_GN=U2AF2_PE=1_SV=4	1.00E-12
comp25354_c0_seq2.p9		
comp25354_c0_seq3.p1	sp|P26369|U2AF2_MOUSE_Splicing_factor_U2AF_65_kDa_subunit_OS=Mus_musculus_GN=U2af2_PE=1_SV=3	8.00E-14
comp25354_c0_seq3.p3	sp|P26368|U2AF2_HUMAN_Splicing_factor_U2AF_65_kDa_subunit_OS=Homo_sapiens_GN=U2AF2_PE=1_SV=4	2.00E-12
comp25354_c0_seq4.p1	sp|P26369|U2AF2_MOUSE_Splicing_factor_U2AF_65_kDa_subunit_OS=Mus_musculus_GN=U2af2_PE=1_SV=3	6.00E-14
comp25354_c0_seq5.p1	sp|P26369|U2AF2_MOUSE_Splicing_factor_U2AF_65_kDa_subunit_OS=Mus_musculus_GN=U2af2_PE=1_SV=3	8.00E-14
comp25354_c0_seq5.p3	sp|P26368|U2AF2_HUMAN_Splicing_factor_U2AF_65_kDa_subunit_OS=Homo_sapiens_GN=U2AF2_PE=1_SV=4	2.00E-12
comp25354_c0_seq6.p1	sp|P26368|U2AF2_HUMAN_Splicing_factor_U2AF_65_kDa_subunit_OS=Homo_sapiens_GN=U2AF2_PE=1_SV=4	3.00E-32
comp25355_c0_seq2.p1		
comp25356_c0_seq1.p1	sp|Q93VR3|GME_ARATH_GDP-mannose_3,5-epimerase_OS=Arabidopsis_thaliana_GN=At5g28840_PE=1_SV=1	1.00E-150
comp25359_c0_seq1.p1		
comp25363_c0_seq1.p1	sp|A3KPW7|PTAR1_DANRE_Protein_prenyltransferase_alpha_subunit_repeat-containing_protein_1_OS=Danio_rerio_GN=ptar1_PE=2_SV=1	1.00E-27
comp25363_c0_seq1.p2	sp|Q84XB6|PSBU_PHATR_Photosystem_II_12_kDa_extrinsic_protein,_chloroplastic_OS=Phaeodactylum_tricornutum_GN=psbU_PE=3_SV=1	4.00E-31
comp25364_c0_seq2.p4	sp|P25387|GBLP_CHLRE_Guanine_nucleotide-binding_protein_subunit_beta-like_protein_OS=Chlamydomonas_reinhardtii_GN=GBLP_PE=2_SV=1	4.00E-46
comp25364_c0_seq5.p4	sp|P25387|GBLP_CHLRE_Guanine_nucleotide-binding_protein_subunit_beta-like_protein_OS=Chlamydomonas_reinhardtii_GN=GBLP_PE=2_SV=1	4.00E-46
comp25366_c0_seq2.p1	sp|Q38920|FNTB_ARATH_Protein_farnesyltransferase_subunit_beta_OS=Arabidopsis_thaliana_GN=FTB_PE=1_SV=3	4.00E-98
comp25367_c0_seq1.p1		
comp25367_c0_seq2.p1		
comp25367_c0_seq3.p1		
comp25368_c0_seq2.p1	sp|P0C1J3|FKBP1_RHIOR_FK506-binding_protein_1_OS=Rhizopus_oryzae_GN=FKBP1_PE=3_SV=1	8.00E-42
comp25370_c0_seq3.p1		
comp25370_c0_seq4.p1		
comp25370_c0_seq4.p2		
comp25371_c0_seq1.p1	sp|P22105|TENX_HUMAN_Tenascin-X_OS=Homo_sapiens_GN=TNXB_PE=1_SV=3	1.00E-19
comp25372_c0_seq1.p1	sp|Q6P2Y1|PAF1_XENTR_RNA_polymerase_II-associated_factor_1_homolog_OS=Xenopus_tropicalis_GN=paf1_PE=2_SV=1	1.00E-14
comp25375_c0_seq1.p1	sp|Q39593|SAC1_CHLRE_Putative_sulfur_deprivation_response_regulator_OS=Chlamydomonas_reinhardtii_GN=SAC1_PE=2_SV=1	1.00E-18
comp25384_c0_seq2.p1		
comp25384_c0_seq3.p1		
comp25384_c0_seq4.p1		
comp25387_c1_seq2.p1		
comp25387_c1_seq3.p1	sp|Q87AD4|Y1892_XYLFT_UPF0394_membrane_protein_PD_1892_OS=Xylella_fastidiosa_(strain_Temecula1_/_ATCC_700964)_GN=PD_1892_PE=3_SV=1	2.00E-12
comp25389_c0_seq1.p1		
comp25389_c1_seq1.p1		
comp25389_c1_seq2.p1		
comp25389_c1_seq3.p1		
comp25389_c1_seq4.p1		
comp25392_c0_seq1.p1		
comp25392_c0_seq2.p1	sp|Q55B06|SPXS1_DICDI_SPX_and_EXS_domain-containing_protein_1_OS=Dictyostelium_discoideum_GN=DDB_G0271664_PE=3_SV=2	3.00E-42
comp25394_c0_seq1.p1		
comp25394_c0_seq2.p1		
comp25395_c1_seq1.p1		
comp25395_c1_seq2.p1		
comp25398_c0_seq2.p1	sp|P33625|TBA_EUGGR_Tubulin_alpha_chain_OS=Euglena_gracilis_GN=TUBA_PE=2_SV=1	0
comp25399_c0_seq1.p1	sp|P55201|BRPF1_HUMAN_Peregrin_OS=Homo_sapiens_GN=BRPF1_PE=1_SV=2	5.00E-15
comp25399_c1_seq1.p1		
comp25400_c0_seq2.p2		
comp25400_c1_seq3.p1		
comp25402_c0_seq1.p2		
comp25403_c0_seq1.p1		
comp25406_c0_seq1.p1		
comp25407_c0_seq1.p1		
comp25409_c0_seq1.p1		
comp25409_c0_seq1.p2	sp|P45524|YHET_ECOLI_Putative_esterase_YheT_OS=Escherichia_coli_(strain_K12)_GN=yheT_PE=3_SV=1	2.00E-30
comp25413_c0_seq1.p1		
comp25414_c0_seq1.p1		
comp25420_c0_seq1.p1	sp|Q9FJ55|CIPKJ_ARATH_CBL-interacting_serine/threonine-protein_kinase_19_OS=Arabidopsis_thaliana_GN=CIPK19_PE=2_SV=1	9.00E-21
comp25421_c0_seq1.p1	sp|Q99PK0|SYF1_RAT_Pre-mRNA-splicing_factor_SYF1_OS=Rattus_norvegicus_GN=Xab2_PE=2_SV=1	0
comp25422_c0_seq1.p1		
comp25423_c0_seq1.p1		
comp25428_c0_seq1.p1		
comp25428_c0_seq4.p1		
comp25428_c0_seq4.p3		
comp25435_c0_seq1.p1	sp|Q28IL6|RL22_XENTR_60S_ribosomal_protein_L22_OS=Xenopus_tropicalis_GN=rpl22_PE=2_SV=3	9.00E-41
comp25437_c0_seq2.p1		
comp25441_c0_seq1.p1		
comp25441_c0_seq2.p1	sp|O69707|Y3740_MYCTU_Putative_diacylglycerol_O-acyltransferase_Rv3740c/MT3848_OS=Mycobacterium_tuberculosis_GN=Rv3740c_PE=2_SV=1	3.00E-11
comp25443_c0_seq1.p2		
comp25443_c0_seq2.p2		
comp25443_c1_seq1.p1	sp|Q0WPT7|Y2104_ARATH_Uncharacterized_methyltransferase_At2g41040,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g41040_PE=1_SV=1	3.00E-36
comp25445_c0_seq1.p1		
comp25446_c0_seq1.p1	sp|Q7PC79|XPOT_ARATH_Exportin-T_OS=Arabidopsis_thaliana_GN=PSD_PE=2_SV=1	3.00E-48
comp25448_c0_seq1.p1		
comp25448_c0_seq2.p1		
comp25451_c0_seq1.p1		
comp25451_c0_seq2.p1		
comp25454_c0_seq1.p1	sp|P32567|PAH1_YEAST_Phosphatidic_acid_phosphohydrolase_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PAH1_PE=1_SV=1	1.00E-21
comp25456_c0_seq2.p2		
comp25457_c0_seq1.p2		
comp2546_c0_seq1.p1	sp|P0AFP0|YADS_ECOLI_UPF0126_inner_membrane_protein_yadS_OS=Escherichia_coli_(strain_K12)_GN=yadS_PE=1_SV=1	2.00E-61
comp25460_c0_seq1.p1		
comp25462_c0_seq2.p1		
comp25462_c0_seq4.p1	sp|Q55909|Y305_SYNY3_TVP38/TMEM64_family_membrane_protein_slr0305_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0305_PE=3_SV=1	9.00E-14
comp25463_c0_seq4.p1		
comp25464_c0_seq1.p1		
comp25466_c0_seq1.p1	sp|Q90YW0|RL9_ICTPU_60S_ribosomal_protein_L9_OS=Ictalurus_punctatus_GN=rpl9_PE=2_SV=1	3.00E-74
comp25468_c0_seq1.p1	sp|B3EN99|GPMA_CHLPB_2,3-bisphosphoglycerate-dependent_phosphoglycerate_mutase_OS=Chlorobium_phaeobacteroides_(strain_BS1)_GN=gpmA_PE=3_SV=1	1.00E-93
comp25469_c0_seq2.p1	sp|Q69TY4|PR2E1_ORYSJ_Peroxiredoxin-2E-1,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=PRXIIE-1_PE=2_SV=1	3.00E-34
comp25470_c0_seq1.p1		
comp25471_c1_seq1.p1		
comp25475_c0_seq1.p1		
comp25477_c1_seq1.p2		
comp25478_c0_seq1.p1	sp|Q6P1R4|DUS1L_HUMAN_tRNA-dihydrouridine(16/17)_synthase_[NAD(P)(+)]-like_OS=Homo_sapiens_GN=DUS1L_PE=1_SV=1	3.00E-24
comp25478_c0_seq1.p2	sp|P53759|DUS1_YEAST_tRNA-dihydrouridine(16/17)_synthase_[NAD(P)(+)]_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=DUS1_PE=1_SV=1	9.00E-51
comp25478_c0_seq3.p1	sp|Q8K582|DUS1L_RAT_tRNA-dihydrouridine(16/17)_synthase_[NAD(P)(+)]-like_OS=Rattus_norvegicus_GN=Dus1l_PE=2_SV=1	2.00E-78
comp25488_c0_seq1.p2		
comp25488_c0_seq2.p1		
comp25489_c0_seq1.p2		
comp25491_c0_seq1.p1		
comp25492_c0_seq1.p1		
comp25493_c1_seq1.p1	sp|P27968|NIA7_HORVU_Nitrate_reductase_[NAD(P)H]_OS=Hordeum_vulgare_GN=NAR-7_PE=2_SV=1	8.00E-12
comp25494_c0_seq1.p1	sp|B4KD90|NMDA1_DROMO_Glutamate_[NMDA]_receptor_subunit_1_OS=Drosophila_mojavensis_GN=Nmdar1_PE=3_SV=1	3.00E-12
comp25495_c0_seq1.p1		
comp25498_c0_seq1.p1	sp|P26300|ENO_SOLLC_Enolase_OS=Solanum_lycopersicum_GN=PGH1_PE=2_SV=1	0
comp25503_c0_seq1.p1		
comp25505_c0_seq1.p1	sp|P19666|SODF_TETPY_Superoxide_dismutase_[Fe]_OS=Tetrahymena_pyriformis_PE=1_SV=1	1.00E-51
comp25506_c0_seq1.p1		
comp25506_c0_seq2.p1		
comp25507_c0_seq1.p1		
comp25507_c0_seq2.p1		
comp25511_c0_seq1.p1	sp|Q07307|UAPA_EMENI_Uric_acid-xanthine_permease_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=uapA_PE=1_SV=3	1.00E-133
comp25511_c0_seq3.p1	sp|Q07307|UAPA_EMENI_Uric_acid-xanthine_permease_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=uapA_PE=1_SV=3	7.00E-77
comp25511_c0_seq5.p1	sp|Q07307|UAPA_EMENI_Uric_acid-xanthine_permease_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=uapA_PE=1_SV=3	6.00E-95
comp25512_c0_seq2.p1		
comp25514_c0_seq1.p1		
comp25516_c0_seq1.p1		
comp25517_c0_seq2.p1		
comp25517_c0_seq3.p1		
comp25518_c0_seq3.p1	sp|Q9FV71|E2FB_ARATH_Transcription_factor_E2FB_OS=Arabidopsis_thaliana_GN=E2FB_PE=1_SV=1	2.00E-47
comp25528_c0_seq1.p1		
comp25528_c0_seq2.p1		
comp25529_c0_seq1.p1		
comp25532_c0_seq1.p1		
comp25534_c0_seq1.p1	sp|Q497B0|NIT2_RAT_Omega-amidase_NIT2_OS=Rattus_norvegicus_GN=Nit2_PE=1_SV=1	7.00E-85
comp25534_c0_seq3.p1	sp|Q497B0|NIT2_RAT_Omega-amidase_NIT2_OS=Rattus_norvegicus_GN=Nit2_PE=1_SV=1	3.00E-77
comp25535_c0_seq1.p1		
comp25537_c0_seq3.p1		
comp25539_c0_seq1.p2	sp|Q09818|YAC4_SCHPO_Putative_general_negative_regulator_of_transcription_C16C9.04c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC16C9.04c_PE=2_SV=1	7.00E-24
comp25539_c0_seq3.p1	sp|P34909|NOT4_YEAST_General_negative_regulator_of_transcription_subunit_4_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=MOT2_PE=1_SV=1	1.00E-46
comp25541_c0_seq1.p1		
comp25546_c0_seq1.p1	sp|P53780|METC_ARATH_Cystathionine_beta-lyase,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g57050_PE=1_SV=1	1.00E-137
comp25548_c0_seq1.p1	sp|Q9SYU4|PEX10_ARATH_Peroxisome_biogenesis_factor_10_OS=Arabidopsis_thaliana_GN=PEX10_PE=1_SV=1	7.00E-24
comp25549_c0_seq3.p1	sp|P0DB61|HASA_STRPQ_Hyaluronan_synthase_OS=Streptococcus_pyogenes_serotype_M3_(strain_SSI-1)_GN=hasA_PE=3_SV=1	2.00E-11
comp25551_c0_seq1.p1	sp|Q9SE42|RPE1_ORYSJ_Ribulose-phosphate_3-epimerase,_cytoplasmic_isoform_OS=Oryza_sativa_subsp._japonica_GN=Os09g0505700_PE=1_SV=1	1.00E-76
comp25555_c0_seq2.p1		
comp25557_c0_seq1.p1	sp|Q8MZS4|PHYSA_PHYPO_Physarolisin_OS=Physarum_polycephalum_PE=1_SV=1	3.00E-21
comp25557_c0_seq2.p1	sp|Q8MZS4|PHYSA_PHYPO_Physarolisin_OS=Physarum_polycephalum_PE=1_SV=1	3.00E-21
comp25559_c0_seq3.p1		
comp25560_c0_seq2.p1		
comp25560_c0_seq4.p1		
comp25563_c0_seq1.p1		
comp25563_c1_seq1.p1		
comp25563_c2_seq1.p1	sp|Q7ZZ25|ATD1A_DANRE_ATPase_family_AAA_domain-containing_protein_1-A_OS=Danio_rerio_GN=atad1a_PE=2_SV=2	3.00E-49
comp25563_c2_seq2.p1	sp|Q7ZZ25|ATD1A_DANRE_ATPase_family_AAA_domain-containing_protein_1-A_OS=Danio_rerio_GN=atad1a_PE=2_SV=2	2.00E-49
comp25566_c0_seq1.p1	sp|Q6AZI2|CCD47_XENLA_Coiled-coil_domain-containing_protein_47_OS=Xenopus_laevis_GN=ccdc47_PE=2_SV=1	2.00E-23
comp25566_c0_seq2.p1	sp|Q94CC0|Y5994_ARATH_Uncharacterized_protein_At5g49945_OS=Arabidopsis_thaliana_GN=At5g49945_PE=1_SV=1	7.00E-13
comp25568_c0_seq1.p1		
comp25568_c1_seq1.p1		
comp25569_c0_seq1.p1	sp|P24280|SEC14_YEAST_SEC14_cytosolic_factor_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=SEC14_PE=1_SV=3	2.00E-15
comp25570_c0_seq1.p1		
comp25570_c0_seq2.p1		
comp25570_c0_seq4.p1		
comp25570_c0_seq5.p1		
comp25572_c0_seq2.p1		

comp25574_c0_seq1.p1				
comp25577_c0_seq1.p1	sp|P30157|TBB6_ECTVR_Tubulin_beta-6_chain_OS=Ectocarpus_variabilis_GN=TUBB6_PE=2_SV=1	4.00E-87	[illegible]	[illegible]
comp25577_c1_seq1.p1	sp|P30156|TBB5_ECTVR_Tubulin_beta-5_chain_OS=Ectocarpus_variabilis_GN=TUBB5_PE=2_SV=1	0	[illegible]	[illegible]
comp25577_c1_seq3.p1	sp|P30157|TBB6_ECTVR_Tubulin_beta-6_chain_OS=Ectocarpus_variabilis_GN=TUBB6_PE=2_SV=1	9.00E-134	[illegible]	[illegible]
comp25580_c0_seq1.p1	sp|Q9WV87|NOX1_RAT_NADPH_oxidase_1_OS=Rattus_norvegicus_GN=Nox1_PE=2_SV=1	2.00E-13	[illegible]	[illegible]
comp25586_c0_seq1.p1				
comp25586_c0_seq2.p1	sp|O88941|MOGS_RAT_Mannosyl-oligosaccharide_glucosidase_OS=Rattus_norvegicus_GN=Mogs_PE=1_SV=1	3.00E-138	[illegible]	[illegible]
comp25590_c1_seq1.p1				
comp25594_c0_seq1.p1	sp|Q8BYR1|LCMT2_MOUSE_Leucine_carboxyl_methyltransferase_2_OS=Mus_musculus_GN=Lcmt2_PE=2_SV=4	2.00E-22	[illegible]	[illegible]
comp25594_c0_seq1.p3	sp|Q60YU0|LCMT1_CAEBR_Probable_leucine_carboxyl_methyltransferase_1_OS=Caenorhabditis_briggsae_GN=CBG18087_PE=3_SV=1	8.00E-16	GO:0008168,GO:0008168,GO:0016740,GO:0032259,GO:0032259	[illegible]
comp25595_c0_seq2.p1	sp|Q99437|VATO_HUMAN_V-type_proton_ATPase_21_kDa_proteolipid_subunit_OS=Homo_sapiens_GN=ATP6V0B_PE=2_SV=1	2.00E-59	[illegible]	[illegible]
comp25595_c0_seq3.p1	sp|Q797A7|YFNA_BACSU_Uncharacterized_amino_acid_permease_YfnA_OS=Bacillus_subtilis_GN=yfnA_PE=3_SV=1	1.00E-52	[illegible]	[illegible]
comp25599_c0_seq1.p1				
comp25600_c0_seq1.p1	sp|Q5SXM8|DNLZ_HUMAN_DNL-type_zinc_finger_protein_OS=Homo_sapiens_GN=DNLZ_PE=2_SV=1	7.00E-12	GO:0005739,GO:0005739,GO:0005739,GO:0008270,GO:0046872	[illegible]
comp25602_c1_seq1.p1	sp|Q60HE9|MA2B1_MACFA_Lysosomal_alpha-mannosidase_OS=Macaca_fascicularis_GN=MAN2B1_PE=2_SV=1	3.00E-55	[illegible]	[illegible]
comp25604_c0_seq2.p1				
comp25606_c0_seq1.p1	sp|Q54GB2|CTSL2_DICDI_CTD_small_phosphatase-like_protein_2_OS=Dictyostelium_discoideum_GN=ctdspl2_PE=3_SV=1	9.00E-23	[illegible]	[illegible]
comp25609_c0_seq2.p1				
comp25609_c0_seq3.p1	sp|O15976|GNAO_MIZYE_Guanine_nucleotide-binding_protein_G(o)_subunit_alpha_OS=Mizuhopecten_yessoensis_GN=SCGOA_PE=2_SV=3	7.00E-90	[illegible]	[illegible]
comp25609_c0_seq4.p1	sp|O13055|GNAI2_ORYLA_Guanine_nucleotide-binding_protein_G(i)_subunit_alpha-2_OS=Oryzias_latipes_GN=gnai2_PE=2_SV=3	2.00E-27	[illegible]	[illegible]
comp25609_c0_seq4.p3	sp|P28052|GPA3_CAEEL_Guanine_nucleotide-binding_protein_alpha-3_subunit_OS=Caenorhabditis_elegans_GN=gpa-3_PE=2_SV=2	2.00E-53	[illegible]	[illegible]
comp25610_c0_seq1.p1	sp|Q802U2|MIO_DANRE_WD_repeat-containing_protein_mio_OS=Danio_rerio_GN=mios_PE=2_SV=1	2.00E-15	GO:0003674,GO:0005575	[illegible]
comp25610_c0_seq1.p3				
comp25612_c0_seq1.p2				
comp25612_c0_seq2.p1				
comp25614_c0_seq1.p1	sp|Q60520|SIN3A_MOUSE_Paired_amphipathic_helix_protein_Sin3a_OS=Mus_musculus_GN=Sin3a_PE=1_SV=3	2.00E-45	[illegible]	[illegible]
comp25616_c0_seq1.p1				
comp25618_c0_seq3.p1	sp|Q6FLH2|GWT1_CANGA_GPI-anchored_wall_transfer_protein_1_OS=Candida_glabrata_(strain_ATCC_2001_/_CBS_138_/_JCM_3761_/_NBRC_0622_/_NRRL_Y-65)_GN=GWT1_PE=3_SV=1	4.00E-46	[illegible]	[illegible]
comp25618_c0_seq5.p1	sp|Q873N1|GWT1_ASPFU_GPI-anchored_wall_transfer_protein_1_OS=Neosartorya_fumigata_(strain_ATCC_MYA-4609_/_Af293_/_CBS_101355_/_FGSC_A1100)_GN=gwt1_PE=3_SV=2	4.00E-62	[illegible]	[illegible]
comp25620_c0_seq1.p3				
comp25623_c0_seq1.p1	sp|Q58DG1|MYG1_BOVIN_UPF0160_protein_MYG1,_mitochondrial_OS=Bos_taurus_PE=2_SV=1	5.00E-90	[illegible]	[illegible]
comp25625_c0_seq2.p1				
comp25627_c0_seq2.p1	sp|P21158|CSGA_MYXXA_C-factor_OS=Myxococcus_xanthus_GN=csgA_PE=1_SV=1	3.00E-29	[illegible]	[illegible]
comp25627_c0_seq3.p1	sp|P21158|CSGA_MYXXA_C-factor_OS=Myxococcus_xanthus_GN=csgA_PE=1_SV=1	2.00E-18	[illegible]	[illegible]
comp25627_c0_seq4.p1	sp|P21158|CSGA_MYXXA_C-factor_OS=Myxococcus_xanthus_GN=csgA_PE=1_SV=1	2.00E-26	[illegible]	[illegible]
comp25631_c0_seq1.p1	sp|Q9JI39|ABCBA_MOUSE_ATP-binding_cassette_sub-family_B_member_10,_mitochondrial_OS=Mus_musculus_GN=Abcb10_PE=2_SV=1	3.00E-110	[illegible]	[illegible]
comp25633_c0_seq1.p1				
comp25633_c0_seq1.p3				
comp25634_c0_seq1.p1				
comp25635_c0_seq1.p1				
comp25635_c1_seq2.p1				
comp25635_c1_seq3.p1				
comp25636_c0_seq1.p1				
comp25636_c0_seq2.p2				
comp25642_c0_seq3.p1				
comp25649_c0_seq1.p1				
comp25651_c0_seq1.p2				
comp25659_c1_seq1.p1				
comp25661_c0_seq5.p1	sp|Q17ZW5|HSLO_CLOD6_33_kDa_chaperonin_OS=Clostridium_difficile_(strain_630)_GN=hslO_PE=3_SV=1	2.00E-48	[illegible]	[illegible]
comp25666_c0_seq1.p2				
comp25666_c0_seq2.p1				
comp25669_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	1.00E-18		
comp25673_c0_seq1.p1				
comp25674_c0_seq2.p1				
comp25675_c0_seq2.p1	sp|O22655|PROF4_MAIZE_Profilin-4_OS=Zea_mays_GN=PRO4_PE=1_SV=1	2.00E-22	[illegible]	[illegible]
comp25677_c0_seq1.p3				
comp25679_c1_seq1.p1				
comp25687_c0_seq3.p1				
comp25690_c0_seq1.p2	sp|P51403|RS2_CAEEL_40S_ribosomal_protein_S2_OS=Caenorhabditis_elegans_GN=rps-2_PE=2_SV=1	9.00E-74	[illegible]	[illegible]
comp25693_c0_seq2.p1	sp|Q9LQV2|RDR1_ARATH_RNA-dependent_RNA_polymerase_1_OS=Arabidopsis_thaliana_GN=RDR1_PE=2_SV=1	7.00E-44	[illegible]	[illegible]
comp25693_c0_seq2.p10				
comp25693_c0_seq2.p2	sp|Q8LHH9|SHL2_ORYSJ_Probable_RNA-dependent_RNA_polymerase_SHL2_OS=Oryza_sativa_subsp._japonica_GN=SHL2_PE=2_SV=1	6.00E-26	[illegible]	[illegible]
comp25693_c0_seq2.p4				
comp25693_c0_seq2.p9				
comp25696_c0_seq5.p1				
comp25698_c0_seq2.p1				
comp25706_c0_seq1.p1				
comp25711_c0_seq1.p1				
comp25714_c0_seq1.p1				
comp25715_c0_seq1.p1				
comp25716_c0_seq3.p1	sp|Q8N0U8|VKORL_HUMAN_Vitamin_K_epoxide_reductase_complex_subunit_1-like_protein_1_OS=Homo_sapiens_GN=VKORC1L1_PE=1_SV=2	2.00E-22	[illegible]	[illegible]
comp25719_c0_seq1.p1				
comp25719_c0_seq3.p1				
comp25720_c0_seq1.p1				
comp25721_c0_seq2.p1	sp|Q4VBT5|MKRN1_DANRE_Probable_E3_ubiquitin-protein_ligase_makorin-1_OS=Danio_rerio_GN=mkrn1_PE=2_SV=1	5.00E-31	[illegible]	[illegible]
comp25721_c0_seq7.p1	sp|Q9TT91|MKRN1_MACEU_E3_ubiquitin-protein_ligase_makorin-1_OS=Macropus_eugenii_GN=MKRN1_PE=2_SV=1	3.00E-19	[illegible]	[illegible]
comp25722_c0_seq2.p2				
comp25726_c0_seq1.p1				
comp25728_c0_seq2.p1	sp|Q96WV1|TRMB_SCHPO_tRNA_(guanine-N(7)-)-methyltransferase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=trm8_PE=2_SV=1	1.00E-71	[illegible]	[illegible]
comp25729_c0_seq2.p1				
comp25736_c0_seq1.p1				
comp25736_c0_seq2.p1				
comp25740_c0_seq1.p1				
comp25740_c0_seq2.p1				
comp25741_c0_seq1.p1	sp|O57429|UBP2_CHICK_Ubiquitin_carboxyl-terminal_hydrolase_2_OS=Gallus_gallus_GN=USP2_PE=2_SV=1	4.00E-22	[illegible]	[illegible]
comp25746_c0_seq1.p1				
comp25748_c0_seq2.p1	sp|O23249|CKS1_ARATH_Cyclin-dependent_kinases_regulatory_subunit_1_OS=Arabidopsis_thaliana_GN=CKS1_PE=1_SV=1	4.00E-34	[illegible]	[illegible]
comp25749_c0_seq1.p1				
comp25751_c0_seq2.p1				
comp25754_c1_seq1.p1				
comp25755_c0_seq1.p1				
comp25757_c0_seq1.p1				
comp25758_c0_seq1.p1	sp|A0JMH0|ASPH2_DANRE_Aspartate_beta-hydroxylase_domain-containing_protein_2_OS=Danio_rerio_GN=asphd2_PE=2_SV=1	4.00E-28	[illegible]	[illegible]
comp25760_c0_seq1.p1	sp|Q5FWM8|GP180_XENLA_Integral_membrane_protein_GPR180_OS=Xenopus_laevis_GN=gpr180_PE=2_SV=1	1.00E-18	[illegible]	[illegible]
comp25764_c0_seq1.p1	sp|Q9QZB7|ARP10_MOUSE_Actin-related_protein_10_OS=Mus_musculus_GN=Actr10_PE=1_SV=2	3.00E-18	[illegible]	[illegible]
comp25764_c0_seq3.p1	sp|Q3ZBD2|ARP10_BOVIN_Actin-related_protein_10_OS=Bos_taurus_GN=ACTR10_PE=2_SV=1	2.00E-26	[illegible]	[illegible]
comp25765_c0_seq1.p1	sp|Q5RAD5|RTF1_PONAB_RNA_polymerase-associated_protein_RTF1_homolog_(Fragment)_OS=Pongo_abelii_GN=RTF1_PE=2_SV=2	1.00E-16	[illegible]	[illegible]
comp25766_c0_seq2.p1				
comp25773_c0_seq1.p1				
comp25774_c0_seq2.p1	sp|Q5BBY1|HAS1_EMENI_ATP-dependent_RNA_helicase_has1_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=has1_PE=3_SV=1	0	[illegible]	[illegible]
comp25775_c0_seq1.p1				
comp25775_c0_seq2.p2				
comp25786_c0_seq1.p1	sp|Q7XJ02|APX7_ORYSJ_Probable_L-ascorbate_peroxidase_7,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=APX7_PE=2_SV=1	8.00E-96	[illegible]	[illegible]
comp25787_c0_seq1.p2				
comp25787_c1_seq1.p1	sp|Q3ULD5|MCCB_MOUSE_Methylcrotonoyl-CoA_carboxylase_beta_chain,_mitochondrial_OS=Mus_musculus_GN=Mccc2_PE=2_SV=1	4.00E-33	[illegible]	[illegible]
comp25787_c1_seq2.p1	sp|Q5XIT9|MCCB_RAT_Methylcrotonoyl-CoA_carboxylase_beta_chain,_mitochondrial_OS=Rattus_norvegicus_GN=Mccc2_PE=2_SV=1	0	[illegible]	[illegible]
comp25790_c0_seq1.p1				
comp25790_c0_seq2.p1				
comp25793_c0_seq2.p1				
comp25793_c0_seq3.p2				
comp25796_c0_seq1.p1				
comp25796_c0_seq3.p1				
comp25796_c0_seq4.p1				
comp25798_c0_seq1.p1	sp|Q6H8D6|COB23_ORYSJ_Putative_coatomer_subunit_beta'-3_OS=Oryza_sativa_subsp._japonica_GN=Os02g0209000_PE=3_SV=2	0	[illegible]	[illegible]
comp25798_c0_seq1.p2	sp|A7I8A7|GPMA_METB6_2,3-bisphosphoglycerate-dependent_phosphoglycerate_mutase_OS=Methanoregula_boonei_(strain_6A8)_GN=gpmA_PE=3_SV=1	2.00E-62	[illegible]	[illegible]
comp25800_c0_seq1.p1	sp|Q55EA1|ZNTD_DICDI_Protein_zntD_OS=Dictyostelium_discoideum_GN=zntD_PE=2_SV=1	3.00E-14	[illegible]	[illegible]
comp25800_c0_seq2.p1	sp|Q55EA1|ZNTD_DICDI_Protein_zntD_OS=Dictyostelium_discoideum_GN=zntD_PE=2_SV=1	2.00E-14	[illegible]	[illegible]
comp25807_c0_seq2.p1				
comp25809_c0_seq1.p1				
comp25816_c0_seq1.p1				
comp25816_c0_seq1.p2	sp|Q15075|EEA1_HUMAN_Early_endosome_antigen_1_OS=Homo_sapiens_GN=EEA1_PE=1_SV=2	5.00E-11	[illegible]	[illegible]
comp25816_c0_seq2.p1	sp|O80925|AGD7_ARATH_ADP-ribosylation_factor_GTPase-activating_protein_AGD7_OS=Arabidopsis_thaliana_GN=AGD7_PE=1_SV=1	5.00E-22	[illegible]	[illegible]
comp25818_c0_seq1.p1				
comp25818_c0_seq1.p2				
comp25819_c0_seq1.p1				
comp25819_c0_seq2.p1				
comp25820_c0_seq1.p3				
comp25821_c1_seq1.p1	sp|Q96C11|FGGY_HUMAN_FGGY_carbohydrate_kinase_domain-containing_protein_OS=Homo_sapiens_GN=FGGY_PE=1_SV=2	8.00E-56	[illegible]	[illegible]
comp25821_c1_seq2.p1	sp|Q9SE42|RPE1_ORYSJ_Ribulose-phosphate_3-epimerase,_cytoplasmic_isoform_OS=Oryza_sativa_subsp._japonica_GN=Os09g0505700_PE=1_SV=1	1.00E-41	[illegible]	[illegible]
comp25821_c1_seq2.p2	sp|P21939|XYLB_LACPE_Xylulose_kinase_OS=Lactobacillus_pentosus_GN=xylB_PE=3_SV=1	1.00E-23	[illegible]	[illegible]
comp25823_c0_seq1.p1				
comp25825_c0_seq2.p1				
comp25827_c0_seq1.p1				
comp25829_c0_seq1.p1				
comp25829_c0_seq4.p1				
comp25835_c0_seq2.p2				
comp25838_c0_seq2.p1	sp|Q6B8U6|PSAA_GRATL_Photosystem_I_P700_chlorophyll_a_apoprotein_A1_OS=Gracilaria_tenuistipitata_var._liui_GN=psaA_PE=3_SV=2	0	[illegible]	[illegible]
comp25838_c0_seq2.p2	sp|P51285|PSAB_PORPU_Photosystem_I_P700_chlorophyll_a_apoprotein_A2_OS=Porphyra_purpurea_GN=psaB_PE=3_SV=1	0	[illegible]	[illegible]
comp25848_c1_seq1.p1				
comp25851_c0_seq1.p1				
comp25855_c0_seq1.p1				
comp25857_c0_seq1.p1				
comp25860_c0_seq1.p1				
comp25860_c0_seq2.p1				
comp25863_c0_seq1.p1	sp|Q9FL69|AGD5_ARATH_Probable_ADP-ribosylation_factor_GTPase-activating_protein_AGD5_OS=Arabidopsis_thaliana_GN=AGD5_PE=1_SV=1	2.00E-32	[illegible]	[illegible]
comp25864_c0_seq3.p1				
comp25867_c0_seq1.p1				
comp25867_c1_seq1.p1	sp|O04921|HEMH2_ARATH_Ferrochelatase-2,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g30390_PE=2_SV=1	2.00E-110	[illegible]	[illegible]
comp25867_c3_seq2.p1	sp|O34524|YOCS_BACSU_Uncharacterized_sodium-dependent_transporter_yocS_OS=Bacillus_subtilis_GN=yocS_PE=3_SV=1	5.00E-42	[illegible]	[illegible]
comp25869_c0_seq2.p1				
comp25871_c0_seq1.p1	sp|P45181|PQQL_HAEIN_Probable_zinc_protease_pqqL_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=pqqL_PE=3_SV=1	2.00E-17	[illegible]	[illegible]
comp25876_c0_seq1.p1				
comp25881_c0_seq3.p1	sp|Q28E13|MFSD5_XENTR_Major_facilitator_superfamily_domain-containing_protein_5_OS=Xenopus_tropicalis_GN=mfsd5_PE=2_SV=1	4.00E-33	[illegible]	[illegible]
comp25881_c0_seq3.p2	sp|Q9ZPQ3|GEK1_ARATH_D-aminoacyl-tRNA_deacylase_OS=Arabidopsis_thaliana_GN=GEK1_PE=1_SV=2	8.00E-33	[illegible]	[illegible]
comp25883_c0_seq1.p1	sp|Q9NX74|DUS2L_HUMAN_tRNA-dihydrouridine(20)_synthase_[NAD(P)+]-like_OS=Homo_sapiens_GN=DUS2L_PE=1_SV=1	3.00E-75	[illegible]	[illegible]
comp25894_c0_seq1.p1				
comp25905_c0_seq2.p1				
comp25907_c0_seq2.p1				
comp25907_c0_seq2.p4				
comp25914_c0_seq1.p1	sp|A8XWW4|SHOC2_CAEBR_Leucine-rich_repeat_protein_soc-2_OS=Caenorhabditis_briggsae_GN=soc-2_PE=3_SV=1	3.00E-12	[illegible]	[illegible]
comp25914_c0_seq1.p2				
comp25914_c0_seq2.p1	sp|A8XWW4|SHOC2_CAEBR_Leucine-rich_repeat_protein_soc-2_OS=Caenorhabditis_briggsae_GN=soc-2_PE=3_SV=1	5.00E-12	[illegible]	[illegible]
comp25914_c0_seq2.p2				
comp25915_c1_seq1.p1	sp|P0ACE2|MBHM_SHIFL_Hydrogenase-2_large_chain_OS=Shigella_flexneri_GN=hybC_PE=3_SV=2	6.00E-84	[illegible]	[illegible]
comp25915_c2_seq1.p1	sp|P0ACE2|MBHM_SHIFL_Hydrogenase-2_large_chain_OS=Shigella_flexneri_GN=hybC_PE=3_SV=2	2.00E-121	[illegible]	[illegible]
comp25915_c2_seq2.p1	sp|P0ACE2|MBHM_SHIFL_Hydrogenase-2_large_chain_OS=Shigella_flexneri_GN=hybC_PE=3_SV=2	2.00E-167	[illegible]	[illegible]
comp25915_c2_seq3.p1	sp|Q3YU11|TYPH_SHISS_Thymidine_phosphorylase_OS=Shigella_sonnei_(strain_Ss046)_GN=deoA_PE=3_SV=1	8.00E-98	[illegible]	[illegible]
comp25920_c0_seq1.p1	sp|A9UZ24|BCAT_MONBE_Branched-chain-amino-acid_aminotransferase_OS=Monosiga_brevicollis_GN=37018_PE=3_SV=1	2.00E-128	[illegible]	[illegible]
comp25923_c0_seq2.p1				
comp25923_c0_seq3.p1				
comp25923_c0_seq4.p1				
comp25923_c1_seq1.p1				
comp25925_c0_seq3.p1				
comp25926_c0_seq1.p1				
comp25927_c0_seq1.p1				
comp25927_c0_seq2.p1				
comp25928_c1_seq2.p1	sp|P38023|RPOD1_SYNE7_RNA_polymerase_sigma_factor_rpoD1_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=rpoD1_PE=3_SV=2	7.00E-44	[illegible]	[illegible]
comp25930_c0_seq1.p1				
comp25930_c1_seq1.p1				
comp25930_c1_seq2.p1				
comp25932_c0_seq1.p2				
comp25932_c0_seq2.p1				
comp25937_c0_seq1.p1				
comp25942_c0_seq3.p1				
comp25943_c0_seq1.p2				
comp25943_c0_seq2.p1				
comp25943_c0_seq3.p1				
comp25943_c0_seq4.p1				
comp25943_c0_seq5.p1				
comp25945_c0_seq2.p1				
comp25945_c1_seq2.p1				
comp25948_c0_seq1.p1				
comp25950_c1_seq1.p2				
comp25952_c1_seq1.p1				
comp25953_c0_seq1.p1				
comp25954_c0_seq2.p1	sp|Q7ZVM9|RMI1_DANRE_RecQ-mediated_genome_instability_protein_1_OS=Danio_rerio_GN=rmi1_PE=2_SV=1	3.00E-13	[illegible]	[illegible]
comp25954_c0_seq2.p3				
comp25955_c0_seq1.p1	sp|Q55403|Y575_SYNY3_Thylakoid_membrane_protein_slr0575_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0575_PE=4_SV=1	4.00E-23	[illegible]	[illegible]
comp25956_c0_seq1.p1	sp|Q9JIM4|DUS12_RAT_Dual_specificity_protein_phosphatase_12_OS=Rattus_norvegicus_GN=Dusp12_PE=2_SV=1	4.00E-22	[illegible]	[illegible]
comp25958_c0_seq1.p1	sp|O18867|KCMA1_MACMU_Calcium-activated_potassium_channel_subunit_alpha-1_(Fragment)_OS=Macaca_mulatta_GN=KCNMA1_PE=2_SV=1	4.00E-31	[illegible]	[illegible]
comp25958_c0_seq2.p1				
comp25959_c0_seq1.p1				
comp25961_c0_seq5.p1				
comp25962_c0_seq1.p1				
comp25964_c0_seq1.p1	sp|D4ARL8|SKP1_ARTBC_E3_ubiquitin_ligase_complex_SCF_subunit_sconC_OS=Arthroderma_benhamiae_(strain_ATCC_MYA-4681_/_CBS_112371)_GN=sconC_PE=3_SV=1	9.00E-26	[illegible]	[illegible]
comp25965_c0_seq1.p1	sp|A4FUN7|UBP12_DANRE_Ubiquitin_carboxyl-terminal_hydrolase_12A_OS=Danio_rerio_GN=usp12a_PE=2_SV=1	4.00E-76	[illegible]	[illegible]
comp25967_c0_seq1.p1	sp|Q8QZZ7|TPRKB_MOUSE_TP53RK-binding_protein_OS=Mus_musculus_GN=Tprkb_PE=2_SV=1	6.00E-18	[illegible]	[illegible]
comp25967_c0_seq2.p1	sp|Q5PQR8|TPRKB_RAT_TP53RK-binding_protein_OS=Rattus_norvegicus_GN=Tprkb_PE=2_SV=1	2.00E-11	[illegible]	[illegible]
comp25968_c0_seq1.p2				
comp25969_c0_seq1.p1	sp|Q96QE3|ATAD5_HUMAN_ATPase_family_AAA_domain-containing_protein_5_OS=Homo_sapiens_GN=ATAD5_PE=1_SV=4	8.00E-18	[illegible]	[illegible]
comp25970_c1_seq1.p1	sp|Q4PEQ5|MCA1_USTMA_Metacaspase-1_OS=Ustilago_maydis_(strain_521_/_FGSC_9021)_GN=MCA1_PE=3_SV=1	2.00E-24	[illegible]	[illegible]
comp25971_c0_seq3.p1	sp|P46875|ATK3_ARATH_Kinesin-3_OS=Arabidopsis_thaliana_GN=ATK3_PE=2_SV=1	2.00E-121	[illegible]	[illegible]
comp25972_c0_seq1.p1				
comp25974_c0_seq1.p1				
comp25975_c1_seq1.p1				
comp25978_c0_seq1.p1				
comp25980_c0_seq2.p1				
comp25981_c0_seq1.p1				
comp25981_c1_seq1.p2				
comp25982_c0_seq2.p1	sp|P40229|CSK2C_ARATH_Casein_kinase_II_subunit_beta'_OS=Arabidopsis_thaliana_GN=CKB2_PE=1_SV=1	1.00E-51	[illegible]	[illegible]
comp25983_c0_seq1.p1				
comp25985_c0_seq1.p1				
comp25986_c0_seq1.p1	sp|Q9AV81|PUB72_ORYSJ_U-box_domain-containing_protein_72_OS=Oryza_sativa_subsp._japonica_GN=PUB72_PE=2_SV=1	4.00E-145	[illegible]	[illegible]
comp25986_c0_seq2.p1	sp|Q9AV81|PUB72_ORYSJ_U-box_domain-containing_protein_72_OS=Oryza_sativa_subsp._japonica_GN=PUB72_PE=2_SV=1	7.00E-46	[illegible]	[illegible]
comp25988_c0_seq1.p1				
comp25990_c0_seq1.p1				
comp25991_c0_seq1.p2	sp|Q55GJ6|PSB6_DICDI_Proteasome_subunit_beta_type-6_OS=Dictyostelium_discoideum_GN=psmB6_PE=1_SV=1	1.00E-91	[illegible]	[illegible]
comp25991_c0_seq1.p5				
comp25993_c0_seq2.p1				
comp25994_c0_seq2.p1	sp|Q2JP65|EFP_SYNJB_Elongation_factor_P_OS=Synechococcus_sp._(strain_JA-2-3B'a(2-13))_GN=efp_PE=3_SV=1	1.00E-64	[illegible]	[illegible]
comp25995_c0_seq1.p1				
comp25996_c0_seq2.p1				
comp25997_c0_seq1.p1				
comp25997_c1_seq1.p2				
comp25998_c0_seq1.p1				
comp26000_c0_seq1.p1	sp|P17202|BADH_SPIOL_Betaine_aldehyde_dehydrogenase,_chloroplastic_OS=Spinacia_oleracea_PE=1_SV=1	2.00E-135	[illegible]	[illegible]
comp26002_c0_seq1.p1				
comp26003_c0_seq1.p1	sp|Q56X76|RH39_ARATH_DEAD-box_ATP-dependent_RNA_helicase_39_OS=Arabidopsis_thaliana_GN=RH39_PE=2_SV=2	1.00E-32	[illegible]	[illegible]
comp26003_c0_seq2.p1	sp|Q56X76|RH39_ARATH_DEAD-box_ATP-dependent_RNA_helicase_39_OS=Arabidopsis_thaliana_GN=RH39_PE=2_SV=2	2.00E-30	[illegible]	[illegible]
comp26004_c0_seq1.p1				
comp26004_c0_seq2.p1	sp|Q08D64|ABCB6_XENTR_ATP-binding_cassette_sub-family_B_member_6,_mitochondrial_OS=Xenopus_tropicalis_GN=abcb6_PE=2_SV=1	7.00E-134	[illegible]	[illegible]
comp26005_c0_seq1.p1	sp|Q62018|CTR9_MOUSE_RNA_polymerase-associated_protein_CTR9_homolog_OS=Mus_musculus_GN=Ctr9_PE=1_SV=2	5.00E-73	[illegible]	[illegible]
comp26006_c0_seq1.p1	sp|Q9C5J9|Y5483_ARATH_Uncharacterized_GTP-binding_protein_At5g64813_OS=Arabidopsis_thaliana_GN=At5g64813_PE=1_SV=1	1.00E-11	[illegible]	[illegible]
comp26009_c0_seq1.p1	sp|Q47KS6|MSHA_THEFY_D-inositol_3-phosphate_glycosyltransferase_OS=Thermobifida_fusca_(strain_YX)_GN=mshA_PE=3_SV=1	6.00E-13	[illegible]	[illegible]
comp26010_c0_seq1.p1	sp|O13853|ITS3_SCHPO_Phosphatidylinositol_4-phosphate_5-kinase_its3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=its3_PE=1_SV=3	1.00E-53	[illegible]	[illegible]
comp26012_c0_seq2.p1				
comp26014_c1_seq2.p1				
comp26014_c1_seq3.p2				
comp26016_c0_seq1.p1	sp|P61315|G3ST3_MOUSE_Galactose-3-O-sulfotransferase_3_OS=Mus_musculus_GN=Gal3st3_PE=2_SV=1	7.00E-11	[illegible]	[illegible]
comp26017_c0_seq1.p2				
comp26018_c0_seq1.p1				
comp26018_c0_seq2.p1				
comp26018_c0_seq2.p3				
comp26019_c0_seq1.p1				
comp26020_c0_seq2.p1				
comp26021_c0_seq1.p1	sp|O50401|OTSB_MYCTU_Trehalose-phosphate_phosphatase_OS=Mycobacterium_tuberculosis_GN=otsB_PE=1_SV=1	7.00E-15		
comp26023_c0_seq1.p1				
comp26023_c0_seq1.p3				
comp26023_c0_seq2.p1				
comp26023_c0_seq2.p3				
comp26024_c0_seq2.p1				
comp26026_c0_seq1.p2				
comp26026_c0_seq4.p1				
comp26027_c0_seq1.p2				
comp26027_c0_seq2.p4				
comp26030_c0_seq1.p1				
comp26031_c0_seq1.p1				
comp26031_c0_seq2.p1				
comp26033_c0_seq1.p1	sp|P54676|PI3K4_DICDI_Phosphatidylinositol_3-kinase_VPS34-like_OS=Dictyostelium_discoideum_GN=pikE_PE=3_SV=2	3.00E-83	[illegible]	[illegible]
comp26033_c0_seq2.p1	sp|P54676|PI3K4_DICDI_Phosphatidylinositol_3-kinase_VPS34-like_OS=Dictyostelium_discoideum_GN=pikE_PE=3_SV=2	2.00E-33	[illegible]	[illegible]
comp26034_c0_seq2.p1				
comp26036_c0_seq2.p1				
comp26036_c0_seq3.p1				
comp26039_c0_seq2.p1				
comp26041_c0_seq1.p1	sp|Q5BCC5|CAN_EMENI_Carbonic_anhydrase_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=AN1805_PE=1_SV=2	2.00E-64	[illegible]	[illegible]
comp26042_c0_seq1.p1	sp|P51399|LOX5_MESAU_Arachidonate_5-lipoxygenase_OS=Mesocricetus_auratus_GN=ALOX5_PE=2_SV=2	8.00E-24	[illegible]	[illegible]
comp26043_c0_seq1.p1				
comp26043_c0_seq2.p1				
comp26043_c0_seq5.p1				
comp26045_c0_seq1.p1	sp|Q9D081|ALG14_MOUSE_UDP-N-acetylglucosamine_transferase_subunit_ALG14_homolog_OS=Mus_musculus_GN=Alg14_PE=2_SV=1	8.00E-46	[illegible]	[illegible]
comp26046_c0_seq1.p2	sp|Q90YR8|RS6_ICTPU_40S_ribosomal_protein_S6_OS=Ictalurus_punctatus_GN=rps6_PE=2_SV=1	7.00E-85	[illegible]	[illegible]
comp26047_c0_seq1.p1	sp|Q8CJ27|ASPM_MOUSE_Abnormal_spindle-like_microcephaly-associated_protein_homolog_OS=Mus_musculus_GN=Aspm_PE=2_SV=2	6.00E-12	[illegible]	[illegible]
comp26049_c0_seq1.p1				
comp26050_c0_seq1.p1				
comp26050_c0_seq3.p1				
comp26054_c0_seq1.p1	sp|Q0WMY5|PP365_ARATH_Pentatricopeptide_repeat-containing_protein_At5g04810,_chloroplastic_OS=Arabidopsis_thaliana_GN=PPR4_PE=1_SV=1	5.00E-11	[illegible]	[illegible]
comp26060_c0_seq3.p1	sp|Q12252|PHM7_YEAST_Phosphate_metabolism_protein_7_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PHM7_PE=1_SV=1	7.00E-36	[illegible]	[illegible]
comp26064_c0_seq2.p1	sp|Q9Z2Y1|TIM_RAT_Protein_timeless_homolog_OS=Rattus_norvegicus_GN=Timeless_PE=1_SV=1	7.00E-19	[illegible]	[illegible]
comp26064_c0_seq2.p2	sp|P34893|CH10_ARATH_10_kDa_chaperonin_OS=Arabidopsis_thaliana_GN=CPN10_PE=2_SV=1	6.00E-28	[illegible]	[illegible]
comp26065_c0_seq1.p1	sp|P94400|YCIC_BACSU_Putative_metal_chaperone_YciC_OS=Bacillus_subtilis_GN=yciC_PE=2_SV=1	5.00E-34	[illegible]	[illegible]
comp26065_c0_seq2.p1	sp|Q869Q0|Y4527_DICDI_COBW_domain-containing_protein_DDB_G0274527_OS=Dictyostelium_discoideum_GN=DDB_G0274527_PE=3_SV=1	3.00E-36	[illegible]	[illegible]
comp26065_c0_seq3.p1	sp|Q869Q0|Y4527_DICDI_COBW_domain-containing_protein_DDB_G0274527_OS=Dictyostelium_discoideum_GN=DDB_G0274527_PE=3_SV=1	3.00E-80	[illegible]	[illegible]
comp26068_c0_seq4.p1				
comp26069_c0_seq1.p2				
comp26069_c0_seq3.p1				
comp26071_c0_seq1.p1				
comp26071_c0_seq4.p1				
comp26072_c0_seq1.p1	sp|Q8IWV8|UBR2_HUMAN_E3_ubiquitin-protein_ligase_UBR2_OS=Homo_sapiens_GN=UBR2_PE=1_SV=1	6.00E-19	[illegible]	[illegible]
comp26075_c0_seq1.p1				
comp26077_c0_seq1.p1	sp|Q9DEE9|ARP6_CHICK_Actin-related_protein_6_OS=Gallus_gallus_GN=ACTR6_PE=2_SV=1	2.00E-69	[illegible]	[illegible]
comp26077_c0_seq2.p1	sp|Q9DEE9|ARP6_CHICK_Actin-related_protein_6_OS=Gallus_gallus_GN=ACTR6_PE=2_SV=1	7.00E-49	[illegible]	[illegible]
comp26077_c0_seq3.p1	sp|Q9DEE9|ARP6_CHICK_Actin-related_protein_6_OS=Gallus_gallus_GN=ACTR6_PE=2_SV=1	4.00E-71	[illegible]	[illegible]
comp26077_c0_seq3.p3	sp|Q5NBI2|ARP6_ORYSJ_Actin-related_protein_6_OS=Oryza_sativa_subsp._japonica_GN=ARP6_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp26079_c0_seq2.p1				
comp26080_c0_seq2.p1				
comp26081_c0_seq1.p1				
comp26081_c0_seq2.p2				
comp26082_c0_seq3.p1				
comp26084_c0_seq1.p1	sp|Q6DW74|DGDG1_LOTJA_Digalactosyldiacylglycerol_synthase_1,_chloroplastic_OS=Lotus_japonicus_GN=DGD1_PE=2_SV=1	8.00E-102	[illegible]	[illegible]
comp26085_c0_seq1.p1				
comp26085_c0_seq1.p4				
comp26086_c0_seq2.p1				
comp26088_c0_seq1.p1	sp|Q8BH79|ANO10_MOUSE_Anoctamin-10_OS=Mus_musculus_GN=Ano10_PE=2_SV=1	1.00E-52	[illegible]	[illegible]
comp26089_c0_seq2.p1				
comp26089_c0_seq5.p1				
comp26089_c0_seq6.p1				
comp26091_c0_seq2.p1				
comp26093_c0_seq1.p1				
comp26094_c0_seq1.p1				
comp26094_c0_seq2.p1				
comp26095_c0_seq1.p1	sp|Q8BSY0|ASPH_MOUSE_Aspartyl/asparaginyl_beta-hydroxylase_OS=Mus_musculus_GN=Asph_PE=2_SV=1	2.00E-12	[illegible]	[illegible]
comp26095_c1_seq1.p1	sp|P42620|YQJG_ECOLI_Uncharacterized_protein_yqjG_OS=Escherichia_coli_(strain_K12)_GN=yqjG_PE=3_SV=1	2.00E-72	[illegible]	[illegible]
comp26097_c0_seq1.p1	sp|P52301|RAN_XENLA_GTP-binding_nuclear_protein_Ran_OS=Xenopus_laevis_GN=ran_PE=1_SV=2	3.00E-128	[illegible]	[illegible]
comp26097_c0_seq1.p6				
comp26098_c0_seq2.p1	sp|Q54KS4|GNL3_DICDI_Guanine_nucleotide-binding_protein-like_3_homolog_OS=Dictyostelium_discoideum_GN=gnl3_PE=3_SV=1	7.00E-96	[illegible]	[illegible]
comp26099_c0_seq1.p2				
comp26099_c0_seq2.p1				
comp26100_c0_seq1.p1	sp|P41151|HFA1A_ARATH_Heat_stress_transcription_factor_A-1a_OS=Arabidopsis_thaliana_GN=HSFA1A_PE=1_SV=2	2.00E-11	[illegible]	[illegible]
comp26102_c0_seq3.p1	sp|B1MTG4|CING_CALMO_Cingulin_OS=Callicebus_moloch_GN=CGN_PE=3_SV=1	3.00E-12	[illegible]	[illegible]
comp26102_c0_seq3.p2				
comp26105_c0_seq1.p2	sp|Q3YVX7|GPMI_SHISS_2,3-bisphosphoglycerate-independent_phosphoglycerate_mutase_OS=Shigella_sonnei_(strain_Ss046)_GN=gpmI_PE=3_SV=1	5.00E-67	[illegible]	[illegible]
comp26105_c0_seq1.p3	sp|P37690|ENVC_ECOLI_Murein_hydrolase_activator_EnvC_OS=Escherichia_coli_(strain_K12)_GN=envC_PE=1_SV=2	8.00E-53	[illegible]	[illegible]
comp26110_c0_seq1.p1				
comp26111_c0_seq1.p1	sp|Q6Q4H1|JMJD6_HYDVU_Bifunctional_arginine_demethylase_and_lysyl-hydroxylase_PSR_OS=Hydra_vulgaris_GN=PSR_PE=1_SV=1	5.00E-21	[illegible]	[illegible]
comp26113_c0_seq2.p1	sp|Q86B11|CDC23_DICDI_Anaphase-promoting_complex_subunit_8_OS=Dictyostelium_discoideum_GN=anapc8_PE=3_SV=1	3.00E-93	[illegible]	[illegible]
comp26115_c0_seq1.p1				
comp26116_c0_seq1.p1				
comp26116_c0_seq2.p1				
comp26117_c0_seq1.p2	sp|P62856|RS26_RAT_40S_ribosomal_protein_S26_OS=Rattus_norvegicus_GN=Rps26_PE=3_SV=3	7.00E-30	[illegible]	[illegible]
comp26118_c0_seq3.p1	sp|P38828|LSM12_YEAST_Protein_LSM12_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=LSM12_PE=1_SV=1	2.00E-14	[illegible]	[illegible]
comp26118_c0_seq3.p3	sp|Q86JJ5|RPB11_DICDI_DNA-directed_RNA_polymerase_II_subunit_rpb11_OS=Dictyostelium_discoideum_GN=polr2j_PE=3_SV=1	3.00E-12	[illegible]	[illegible]
comp26119_c0_seq1.p1				
comp26119_c0_seq2.p1				
comp26121_c0_seq1.p1	sp|P61315|G3ST3_MOUSE_Galactose-3-O-sulfotransferase_3_OS=Mus_musculus_GN=Gal3st3_PE=2_SV=1	5.00E-15	[illegible]	[illegible]
comp26121_c0_seq2.p1				
comp26124_c0_seq1.p1				
comp26124_c0_seq1.p3	sp|Q54FB6|DAD1_DICDI_Dolichyl-diphosphooligosaccharide--protein_glycosyltransferase_subunit_2_OS=Dictyostelium_discoideum_GN=ost2_PE=3_SV=1	2.00E-18	[illegible]	[illegible]

comp26125_c0_seq1.p1	sp|Q04637|IF4G1_HUMAN_Eukaryotic_translation_initiation_factor_4_gamma_1_OS=Homo_sapiens_GN=EIF4G1_PE=1_SV=4	9.00E-29	GO:0000184,GO:0000288,GO:0000289,GO:0003723,GO:0003723,GO:0003743,GO:0003743,GO:0003743,GO:0005515,GO:0005737,GO:0005829,GO:0006412,GO:0006412,GO:0006413,GO:0006413,GO:0006417,GO:0006446,GO:0006446,GO:0006446,GO:0008135,GO:0008135,GO:0008286,GO:0010467,GO:0016020,GO:0016032,GO:0016070,GO:0016071,GO:0016281,GO:0019221,GO:0044267,GO:0044822	[illegible]
comp26127_c0_seq1.p1				
comp26127_c1_seq1.p1	sp|Q96M32|KAD7_HUMAN_Adenylate_kinase_7_OS=Homo_sapiens_GN=AK7_PE=1_SV=3	3.00E-15	GO:0000166,GO:0002437,GO:0003351,GO:0004017,GO:0004017,GO:0004127,GO:0004550,GO:0004550,GO:0005524,GO:0005524,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0006139,GO:0006165,GO:0007283,GO:0007420,GO:0009142,GO:0016301,GO:0016310,GO:0016740,GO:0019205,GO:0030030,GO:0035082	[illegible]
comp26127_c2_seq1.p1				
comp26128_c0_seq1.p1	sp|Q499P8|CP058_RAT_UPF0420_protein_C16orf58_homolog_OS=Rattus_norvegicus_PE=2_SV=1	5.00E-32	GO:0016020,GO:0016020,GO:0016021	[illegible]
comp26128_c0_seq3.p1	sp|Q499P8|CP058_RAT_UPF0420_protein_C16orf58_homolog_OS=Rattus_norvegicus_PE=2_SV=1	1.00E-31	GO:0016020,GO:0016020,GO:0016021	[illegible]
comp26128_c0_seq4.p1				
comp26129_c0_seq1.p1				
comp26129_c0_seq2.p1				
comp26130_c0_seq2.p1				
comp26130_c0_seq2.p2				
comp26131_c0_seq1.p1				
comp26133_c0_seq2.p1	sp|P08466|NUC1_YEAST_Mitochondrial_nuclease_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=NUC1_PE=1_SV=1	3.00E-24	GO:0000738,GO:0003676,GO:0004518,GO:0004519,GO:0004520,GO:0004529,GO:0004540,GO:0005634,GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0005743,GO:0006308,GO:0006309,GO:0006310,GO:0006401,GO:0006915,GO:0016020,GO:0016787,GO:0016787,GO:0046872,GO:0046872,GO:0090501	[illegible]
comp26133_c0_seq2.p4				
comp26135_c0_seq2.p1	sp|Q9LMK5|STN1_ARATH_CST_complex_subunit_STN1_OS=Arabidopsis_thaliana_GN=STN1_PE=1_SV=1	2.00E-11	GO:0000781,GO:0000781,GO:0000784,GO:0003676,GO:0003677,GO:0005515,GO:0005634,GO:0005634,GO:0005694,GO:0006355,GO:0016233,GO:0043687,GO:0045893	[illegible]
comp26138_c0_seq1.p1	sp|Q56XP4|NHX2_ARATH_Sodium/hydrogen_exchanger_2_OS=Arabidopsis_thaliana_GN=NHX2_PE=1_SV=2	6.00E-60	GO:0005773,GO:0005774,GO:0006810,GO:0006811,GO:0006812,GO:0006814,GO:0006814,GO:0006814,GO:0006885,GO:0010107,GO:0010351,GO:0015297,GO:0015299,GO:0015385,GO:0015385,GO:0015386,GO:0016020,GO:0016021,GO:0016021,GO:0035725,GO:0035725,GO:0055075,GO:0055085,GO:0090333,GO:1902600	[illegible]
comp26139_c0_seq1.p1	sp|Q8W033|AL3I1_ARATH_Aldehyde_dehydrogenase_family_3_member_I1,_chloroplastic_OS=Arabidopsis_thaliana_GN=ALDH3I1_PE=2_SV=2	4.00E-24	GO:0004028,GO:0004028,GO:0004029,GO:0004029,GO:0004029,GO:0004030,GO:0006081,GO:0008152,GO:0009414,GO:0009507,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009536,GO:0009737,GO:0009941,GO:0016491,GO:0016491,GO:0016620,GO:0033721,GO:0055114,GO:0055114	[illegible]
comp26140_c0_seq1.p1				
comp26142_c0_seq2.p1				
comp26143_c1_seq1.p1				
comp26143_c1_seq4.p1				
comp26144_c0_seq1.p1	sp|Q9CAN6|PPR97_ARATH_Pentatricopeptide_repeat-containing_protein_At1g63070,_mitochondrial_OS=Arabidopsis_thaliana_GN=At1g63070_PE=1_SV=1	3.00E-17	GO:0005739,GO:0005739	[illegible]
comp26148_c0_seq1.p1				
comp26149_c0_seq1.p1	sp|Q55311|SRP54_SYNE7_Signal_sequence-binding_protein_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=ffh_PE=3_SV=1	2.00E-115	GO:0000166,GO:0003723,GO:0003723,GO:0003924,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0005737,GO:0005737,GO:0006184,GO:0006184,GO:0006612,GO:0006614,GO:0008312,GO:0030529,GO:0030529,GO:0048500,GO:0048500	[illegible]
comp26149_c0_seq2.p1	sp|Q55311|SRP54_SYNE7_Signal_sequence-binding_protein_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=ffh_PE=3_SV=1	3.00E-130	GO:0000166,GO:0003723,GO:0003723,GO:0003924,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0005737,GO:0005737,GO:0006184,GO:0006184,GO:0006612,GO:0006614,GO:0008312,GO:0030529,GO:0030529,GO:0048500,GO:0048500	[illegible]
comp26149_c0_seq2.p2	sp|Q9VTC4|U195A_DROME_MIP18_family_protein_CG7949_OS=Drosophila_melanogaster_GN=CG7949_PE=1_SV=1	1.00E-62	GO:0003674,GO:0005515,GO:0005515,GO:0005575,GO:0005634,GO:0005737,GO:0007059,GO:0007059,GO:0008150,GO:0016226	[illegible]
comp26151_c0_seq1.p1	sp|Q94A97|UBC35_ARATH_Ubiquitin-conjugating_enzyme_E2_35_OS=Arabidopsis_thaliana_GN=UBC35_PE=1_SV=1	3.00E-86	GO:0000166,GO:0004842,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0006301,GO:0006511,GO:0010039,GO:0010053,GO:0016567,GO:0016567,GO:0016874,GO:0016881,GO:0031372,GO:0046686	[illegible]
comp26152_c0_seq4.p1				
comp26154_c0_seq1.p1				
comp26154_c0_seq2.p1				
comp26156_c0_seq1.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	5.00E-38		
comp26157_c1_seq1.p1	sp|Q7TNH6|NPHP3_MOUSE_Nephrocystin-3_OS=Mus_musculus_GN=Nphp3_PE=1_SV=2	1.00E-43	GO:0003674,GO:0005929,GO:0005929,GO:0005929,GO:0006629,GO:0007163,GO:0007368,GO:0016055,GO:0030198,GO:0030814,GO:0042995,GO:0048496,GO:0060271,GO:0060271,GO:0060271,GO:0060993,GO:0072372,GO:0090090,GO:0097543,GO:0097546,GO:2000095	[illegible]
comp26158_c0_seq2.p1	sp|Q8LHP0|ELOF1_ORYSJ_Transcription_elongation_factor_1_homolog_OS=Oryza_sativa_subsp._japonica_GN=Os07g0631100_PE=3_SV=1	2.00E-21	GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0046872	[illegible]
comp26159_c0_seq4.p1				
comp26160_c0_seq1.p1	sp|Q54KR9|NCBP2_DICDI_Nuclear_cap-binding_protein_subunit_2_OS=Dictyostelium_discoideum_GN=ncbp2_PE=3_SV=1	2.00E-49	GO:0000166,GO:0000339,GO:0000339,GO:0000339,GO:0000398,GO:0000398,GO:0003676,GO:0003723,GO:0005634,GO:0005634,GO:0005846,GO:0005846,GO:0005846,GO:0006370,GO:0006397,GO:0008380,GO:0031047,GO:0045292	[illegible]
comp26161_c0_seq1.p1				
comp26163_c0_seq1.p1	sp|P0CF85|INSF_ECO11_Transposase_insF_for_insertion_sequence_IS3_OS=Escherichia_coli_O111:H-_GN=insF_PE=3_SV=1	1.00E-102	GO:0003676,GO:0003677,GO:0006310,GO:0015074,GO:0032196	[illegible]
comp26163_c0_seq1.p2	sp|P59445|INSE_SHIFL_Transposase_insE_for_insertion_sequence_IS3_OS=Shigella_flexneri_GN=insE1_PE=3_SV=2	4.00E-62	GO:0003677,GO:0003677,GO:0004803,GO:0006310,GO:0006313,GO:0032196	[illegible]
comp26164_c0_seq1.p1	sp|Q96JK4|HIPL1_HUMAN_HHIP-like_protein_1_OS=Homo_sapiens_GN=HHIPL1_PE=2_SV=2	1.00E-12	GO:0003674,GO:0003824,GO:0005044,GO:0005575,GO:0005576,GO:0005576,GO:0005975,GO:0006898,GO:0008150,GO:0016020,GO:0016901,GO:0048038,GO:0055114	[illegible]
comp26165_c0_seq1.p1	sp|Q54B20|SDHF2_DICDI_Succinate_dehydrogenase_assembly_factor_2,_mitochondrial_OS=Dictyostelium_discoideum_GN=DDB_G0293946_PE=3_SV=1	1.00E-11	GO:0003674,GO:0003674,GO:0005575,GO:0005575,GO:0005739,GO:0005739,GO:0005739,GO:0005759,GO:0005759,GO:0006121,GO:0006121,GO:0008150,GO:0008150,GO:0018293,GO:0018293,GO:0018293	[illegible]
comp26166_c0_seq1.p1	sp|Q02357|ANK1_MOUSE_Ankyrin-1_OS=Mus_musculus_GN=Ank1_PE=1_SV=2	2.00E-15	GO:0005634,GO:0005737,GO:0005856,GO:0005856,GO:0005886,GO:0005886,GO:0006779,GO:0006888,GO:0007165,GO:0010638,GO:0014731,GO:0014731,GO:0015672,GO:0016020,GO:0016020,GO:0016020,GO:0016529,GO:0016529,GO:0016529,GO:0030018,GO:0030507,GO:0030673,GO:0030863,GO:0031430,GO:0031672,GO:0042383,GO:0043005,GO:0045211,GO:0048821,GO:0048821,GO:0051117,GO:0055072,GO:0072661	[illegible]
comp26166_c0_seq2.p1				
comp26167_c0_seq2.p1				
comp26169_c0_seq1.p1	sp|Q501S4|MET12_DANRE_Methyltransferase-like_protein_12,_mitochondrial_OS=Danio_rerio_GN=mettl12_PE=2_SV=2	4.00E-13	GO:0005739,GO:0005739,GO:0008168,GO:0016740,GO:0032259	[illegible]
comp26169_c0_seq2.p1	sp|Q501S4|MET12_DANRE_Methyltransferase-like_protein_12,_mitochondrial_OS=Danio_rerio_GN=mettl12_PE=2_SV=2	2.00E-13	GO:0005739,GO:0005739,GO:0008168,GO:0016740,GO:0032259	[illegible]
comp26172_c0_seq1.p1				
comp26173_c0_seq1.p2	sp|Q3UX43|AN13C_MOUSE_Ankyrin_repeat_domain-containing_protein_13C_OS=Mus_musculus_GN=Ankrd13c_PE=2_SV=2	3.00E-11	GO:0005102,GO:0005783,GO:0005783,GO:0005789,GO:0006621,GO:0010869,GO:0016020,GO:0048471,GO:2000209	[illegible]
comp26174_c0_seq1.p1	sp|Q9SJM7|URH1_ARATH_Uridine_nucleosidase_1_OS=Arabidopsis_thaliana_GN=URH1_PE=1_SV=2	3.00E-11	GO:0005737,GO:0005737,GO:0005829,GO:0006152,GO:0006218,GO:0008152,GO:0016787,GO:0016798,GO:0045437,GO:0045437,GO:0047622,GO:0047724,GO:0072585	[illegible]
comp26176_c0_seq1.p1				
comp26177_c0_seq1.p1	sp|A5GQN5|AROK_SYNR3_Shikimate_kinase_OS=Synechococcus_sp._(strain_RCC307)_GN=aroK_PE=3_SV=1	1.00E-46	GO:0000166,GO:0000287,GO:0004765,GO:0004765,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0008652,GO:0009073,GO:0009073,GO:0009423,GO:0016301,GO:0016310,GO:0016740,GO:0046872	[illegible]
comp26177_c0_seq2.p1	sp|A5GQN5|AROK_SYNR3_Shikimate_kinase_OS=Synechococcus_sp._(strain_RCC307)_GN=aroK_PE=3_SV=1	8.00E-43	GO:0000166,GO:0000287,GO:0004765,GO:0004765,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0008652,GO:0009073,GO:0009073,GO:0009423,GO:0016301,GO:0016310,GO:0016740,GO:0046872	[illegible]
comp26178_c0_seq1.p1	sp|Q9V3D6|CPSF2_DROME_Probable_cleavage_and_polyadenylation_specificity_factor_subunit_2_OS=Drosophila_melanogaster_GN=Cpsf100_PE=1_SV=1	3.00E-78	GO:0003723,GO:0005515,GO:0005634,GO:0005634,GO:0005847,GO:0005847,GO:0006378,GO:0006378,GO:0006378,GO:0006379,GO:0006379,GO:0006397,GO:0006398,GO:0006398,GO:0022008	[illegible]
comp26178_c0_seq1.p2				
comp26179_c0_seq2.p1				
comp26179_c0_seq4.p1				
comp26180_c0_seq2.p1	sp|Q9LX49|PRN1_ARATH_Pirin-1_OS=Arabidopsis_thaliana_GN=PRN1_PE=1_SV=1	6.00E-38	GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0006826,GO:0009737,GO:0009738,GO:0009738,GO:0009785,GO:0010106,GO:0010167,GO:0015706	[illegible]
comp26181_c0_seq2.p2				
comp26183_c0_seq1.p1	sp|O14841|OPLA_HUMAN_5-oxoprolinase_OS=Homo_sapiens_GN=OPLAH_PE=1_SV=3	0	GO:0000166,GO:0003824,GO:0005524,GO:0005829,GO:0006750,GO:0006805,GO:0006805,GO:0016787,GO:0016787,GO:0017168,GO:0017168,GO:0044281,GO:1901687	[illegible]
comp26184_c0_seq1.p1				
comp26185_c0_seq2.p1	sp|Q5JLD8|CIPK8_ORYSJ_CBL-interacting_protein_kinase_8_OS=Oryza_sativa_subsp._japonica_GN=CIPK8_PE=2_SV=1	3.00E-38	GO:0000166,GO:0000166,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005524,GO:0005886,GO:0006468,GO:0006468,GO:0007165,GO:0007165,GO:0009749,GO:0016301,GO:0016301,GO:0016310,GO:0016740,GO:0016740,GO:0016772,GO:0016772,GO:0046777,GO:0048364	[illegible]
comp26186_c0_seq1.p1				
comp26187_c0_seq4.p1				
comp26189_c0_seq1.p1				
comp26192_c0_seq3.p1				
comp26193_c0_seq1.p1				
comp26193_c0_seq2.p1				
comp26195_c0_seq1.p1				
comp26195_c0_seq2.p1				
comp26196_c0_seq2.p1	sp|Q9XFH4|DDM1_ARATH_ATP-dependent_DNA_helicase_DDM1_OS=Arabidopsis_thaliana_GN=DDM1_PE=1_SV=1	8.00E-148	GO:0000166,GO:0000786,GO:0003677,GO:0003677,GO:0004003,GO:0004386,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006200,GO:0006342,GO:0006344,GO:0006346,GO:0006349,GO:0006351,GO:0006355,GO:0008283,GO:0009294,GO:0016246,GO:0016572,GO:0016787,GO:0016887,GO:0031048,GO:0032197,GO:0032508,GO:0044030,GO:0051567,GO:0051574,GO:0051574,GO:0090241	[illegible]
comp26197_c0_seq1.p1	sp|P23921|RIR1_HUMAN_Ribonucleoside-diphosphate_reductase_large_subunit_OS=Homo_sapiens_GN=RRM1_PE=1_SV=1	0	GO:0000166,GO:0000278,GO:0003824,GO:0004748,GO:0004748,GO:0004748,GO:0005515,GO:0005524,GO:0005524,GO:0005635,GO:0005654,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0006206,GO:0006260,GO:0006260,GO:0006260,GO:0008152,GO:0008584,GO:0009263,GO:0009263,GO:0010212,GO:0015949,GO:0016491,GO:0017076,GO:0021846,GO:0042995,GO:0043025,GO:0044281,GO:0051259,GO:0051290,GO:0055086,GO:0055114,GO:0055114,GO:0060041,GO:0070062	[illegible]
comp26197_c1_seq2.p1	sp|P21672|RIR3_YEAST_Ribonucleoside-diphosphate_reductase_large_chain_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=RNR3_PE=1_SV=4	9.00E-72	GO:0000166,GO:0003824,GO:0004748,GO:0004748,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005971,GO:0006260,GO:0006260,GO:0006260,GO:0008152,GO:0009263,GO:0016491,GO:0055114,GO:0055114,GO:0004748	[illegible]
comp26197_c1_seq4.p1	sp|P36602|RIR1_SCHPO_Ribonucleoside-diphosphate_reductase_large_chain_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=cdc22_PE=1_SV=2	1.00E-91	GO:0000166,GO:0003824,GO:0004550,GO:0004748,GO:0004748,GO:0004748,GO:0004748,GO:0005515,GO:0005524,GO:0005524,GO:0005737,GO:0005829,GO:0005971,GO:0006165,GO:0006235,GO:0006240,GO:0006260,GO:0006260,GO:0006260,GO:0008152,GO:0009216,GO:0009263,GO:0016491,GO:0042278,GO:0046704,GO:0051063,GO:0051063,GO:0055114,GO:0055114,GO:0051063	[illegible]
comp26198_c0_seq1.p1	sp|Q9NZN3|EHD3_HUMAN_EH_domain-containing_protein_3_OS=Homo_sapiens_GN=EHD3_PE=1_SV=2	4.00E-162	GO:0000166,GO:0003676,GO:0003924,GO:0005509,GO:0005515,GO:0005515,GO:0005524,GO:0005525,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005768,GO:0005886,GO:0005886,GO:0005925,GO:0006184,GO:0007596,GO:0010008,GO:0010008,GO:0016020,GO:0030139,GO:0032456,GO:0046872,GO:0048471,GO:0051260,GO:0055038,GO:0055038,GO:0072661,GO:0072661,GO:0086036,GO:0086036	[illegible]
comp26198_c0_seq1.p2	sp|Q940S5|COPZ1_ARATH_Coatomer_subunit_zeta-1_OS=Arabidopsis_thaliana_GN=At1g60970_PE=2_SV=1	3.00E-36	GO:0000139,GO:0005737,GO:0005737,GO:0005794,GO:0006457,GO:0006810,GO:0006810,GO:0009408,GO:0009644,GO:0015031,GO:0016020,GO:0016192,GO:0030663,GO:0031410,GO:0034976,GO:0042542,GO:0045893	[illegible]
comp26199_c0_seq2.p1	sp|Q96RY7|IF140_HUMAN_Intraflagellar_transport_protein_140_homolog_OS=Homo_sapiens_GN=IFT140_PE=1_SV=1	2.00E-28	GO:0003674,GO:0005737,GO:0005813,GO:0005815,GO:0005856,GO:0005929,GO:0005929,GO:0005930,GO:0005930,GO:0005930,GO:0030030,GO:0030991,GO:0030991,GO:0030991,GO:0032391,GO:0035721,GO:0036064,GO:0036064,GO:0042384,GO:0042995,GO:0048705,GO:0048705,GO:0060041,GO:0060041,GO:0060271,GO:0061512,GO:0061512,GO:0072001,GO:0072001,GO:0072372,GO:1902017	[illegible]
comp26200_c0_seq1.p1				
comp26203_c0_seq1.p1				
comp26206_c0_seq1.p1				
comp26209_c0_seq1.p2				
comp26211_c0_seq1.p1	sp|Q5UQG7|YR818_MIMIV_Putative_serine/threonine-protein_kinase/receptor_R818_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R818_PE=4_SV=1	5.00E-37	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0009190,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016849,GO:0035556	[illegible]
comp26212_c0_seq1.p1	sp|P50944|AVT4_YEAST_Vacuolar_amino_acid_transporter_4_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=AVT4_PE=1_SV=1	1.00E-46	GO:0000324,GO:0000329,GO:0005302,GO:0005302,GO:0005773,GO:0005774,GO:0006810,GO:0006812,GO:0006812,GO:0006865,GO:0006868,GO:0006868,GO:0015186,GO:0015186,GO:0015188,GO:0015188,GO:0015803,GO:0015803,GO:0015804,GO:0015804,GO:0015807,GO:0015807,GO:0015828,GO:0015828,GO:0016020,GO:0016021,GO:0032974,GO:0032974,GO:0098655,GO:0098655,GO:1902475,GO:1902475	[illegible]
comp26213_c0_seq1.p1	sp|O53870|DAPC_MYCTU_Probable_N-succinyldiaminopimelate_aminotransferase_DapC_OS=Mycobacterium_tuberculosis_GN=dapC_PE=1_SV=1	9.00E-66		

comp26474_c0_seq1.p1				
comp26476_c0_seq2.p1	sp|O22212|PRP4_ARATH_U4/U6_small_nuclear_ribonucleoprotein_PRP4-like_protein_OS=Arabidopsis_thaliana_GN=EMB2776_PE=2_SV=1	1.00E-96	[illegible]	[illegible]
comp26477_c0_seq1.p1	sp|Q9ZU35|AB7G_ARATH_ABC_transporter_G_family_member_7_OS=Arabidopsis_thaliana_GN=ABCG7_PE=1_SV=1	1.00E-87	[illegible]	[illegible]
comp26477_c0_seq1.p4	sp|Q9ZU35|AB7G_ARATH_ABC_transporter_G_family_member_7_OS=Arabidopsis_thaliana_GN=ABCG7_PE=1_SV=1	2.00E-12	[illegible]	[illegible]
comp26477_c0_seq2.p1	sp|Q9ZU35|AB7G_ARATH_ABC_transporter_G_family_member_7_OS=Arabidopsis_thaliana_GN=ABCG7_PE=1_SV=1	6.00E-85	[illegible]	[illegible]
comp26478_c0_seq1.p1				
comp26480_c0_seq1.p1				
comp26482_c0_seq1.p1				
comp26483_c1_seq2.p1				
comp26483_c1_seq2.p4				
comp26487_c0_seq4.p1				
comp26488_c0_seq2.p1				
comp26489_c0_seq1.p1	sp|Q84WV9|QPCT_ARATH_Glutaminyl-peptide_cyclotransferase_OS=Arabidopsis_thaliana_GN=QCT_PE=1_SV=1	3.00E-54	[illegible]	[illegible]
comp26490_c0_seq1.p2				
comp26492_c0_seq2.p1	sp|P51799|CLCN7_RAT_H(+)/Cl(-)_exchange_transporter_7_OS=Rattus_norvegicus_GN=Clcn7_PE=2_SV=1	4.00E-32	[illegible]	[illegible]
comp26495_c0_seq2.p1				
comp26499_c0_seq1.p1	sp|Q921L7|HEMK1_MOUSE_HemK_methyltransferase_family_member_1_OS=Mus_musculus_GN=Hemk1_PE=2_SV=1	2.00E-27	[illegible]	[illegible]
comp26499_c0_seq3.p1				
comp26499_c0_seq3.p6	sp|Q9Y5R4|HEMK1_HUMAN_HemK_methyltransferase_family_member_1_OS=Homo_sapiens_GN=HEMK1_PE=2_SV=1	1.00E-11	[illegible]	[illegible]
comp26500_c0_seq1.p1	sp|Q80UY1|CI041_MOUSE_UPF0586_protein_C9orf41_homolog_OS=Mus_musculus_PE=2_SV=1	2.00E-15	GO:0003674,GO:0005575,GO:0008150	[illegible]
comp26500_c0_seq1.p2				
comp26502_c0_seq1.p1				
comp26504_c0_seq1.p1				
comp26505_c0_seq1.p1				
comp26506_c0_seq3.p1				
comp26510_c0_seq2.p1	sp|Q6AYB3|ISY1_RAT_Pre-mRNA-splicing_factor_ISY1_homolog_OS=Rattus_norvegicus_GN=Isy1_PE=2_SV=1	4.00E-66	[illegible]	[illegible]
comp26510_c0_seq2.p2	sp|Q6C537|YKT6_YARLI_Synaptobrevin_homolog_YKT6_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=YKT6_PE=3_SV=1	2.00E-13	[illegible]	[illegible]
comp26511_c0_seq1.p1				
comp26512_c0_seq2.p1				
comp26515_c0_seq1.p1				
comp26518_c0_seq1.p1	sp|Q8RNT4|LOX_PSEAI_Oleic_acid_lipoxygenase_OS=Pseudomonas_aeruginosa_GN=lox_PE=1_SV=2	3.00E-58	[illegible]	[illegible]
comp26519_c0_seq1.p2	sp|P30175|ADF_LILLO_Actin-depolymerizing_factor_OS=Lilium_longiflorum_PE=2_SV=1	8.00E-37	[illegible]	[illegible]
comp26519_c0_seq1.p3				
comp26520_c0_seq2.p1				
comp26523_c0_seq1.p1	sp|A1APP9|SELD_PELPD_Selenide,_water_dikinase_OS=Pelobacter_propionicus_(strain_DSM_2379)_GN=selD_PE=3_SV=1	8.00E-44	[illegible]	[illegible]
comp26524_c0_seq2.p1				
comp26526_c0_seq3.p1	sp|Q9NRK6|ABCBA_HUMAN_ATP-binding_cassette_sub-family_B_member_10,_mitochondrial_OS=Homo_sapiens_GN=ABCB10_PE=1_SV=2	4.00E-94	[illegible]	[illegible]
comp26528_c0_seq1.p1				
comp26529_c0_seq1.p1				
comp26532_c0_seq1.p1				
comp26532_c1_seq1.p1				
comp26534_c0_seq1.p1	sp|Q9W3J5|SYFA_DROME_Probable_phenylalanine--tRNA_ligase_alpha_subunit_OS=Drosophila_melanogaster_GN=CG2263_PE=2_SV=1	0	[illegible]	[illegible]
comp26534_c0_seq1.p2	sp|P42784|CTPA_SYNP2_Carboxyl-terminal-processing_protease_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=ctpA_PE=3_SV=2	8.00E-56	[illegible]	[illegible]
comp26535_c0_seq2.p1	sp|B1GZ18|RNH2_UNCTG_Ribonuclease_HII_OS=Uncultured_termite_group_1_bacterium_phylotype_Rs-D17_GN=rnhB_PE=3_SV=1	3.00E-46	[illegible]	[illegible]
comp26536_c0_seq2.p1				
comp26538_c0_seq1.p1	sp|P28606|Y1628_SYNP2_Uncharacterized_protein_SYNPCC7002_A1628_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=SYNPCC7002_A1628_PE=3_SV=2	5.00E-98	GO:0008152,GO:0016787	[illegible]
comp26538_c0_seq3.p1	sp|P28606|Y1628_SYNP2_Uncharacterized_protein_SYNPCC7002_A1628_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=SYNPCC7002_A1628_PE=3_SV=2	7.00E-53	GO:0008152,GO:0016787	[illegible]
comp26539_c0_seq2.p1	sp|Q4WPF8|CCPR_ASPFU_Cytochrome_c_peroxidase,_mitochondrial_OS=Neosartorya_fumigata_(strain_ATCC_MYA-4609_/_Af293_/_CBS_101355_/_FGSC_A1100)_GN=ccp1_PE=3_SV=1	4.00E-92	[illegible]	[illegible]
comp26539_c0_seq3.p1	sp|Q4WPF8|CCPR_ASPFU_Cytochrome_c_peroxidase,_mitochondrial_OS=Neosartorya_fumigata_(strain_ATCC_MYA-4609_/_Af293_/_CBS_101355_/_FGSC_A1100)_GN=ccp1_PE=3_SV=1	6.00E-39	[illegible]	[illegible]
comp26540_c0_seq1.p1	sp|Q99PV0|PRP8_MOUSE_Pre-mRNA-processing-splicing_factor_8_OS=Mus_musculus_GN=Prpf8_PE=1_SV=2	0	[illegible]	[illegible]
comp26542_c0_seq1.p1				
comp26543_c0_seq1.p1				
comp26543_c0_seq2.p1				
comp26543_c0_seq6.p1				
comp26546_c0_seq4.p1	sp|Q3MHG1|SPTC1_BOVIN_Serine_palmitoyltransferase_1_OS=Bos_taurus_GN=SPTLC1_PE=2_SV=1	5.00E-102	[illegible]	[illegible]
comp26547_c0_seq2.p1				
comp26554_c0_seq1.p1				
comp26555_c0_seq4.p1				
comp26557_c0_seq1.p1				
comp26558_c0_seq1.p1				
comp26559_c0_seq1.p1	sp|Q9SUR9|SGT1A_ARATH_Protein_SGT1_homolog_A_OS=Arabidopsis_thaliana_GN=SGT1A_PE=1_SV=1	1.00E-40	[illegible]	[illegible]
comp26559_c0_seq1.p2	sp|O24633|PSB2B_ARATH_Proteasome_subunit_beta_type-2-B_OS=Arabidopsis_thaliana_GN=PBD2_PE=1_SV=1	5.00E-56	[illegible]	[illegible]
comp26560_c0_seq2.p1				
comp26561_c0_seq1.p3				
comp26563_c0_seq1.p1				
comp26563_c0_seq2.p1				
comp26564_c0_seq2.p1				
comp26565_c0_seq1.p1	sp|Q28GQ2|MECR_XENTR_Trans-2-enoyl-CoA_reductase,_mitochondrial_OS=Xenopus_tropicalis_GN=mecr_PE=2_SV=1	3.00E-93	[illegible]	[illegible]
comp26565_c0_seq4.p1	sp|Q28GQ2|MECR_XENTR_Trans-2-enoyl-CoA_reductase,_mitochondrial_OS=Xenopus_tropicalis_GN=mecr_PE=2_SV=1	9.00E-90	[illegible]	[illegible]
comp26566_c0_seq1.p1				
comp26568_c0_seq1.p1				
comp26569_c0_seq1.p1				
comp26569_c0_seq4.p1	sp|Q8L840|RQL4A_ARATH_ATP-dependent_DNA_helicase_Q-like_4A_OS=Arabidopsis_thaliana_GN=RECQL4A_PE=2_SV=1	9.00E-112	[illegible]	[illegible]
comp26569_c1_seq2.p1				
comp26570_c0_seq1.p1				
comp26571_c0_seq1.p1				
comp26571_c1_seq1.p1				
comp26571_c2_seq1.p1				
comp26572_c0_seq1.p1				
comp26573_c0_seq1.p1	sp|Q5ZI34|F213A_CHICK_Redox-regulatory_protein_FAM213A_OS=Gallus_gallus_GN=FAM213A_PE=2_SV=2	2.00E-17	[illegible]	[illegible]
comp26573_c0_seq4.p1				
comp26574_c0_seq1.p1	sp|P0CD62|LIMKB_DICDI_Probable_LIM_domain-containing_serine/threonine-protein_kinase_DDB_G0286997_OS=Dictyostelium_discoideum_GN=DDB_G0286997_PE=3_SV=1	2.00E-26	[illegible]	[illegible]
comp26575_c0_seq2.p1	sp|Q9H777|RNZ1_HUMAN_Zinc_phosphodiesterase_ELAC_protein_1_OS=Homo_sapiens_GN=ELAC1_PE=1_SV=2	7.00E-58	[illegible]	[illegible]
comp26575_c0_seq2.p3				
comp26575_c0_seq4.p1	sp|Q9H777|RNZ1_HUMAN_Zinc_phosphodiesterase_ELAC_protein_1_OS=Homo_sapiens_GN=ELAC1_PE=1_SV=2	3.00E-27	[illegible]	[illegible]
comp26576_c0_seq2.p1				
comp26576_c0_seq2.p2	sp|Q3EDF8|PPR28_ARATH_Pentatricopeptide_repeat-containing_protein_At1g09900_OS=Arabidopsis_thaliana_GN=At1g09900_PE=2_SV=1	6.00E-15	GO:0003674,GO:0016020	[illegible]
comp26576_c0_seq3.p1	sp|Q9SR00|PP213_ARATH_Pentatricopeptide_repeat-containing_protein_At3g04760,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g04760_PE=2_SV=1	2.00E-22	[illegible]	[illegible]
comp26578_c0_seq1.p1				
comp26578_c0_seq2.p1				
comp26581_c0_seq1.p1	sp|Q15269|PWP2_HUMAN_Periodic_tryptophan_protein_2_homolog_OS=Homo_sapiens_GN=PWP2_PE=1_SV=2	0	[illegible]	[illegible]
comp26581_c0_seq1.p2				
comp26583_c0_seq1.p2				
comp26583_c1_seq1.p1	sp|Q04832|HEXP_LEIMA_DNA-binding_protein_HEXBP_OS=Leishmania_major_GN=HEXBP_PE=4_SV=1	7.00E-17	[illegible]	[illegible]
comp26584_c0_seq1.p1				
comp26584_c0_seq2.p1				
comp26585_c0_seq1.p1	sp|Q8N0W3|FUK_HUMAN_L-fucose_kinase_OS=Homo_sapiens_GN=FUK_PE=2_SV=2	2.00E-84	[illegible]	[illegible]
comp26585_c0_seq2.p1	sp|Q8N0W3|FUK_HUMAN_L-fucose_kinase_OS=Homo_sapiens_GN=FUK_PE=2_SV=2	9.00E-21	[illegible]	[illegible]
comp26585_c0_seq3.p1	sp|O14772|FPGT_HUMAN_Fucose-1-phosphate_guanylyltransferase_OS=Homo_sapiens_GN=FPGT_PE=1_SV=2	3.00E-11	[illegible]	[illegible]
comp26586_c0_seq1.p1				
comp26587_c0_seq1.p1	sp|Q39593|SAC1_CHLRE_Putative_sulfur_deprivation_response_regulator_OS=Chlamydomonas_reinhardtii_GN=SAC1_PE=2_SV=1	2.00E-29	[illegible]	[illegible]
comp26587_c0_seq2.p1	sp|Q39593|SAC1_CHLRE_Putative_sulfur_deprivation_response_regulator_OS=Chlamydomonas_reinhardtii_GN=SAC1_PE=2_SV=1	7.00E-30	[illegible]	[illegible]
comp26588_c0_seq1.p1	sp|P59114|PCIF1_MOUSE_Phosphorylated_CTD-interacting_factor_1_OS=Mus_musculus_GN=Pcif1_PE=1_SV=1	1.00E-20	[illegible]	[illegible]
comp26588_c0_seq2.p1	sp|P59114|PCIF1_MOUSE_Phosphorylated_CTD-interacting_factor_1_OS=Mus_musculus_GN=Pcif1_PE=1_SV=1	1.00E-36	[illegible]	[illegible]
comp26589_c0_seq2.p1				
comp26590_c0_seq2.p1	sp|B5DFA1|TBD2A_RAT_TBC1_domain_family_member_2A_OS=Rattus_norvegicus_GN=Tbc1d2_PE=2_SV=1	4.00E-19	[illegible]	[illegible]
comp26590_c0_seq2.p2				
comp26592_c0_seq1.p2	sp|Q98TZ8|FLOT2_DANRE_Flotillin-2a_OS=Danio_rerio_GN=flot2a_PE=2_SV=2	6.00E-12	[illegible]	[illegible]
comp26593_c0_seq3.p1	sp|Q01581|HMCS1_HUMAN_Hydroxymethylglutaryl-CoA_synthase,_cytoplasmic_OS=Homo_sapiens_GN=HMGCS1_PE=1_SV=2	6.00E-129	[illegible]	[illegible]
comp26593_c0_seq3.p2				
comp26593_c0_seq3.p3				
comp26594_c0_seq3.p1	sp|B4EVG2|MNMA_PROMH_tRNA-specific_2-thiouridylase_mnmA_OS=Proteus_mirabilis_(strain_HI4320)_GN=mnmA_PE=3_SV=1	6.00E-59	[illegible]	[illegible]
comp26594_c0_seq3.p2	sp|P95041|MFTE_MYCTU_Putative_mycofactocin_biosynthesis_creatinase_MftE_OS=Mycobacterium_tuberculosis_GN=mftE_PE=3_SV=2	4.00E-11		
comp26594_c0_seq4.p1				
comp26595_c0_seq1.p1	sp|P27431|YCFD_ECOLI_Uncharacterized_protein_ycfD_OS=Escherichia_coli_(strain_K12)_GN=ycfD_PE=4_SV=2	3.00E-54	[illegible]	[illegible]
comp26596_c0_seq1.p1	sp|P06715|GSHR_ECOLI_Glutathione_reductase_OS=Escherichia_coli_(strain_K12)_GN=gor_PE=1_SV=1	2.00E-144	[illegible]	[illegible]
comp26596_c0_seq2.p1	sp|P78965|GSHR_SCHPO_Glutathione_reductase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=pgr1_PE=2_SV=2	2.00E-66	[illegible]	[illegible]
comp26596_c0_seq3.p1	sp|Q8RB46|SYG_THETN_Glycine--tRNA_ligase_OS=Thermoanaerobacter_tengcongensis_(strain_DSM_15242_/_JCM_11007_/_NBRC_100824_/_MB4)_GN=glyQS_PE=3_SV=1	3.00E-146	[illegible]	[illegible]
comp26598_c0_seq1.p1				
comp26599_c0_seq2.p1	sp|Q9EQW8|NDST4_MOUSE_Bifunctional_heparan_sulfate_N-deacetylase/N-sulfotransferase_4_OS=Mus_musculus_GN=Ndst4_PE=2_SV=2	4.00E-14	[illegible]	[illegible]
comp26600_c0_seq1.p1				
comp26601_c0_seq1.p1				
comp26601_c1_seq1.p1				
comp26602_c0_seq1.p2				
comp26602_c0_seq2.p1	sp|Q822B9|TILS_CHLCV_tRNA(Ile)-lysidine_synthase_OS=Chlamydophila_caviae_(strain_GPIC)_GN=tilS_PE=3_SV=1	2.00E-20	[illegible]	[illegible]
comp26604_c0_seq2.p1				
comp26604_c0_seq2.p3				
comp26606_c0_seq1.p1	sp|Q32L22|RPAC1_BOVIN_DNA-directed_RNA_polymerases_I_and_III_subunit_RPAC1_OS=Bos_taurus_GN=POLR1C_PE=2_SV=1	2.00E-49	[illegible]	[illegible]
comp26606_c0_seq3.p1	sp|Q32L22|RPAC1_BOVIN_DNA-directed_RNA_polymerases_I_and_III_subunit_RPAC1_OS=Bos_taurus_GN=POLR1C_PE=2_SV=1	2.00E-78	[illegible]	[illegible]
comp26607_c0_seq1.p1	sp|O74916|YJ75_SCHPO_Peptidase_M20_domain-containing_protein_C757.05c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC757.05c_PE=2_SV=1	1.00E-52	[illegible]	[illegible]
comp26607_c0_seq2.p1	sp|O74916|YJ75_SCHPO_Peptidase_M20_domain-containing_protein_C757.05c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC757.05c_PE=2_SV=1	5.00E-38	[illegible]	[illegible]
comp26608_c0_seq1.p1	sp|P73846|Y1717_SYNY3_Uncharacterized_protein_slr1717_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr1717_PE=4_SV=1	9.00E-29		
comp26608_c0_seq2.p1	sp|P73846|Y1717_SYNY3_Uncharacterized_protein_slr1717_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr1717_PE=4_SV=1	9.00E-29		
comp26609_c0_seq1.p1	sp|Q8BZ20|PAR12_MOUSE_Poly_[ADP-ribose]_polymerase_12_OS=Mus_musculus_GN=Parp12_PE=2_SV=3	9.00E-28	[illegible]	[illegible]
comp26610_c0_seq1.p1				
comp26612_c0_seq1.p1	sp|Q2TBN6|PCID2_BOVIN_PCI_domain-containing_protein_2_OS=Bos_taurus_GN=PCID2_PE=2_SV=1	9.00E-23	[illegible]	[illegible]
comp26612_c0_seq1.p3				
comp26612_c0_seq3.p1	sp|Q2TBN6|PCID2_BOVIN_PCI_domain-containing_protein_2_OS=Bos_taurus_GN=PCID2_PE=2_SV=1	1.00E-22	[illegible]	[illegible]
comp26612_c0_seq3.p3				
comp26614_c0_seq2.p1				
comp26615_c0_seq1.p1	sp|F8W2M1|HACE1_DANRE_E3_ubiquitin-protein_ligase_HACE1_OS=Danio_rerio_GN=hace1_PE=3_SV=2	4.00E-29	[illegible]	[illegible]
comp26616_c0_seq1.p1	sp|A1L4W5|BPM6_ARATH_BTB/POZ_and_MATH_domain-containing_protein_6_OS=Arabidopsis_thaliana_GN=BPM6_PE=1_SV=1	8.00E-14	[illegible]	[illegible]
comp26617_c0_seq2.p2				
comp26617_c0_seq3.p1	sp|Q55720|YC49L_SYNY3_Ycf49-like_protein_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll0608_PE=3_SV=1	7.00E-20	[illegible]	[illegible]
comp26618_c0_seq2.p1				
comp26618_c0_seq3.p1				
comp26620_c0_seq2.p1				
comp26620_c0_seq2.p2				
comp26622_c0_seq1.p2	sp|P70805|ALGG_AZOVI_Poly(beta-D-mannuronate)_C5_epimerase_OS=Azotobacter_vinelandii_GN=algG_PE=2_SV=1	1.00E-15	[illegible]	[illegible]
comp26622_c1_seq1.p2				
comp26622_c1_seq3.p2				
comp26622_c1_seq4.p1				
comp26623_c0_seq1.p1				
comp26623_c0_seq2.p1				
comp26625_c0_seq1.p1				
comp26625_c0_seq4.p1				
comp26626_c0_seq1.p1	sp|P46825|KLC_LOLPE_Kinesin_light_chain_OS=Loligo_pealeii_PE=2_SV=1	9.00E-30	[illegible]	[illegible]
comp26627_c0_seq3.p1				
comp26627_c0_seq3.p6				
comp26627_c0_seq3.p9				
comp26628_c0_seq1.p1	sp|Q7D745|Y2525_MYCTU_Putative_trans-acting_enoyl_reductase_MT2525_OS=Mycobacterium_tuberculosis_GN=MT2525_PE=3_SV=2	2.00E-56	[illegible]	[illegible]
comp26628_c0_seq2.p1				
comp26630_c0_seq1.p1	sp|P38576|IPYR_THET8_Inorganic_pyrophosphatase_OS=Thermus_thermophilus_(strain_HB8_/_ATCC_27634_/_DSM_579)_GN=ppa_PE=1_SV=2	3.00E-42	[illegible]	[illegible]
comp26630_c0_seq1.p2	sp|Q54EH6|PSF3_DICDI_Probable_DNA_replication_complex_GINS_protein_PSF3_OS=Dictyostelium_discoideum_GN=gins3_PE=3_SV=1	8.00E-30	[illegible]	[illegible]
comp26631_c0_seq1.p1				
comp26631_c0_seq2.p1				
comp26631_c0_seq3.p1				
comp26632_c0_seq1.p1	sp|Q54FQ8|EI2BG_DICDI_Translation_initiation_factor_eIF-2B_subunit_gamma_OS=Dictyostelium_discoideum_GN=eif2b3_PE=3_SV=1	5.00E-52	[illegible]	[illegible]
comp26632_c0_seq2.p1	sp|Q54FQ8|EI2BG_DICDI_Translation_initiation_factor_eIF-2B_subunit_gamma_OS=Dictyostelium_discoideum_GN=eif2b3_PE=3_SV=1	5.00E-52	[illegible]	[illegible]
comp26632_c0_seq3.p1	sp|Q54FQ8|EI2BG_DICDI_Translation_initiation_factor_eIF-2B_subunit_gamma_OS=Dictyostelium_discoideum_GN=eif2b3_PE=3_SV=1	9.00E-39	[illegible]	[illegible]
comp26632_c0_seq3.p3				
comp26633_c0_seq1.p1	sp|Q93YN9|IPPK_ARATH_Inositol-pentakisphosphate_2-kinase_OS=Arabidopsis_thaliana_GN=IPK1_PE=1_SV=1	1.00E-23	[illegible]	[illegible]
comp26633_c0_seq1.p2				
comp26633_c0_seq4.p1				
comp26634_c0_seq2.p1	sp|P73177|RN2H_SYNY3_Uncharacterized_ribonuclease_sll1290_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll1290_PE=3_SV=1	5.00E-79	[illegible]	[illegible]
comp26635_c0_seq1.p1				
comp26635_c0_seq3.p1				
comp26636_c0_seq1.p1				
comp26636_c0_seq3.p2				
comp26636_c0_seq4.p1				
comp26636_c1_seq1.p2				
comp26637_c1_seq1.p1				
comp26638_c0_seq1.p1	sp|Q119H9|MIAB_TRIEI_(Dimethylallyl)adenosine_tRNA_methylthiotransferase_MiaB_OS=Trichodesmium_erythraeum_(strain_IMS101)_GN=miaB_PE=3_SV=1	0	[illegible]	[illegible]
comp26639_c0_seq1.p1	sp|Q9JHF7|HPGDS_MOUSE_Hematopoietic_prostaglandin_D_synthase_OS=Mus_musculus_GN=Hpgds_PE=1_SV=3	2.00E-29	[illegible]	[illegible]
comp26639_c0_seq5.p1	sp|Q9JHF7|HPGDS_MOUSE_Hematopoietic_prostaglandin_D_synthase_OS=Mus_musculus_GN=Hpgds_PE=1_SV=3	7.00E-27	[illegible]	[illegible]
comp26641_c0_seq2.p2				
comp26643_c0_seq1.p1	sp|P46250|SEC14_CANAL_SEC14_cytosolic_factor_OS=Candida_albicans_(strain_SC5314_/_ATCC_MYA-2876)_GN=SEC14_PE=2_SV=1	4.00E-22	[illegible]	[illegible]
comp26643_c0_seq1.p4				
comp26644_c1_seq2.p1	sp|Q54RA4|Y3291_DICDI_Probable_iron/ascorbate_oxidoreductase_DDB_G0283291_OS=Dictyostelium_discoideum_GN=DDB_G0283291_PE=3_SV=1	5.00E-36	[illegible]	[illegible]
comp26644_c1_seq3.p1	sp|Q7LL04|YQK1_SCHPO_UPF0676_protein_C1494.01_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC1494.01_PE=3_SV=2	6.00E-18	[illegible]	[illegible]
comp26645_c0_seq1.p1	sp|O22609|DEGP1_ARATH_Protease_Do-like_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=DEGP1_PE=1_SV=2	7.00E-101	[illegible]	[illegible]
comp26645_c0_seq3.p1	sp|O22609|DEGP1_ARATH_Protease_Do-like_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=DEGP1_PE=1_SV=2	9.00E-93	[illegible]	[illegible]
comp26646_c0_seq2.p1				
comp26647_c0_seq1.p1				
comp26647_c0_seq2.p1	sp|Q8BLQ7|CTR4_MOUSE_Cationic_amino_acid_transporter_4_OS=Mus_musculus_GN=Slc7a4_PE=1_SV=1	7.00E-49	[illegible]	[illegible]
comp26649_c0_seq1.p1				
comp26649_c0_seq2.p1				
comp26649_c0_seq3.p1				
comp26650_c2_seq3.p1	sp|Q9CSH3|RRP44_MOUSE_Exosome_complex_exonuclease_RRP44_OS=Mus_musculus_GN=Dis3_PE=2_SV=4	0	[illegible]	[illegible]
comp26651_c0_seq2.p1				
comp26653_c0_seq1.p1	sp|P74391|RADA_SYNY3_DNA_repair_protein_RadA_homolog_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=radA_PE=3_SV=1	4.00E-94	[illegible]	[illegible]
comp26653_c0_seq2.p1	sp|P74391|RADA_SYNY3_DNA_repair_protein_RadA_homolog_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=radA_PE=3_SV=1	4.00E-90	[illegible]	[illegible]
comp26653_c0_seq2.p5				
comp26654_c0_seq1.p1	sp|Q6NRC7|TBC23_XENLA_TBC1_domain_family_member_23_OS=Xenopus_laevis_GN=tbc1d23_PE=2_SV=1	6.00E-23	[illegible]	[illegible]
comp26657_c0_seq2.p1	sp|Q8BW96|KCC1D_MOUSE_Calcium/calmodulin-dependent_protein_kinase_type_1D_OS=Mus_musculus_GN=Camk1d_PE=1_SV=2	1.00E-47	[illegible]	[illegible]
comp26659_c0_seq1.p1	sp|Q9R6X4|ZDS_NOSS1_Zeta-carotene_desaturase_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=crtQ_PE=3_SV=2	0	[illegible]	[illegible]
comp26661_c1_seq1.p1				
comp26662_c0_seq1.p3	sp|P62313|LSM6_MOUSE_U6_snRNA-associated_Sm-like_protein_LSm6_OS=Mus_musculus_GN=Lsm6_PE=2_SV=1	8.00E-40	[illegible]	[illegible]
comp26663_c0_seq1.p1	sp|P54697|MYOJ_DICDI_Myosin-J_heavy_chain_OS=Dictyostelium_discoideum_GN=myoJ_PE=4_SV=2	3.00E-145	[illegible]	[illegible]
comp26664_c0_seq1.p1				
comp26664_c0_seq2.p1				
comp26664_c0_seq3.p1				
comp26664_c0_seq4.p1				
comp26665_c0_seq2.p1	sp|Q8NFI3|ENASE_HUMAN_Cytosolic_endo-beta-N-acetylglucosaminidase_OS=Homo_sapiens_GN=ENGASE_PE=1_SV=1	1.00E-76	[illegible]	[illegible]
comp26666_c0_seq2.p1	sp|Q5U680|SAMC_MOUSE_S-adenosylmethionine_mitochondrial_carrier_protein_OS=Mus_musculus_GN=Slc25a26_PE=2_SV=2	3.00E-77	[illegible]	[illegible]
comp26666_c0_seq4.p2	sp|Q9P3U4|YKX2_SCHPO_Uncharacterized_RING_finger_protein_C328.02_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC328.02_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp26666_c0_seq4.p3				
comp26666_c0_seq5.p2	sp|Q5U680|SAMC_MOUSE_S-adenosylmethionine_mitochondrial_carrier_protein_OS=Mus_musculus_GN=Slc25a26_PE=2_SV=2	3.00E-21	[illegible]	[illegible]
comp26667_c0_seq2.p3				
comp26668_c0_seq3.p1	sp|Q96CS3|FAF2_HUMAN_FAS-associated_factor_2_OS=Homo_sapiens_GN=FAF2_PE=1_SV=2	1.00E-15	[illegible]	[illegible]
comp26669_c0_seq1.p1				
comp26669_c0_seq1.p2				
comp26670_c0_seq1.p1				
comp26671_c0_seq3.p1	sp|P54683|TAGB_DICDI_Serine_protease/ABC_transporter_B_family_protein_tagB_OS=Dictyostelium_discoideum_GN=tagB_PE=3_SV=2	7.00E-21	[illegible]	[illegible]
comp26674_c0_seq1.p1	sp|Q5C9Z4|NOM1_HUMAN_Nucleolar_MIF4G_domain-containing_protein_1_OS=Homo_sapiens_GN=NOM1_PE=1_SV=1	3.00E-22	[illegible]	[illegible]
comp26674_c0_seq2.p1	sp|Q07204|F16P1_BRANA_Fructose-1,6-bisphosphatase,_chloroplastic_OS=Brassica_napus_GN=FBP_PE=2_SV=1	4.00E-57	[illegible]	[illegible]
comp26674_c0_seq2.p3	sp|Q3UFM5|NOM1_MOUSE_Nucleolar_MIF4G_domain-containing_protein_1_OS=Mus_musculus_GN=Nom1_PE=2_SV=2	6.00E-27	[illegible]	[illegible]
comp26676_c0_seq2.p2				
comp26677_c0_seq2.p1				
comp26679_c0_seq1.p1				
comp26680_c0_seq1.p1	sp|Q08759|MYB_XENLA_Transcriptional_activator_Myb_OS=Xenopus_laevis_GN=myb_PE=2_SV=1	8.00E-58	[illegible]	[illegible]
comp26681_c0_seq1.p1				
comp26681_c0_seq1.p2				
comp26681_c0_seq1.p5				
comp26681_c0_seq2.p1				
comp26681_c0_seq2.p2				
comp26683_c0_seq2.p1				
comp26683_c0_seq2.p2				
comp26684_c0_seq1.p1				
comp26684_c0_seq4.p1				
comp26685_c0_seq2.p3				
comp26685_c0_seq3.p1				
comp26686_c0_seq1.p1	sp|P74838|FKBM_STRTA_31-O-demethyl-FK506_methyltransferase_FkbM_OS=Streptomyces_tacrolimicus_GN=fkbM_PE=1_SV=1	2.00E-15	[illegible]	[illegible]
comp26686_c0_seq1.p2				
comp26686_c0_seq2.p1	sp|P74838|FKBM_STRTA_31-O-demethyl-FK506_methyltransferase_FkbM_OS=Streptomyces_tacrolimicus_GN=fkbM_PE=1_SV=1	3.00E-15	[illegible]	[illegible]
comp26687_c0_seq1.p2	sp|Q9S7E9|GGT2_ARATH_Glutamate--glyoxylate_aminotransferase_2_OS=Arabidopsis_thaliana_GN=GGAT2_PE=1_SV=1	1.00E-19	[illegible]	[illegible]
comp26687_c0_seq2.p1	sp|Q9LR30|GGT1_ARATH_Glutamate--glyoxylate_aminotransferase_1_OS=Arabidopsis_thaliana_GN=GGAT1_PE=1_SV=1	0	[illegible]	[illegible]
comp26690_c0_seq1.p1				
comp26691_c0_seq2.p1	sp|Q7M3S9|RNGB_DICDI_RING_finger_protein_B_OS=Dictyostelium_discoideum_GN=rngB_PE=2_SV=2	2.00E-20	[illegible]	[illegible]
comp26691_c0_seq6.p1	sp|P80197|AFK_PHYPO_Actin-fragmin_kinase_OS=Physarum_polycephalum_PE=1_SV=2	4.00E-22	[illegible]	[illegible]
comp26693_c0_seq1.p2	sp|P49373|TFS2_SCHPO_Transcription_elongation_factor_S-II_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=tfs1_PE=2_SV=1	6.00E-11	[illegible]	[illegible]
comp26693_c0_seq1.p3				
comp26694_c0_seq1.p1	sp|Q5REA7|FADS2_PONAB_Fatty_acid_desaturase_2_OS=Pongo_abelii_GN=FADS2_PE=2_SV=1	5.00E-25	[illegible]	[illegible]
comp26694_c0_seq2.p1	sp|A4IFP3|FADS3_BOVIN_Fatty_acid_desaturase_3_OS=Bos_taurus_GN=FADS3_PE=2_SV=1	7.00E-13	[illegible]	[illegible]
comp26695_c0_seq2.p1	sp|Q10MQ2|DAPAT_ORYSJ_Probable_LL-diaminopimelate_aminotransferase,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=AGD2_PE=2_SV=1	8.00E-149	[illegible]	[illegible]
comp26695_c0_seq2.p3				
comp26697_c0_seq1.p2				
comp26697_c0_seq3.p1	sp|Q99797|MIPEP_HUMAN_Mitochondrial_intermediate_peptidase_OS=Homo_sapiens_GN=MIPEP_PE=1_SV=2	1.00E-95	[illegible]	[illegible]
comp26698_c0_seq1.p2				
comp26699_c0_seq2.p1				
comp26700_c0_seq2.p1				
comp26700_c0_seq3.p1				
comp26701_c0_seq2.p1				
comp26701_c0_seq3.p1				
comp26702_c0_seq1.p1	sp|Q5UR04|YR911_MIMIV_Putative_ankyrin_repeat_protein_R911_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R911_PE=4_SV=1	6.00E-19		
comp26702_c0_seq1.p2				
comp26702_c0_seq2.p2	sp|Q5UP39|YR873_MIMIV_Putative_ankyrin_repeat_protein_R873_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R873_PE=4_SV=1	6.00E-16		
comp26704_c0_seq1.p1				
comp26704_c0_seq2.p1				
comp26705_c0_seq3.p1	sp|P55826|PPOC_ARATH_Protoporphyrinogen_oxidase,_chloroplastic_OS=Arabidopsis_thaliana_GN=PPOX_PE=2_SV=1	3.00E-120	[illegible]	[illegible]
comp26706_c0_seq1.p1				
comp26706_c0_seq2.p1				
comp26707_c0_seq1.p1	sp|P71020|YLMH_BACSU_Putative_RNA-binding_protein_ylmH_OS=Bacillus_subtilis_GN=ylmH_PE=4_SV=1	4.00E-23	GO:0003723,GO:0003723	[illegible]
comp26707_c0_seq3.p1				
comp26707_c0_seq4.p1				
comp26709_c1_seq1.p1	sp|P54680|FIMB_DICDI_Fimbrin_OS=Dictyostelium_discoideum_GN=fimA_PE=2_SV=2	2.00E-117	[illegible]	[illegible]
comp26709_c1_seq2.p1	sp|P54680|FIMB_DICDI_Fimbrin_OS=Dictyostelium_discoideum_GN=fimA_PE=2_SV=2	2.00E-117	[illegible]	[illegible]
comp26710_c0_seq1.p1	sp|O65781|GALE2_CYATE_UDP-glucose_4-epimerase_GEPI48_OS=Cyamopsis_tetragonoloba_PE=2_SV=1	1.00E-123	[illegible]	[illegible]
comp26710_c0_seq3.p1	sp|Q9T0A7|GALE3_ARATH_UDP-glucose_4-epimerase_3_OS=Arabidopsis_thaliana_GN=At4g23920_PE=2_SV=1	4.00E-100	[illegible]	[illegible]
comp26711_c0_seq2.p1	sp|Q9JLR1|S61A2_MOUSE_Protein_transport_protein_Sec61_subunit_alpha_isoform_2_OS=Mus_musculus_GN=Sec61a2_PE=2_SV=3	0	[illegible]	[illegible]
comp26712_c0_seq1.p1				
comp26713_c0_seq1.p1	sp|Q8LAP6|PAP12_ARATH_Probable_plastid-lipid-associated_protein_12,_chloroplastic_OS=Arabidopsis_thaliana_GN=PAP12_PE=2_SV=1	5.00E-49	[illegible]	[illegible]
comp26713_c0_seq2.p1	sp|Q8LAP6|PAP12_ARATH_Probable_plastid-lipid-associated_protein_12,_chloroplastic_OS=Arabidopsis_thaliana_GN=PAP12_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp26714_c0_seq2.p1	sp|Q99145|HIS1_YARLI_ATP_phosphoribosyltransferase_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=HIS1_PE=3_SV=1	8.00E-89	[illegible]	[illegible]
comp26717_c0_seq1.p1				
comp26717_c0_seq1.p3				
comp26717_c0_seq3.p1				
comp26719_c0_seq1.p1	sp|Q6AUQ4|P2C47_ORYSJ_Probable_protein_phosphatase_2C_47_OS=Oryza_sativa_subsp._japonica_GN=Os05g0134200_PE=2_SV=1	8.00E-30	[illegible]	[illegible]
comp26720_c0_seq2.p1	sp|Q9SL02|RAD50_ARATH_DNA_repair_protein_RAD50_OS=Arabidopsis_thaliana_GN=RAD50_PE=1_SV=2	1.00E-172	[illegible]	[illegible]
comp26721_c1_seq1.p1				
comp26722_c0_seq1.p1	sp|Q9C7S7|ERO1_ARATH_Endoplasmic_oxidoreductin-1_OS=Arabidopsis_thaliana_GN=AERO1_PE=1_SV=1	6.00E-95	[illegible]	[illegible]
comp26722_c0_seq2.p1	sp|Q9C7S7|ERO1_ARATH_Endoplasmic_oxidoreductin-1_OS=Arabidopsis_thaliana_GN=AERO1_PE=1_SV=1	1.00E-92	[illegible]	[illegible]
comp26724_c0_seq1.p1				
comp26726_c0_seq2.p1				
comp26728_c0_seq1.p1	sp|P27119|DCOR_MUSPA_Ornithine_decarboxylase_OS=Mus_pahari_GN=Odc1_PE=2_SV=1	1.00E-72	[illegible]	[illegible]
comp26728_c0_seq3.p1	sp|P27119|DCOR_MUSPA_Ornithine_decarboxylase_OS=Mus_pahari_GN=Odc1_PE=2_SV=1	1.00E-72	[illegible]	[illegible]
comp26729_c0_seq2.p1	sp|Q7SXP4|SRS1A_DANRE_Serine/arginine-rich_splicing_factor_1A_OS=Danio_rerio_GN=srsf1a_PE=2_SV=2	4.00E-25	[illegible]	[illegible]
comp26730_c0_seq1.p1	sp|Q17R09|PRP16_BOVIN_Pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_PRP16_OS=Bos_taurus_GN=DHX38_PE=2_SV=1	0	[illegible]	[illegible]
comp26731_c0_seq1.p1	sp|Q7Z494|NPHP3_HUMAN_Nephrocystin-3_OS=Homo_sapiens_GN=NPHP3_PE=1_SV=1	6.00E-45	[illegible]	[illegible]
comp26732_c0_seq1.p1	sp|Q9P4S5|CCA1_CANGA_CCA_tRNA_nucleotidyltransferase,_mitochondrial_OS=Candida_glabrata_(strain_ATCC_2001_/_CBS_138_/_JCM_3761_/_NBRC_0622_/_NRRL_Y-65)_GN=CCA1_PE=1_SV=2	3.00E-58	[illegible]	[illegible]
comp26732_c0_seq1.p2				
comp26733_c0_seq1.p1				
comp26733_c0_seq2.p1	sp|P34913|HYES_HUMAN_Epoxide_hydrolase_2_OS=Homo_sapiens_GN=EPHX2_PE=1_SV=2	5.00E-14	[illegible]	[illegible]
comp26733_c0_seq2.p2				
comp26733_c0_seq3.p1	sp|Q0IIS3|EPHX3_XENTR_Epoxide_hydrolase_3_OS=Xenopus_tropicalis_GN=ephx3_PE=2_SV=1	8.00E-12	[illegible]	[illegible]
comp26734_c0_seq1.p1				
comp26734_c0_seq2.p1				
comp26734_c0_seq4.p1				
comp26734_c0_seq5.p1				
comp26735_c0_seq1.p1	sp|P16970|ABCD3_RAT_ATP-binding_cassette_sub-family_D_member_3_OS=Rattus_norvegicus_GN=Abcd3_PE=1_SV=3	2.00E-97	[illegible]	[illegible]
comp26735_c0_seq3.p1	sp|P55096|ABCD3_MOUSE_ATP-binding_cassette_sub-family_D_member_3_OS=Mus_musculus_GN=Abcd3_PE=1_SV=2	9.00E-63	[illegible]	[illegible]
comp26738_c0_seq1.p1				
comp26739_c0_seq2.p1	sp|Q54QB1|ERK2_DICDI_Extracellular_signal-regulated_kinase_2_OS=Dictyostelium_discoideum_GN=erkB_PE=1_SV=1	4.00E-164	[illegible]	[illegible]
comp26739_c0_seq3.p1	sp|Q54QB1|ERK2_DICDI_Extracellular_signal-regulated_kinase_2_OS=Dictyostelium_discoideum_GN=erkB_PE=1_SV=1	1.00E-36	[illegible]	[illegible]
comp26739_c0_seq3.p2	sp|Q54QB1|ERK2_DICDI_Extracellular_signal-regulated_kinase_2_OS=Dictyostelium_discoideum_GN=erkB_PE=1_SV=1	1.00E-59	[illegible]	[illegible]
comp26740_c0_seq1.p1				
comp26740_c0_seq2.p1				
comp26741_c0_seq1.p1				
comp26741_c0_seq2.p1				
comp26741_c0_seq3.p1				
comp26743_c0_seq3.p1	sp|Q7Z4G4|TRM11_HUMAN_tRNA_(guanine(10)-N2)-methyltransferase_homolog_OS=Homo_sapiens_GN=TRMT11_PE=1_SV=1	5.00E-15	[illegible]	[illegible]
comp26743_c0_seq4.p1	sp|Q5R962|TRM11_PONAB_tRNA_(guanine(10)-N2)-methyltransferase_homolog_OS=Pongo_abelii_GN=TRMT11_PE=2_SV=1	3.00E-14	[illegible]	[illegible]
comp26743_c0_seq4.p3	sp|Q5DHJ5|IFT46_SCHJA_Intraflagellar_transport_protein_46_homolog_OS=Schistosoma_japonicum_GN=SJCHGC08984_PE=2_SV=1	2.00E-46	[illegible]	[illegible]
comp26743_c0_seq6.p1	sp|Q8BX09|RBBP5_MOUSE_Retinoblastoma-binding_protein_5_OS=Mus_musculus_GN=Rbbp5_PE=1_SV=2	2.00E-42	[illegible]	[illegible]
comp26743_c0_seq6.p2				
comp26743_c0_seq6.p7				
comp26744_c0_seq1.p1	sp|P45482|FTSZ_NOSS1_Cell_division_protein_FtsZ_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=ftsZ_PE=3_SV=2	3.00E-94	[illegible]	[illegible]
comp26744_c0_seq2.p1	sp|P45482|FTSZ_NOSS1_Cell_division_protein_FtsZ_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=ftsZ_PE=3_SV=2	4.00E-99	[illegible]	[illegible]
comp26744_c0_seq3.p1	sp|P45482|FTSZ_NOSS1_Cell_division_protein_FtsZ_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=ftsZ_PE=3_SV=2	7.00E-94	[illegible]	[illegible]
comp26744_c0_seq4.p1	sp|P45482|FTSZ_NOSS1_Cell_division_protein_FtsZ_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=ftsZ_PE=3_SV=2	1.00E-98	[illegible]	[illegible]
comp26745_c0_seq3.p1	sp|O21272|NDUS7_RECAM_NADH-ubiquinone_oxidoreductase_20_kDa_subunit_OS=Reclinomonas_americana_GN=NAD10_PE=3_SV=1	6.00E-83	[illegible]	[illegible]
comp26745_c0_seq3.p3				
comp26746_c0_seq2.p1				
comp26746_c1_seq1.p1				
comp26748_c0_seq1.p1	sp|Q5FVR8|TBCC1_RAT_TBCC_domain-containing_protein_1_OS=Rattus_norvegicus_GN=Tbccd1_PE=2_SV=1	2.00E-28	[illegible]	[illegible]

comp26748_c0_seq1.p3			
comp26750_c0_seq1.p1	sp|Q8AVX5|XRP2_XENLA_Protein_XRP2_OS=Xenopus_laevis_GN=rp2_PE=2_SV=3	3.00E-19	GO:0000166,GO:0000902,GO:0003779,GO:0004550,GO:0005096,GO:0005096,GO:0005524,GO:0005525,GO:0005737,GO:0005886,GO:0005886,GO:0005886,GO:0006165,GO:0006183,GO:0006228,GO:0006241,GO:0007010,GO:0016020,GO:0043547,GO:0043547,GO:0007023
comp26750_c0_seq2.p1	sp|Q8AVX5|XRP2_XENLA_Protein_XRP2_OS=Xenopus_laevis_GN=rp2_PE=2_SV=3	6.00E-19	GO:0000166,GO:0000902,GO:0003779,GO:0004550,GO:0005096,GO:0005096,GO:0005524,GO:0005525,GO:0005737,GO:0005886,GO:0005886,GO:0005886,GO:0006165,GO:0006183,GO:0006228,GO:0006241,GO:0007010,GO:0016020,GO:0043547,GO:0043547,GO:0007023
comp26750_c0_seq3.p1	sp|Q8AVX5|XRP2_XENLA_Protein_XRP2_OS=Xenopus_laevis_GN=rp2_PE=2_SV=3	3.00E-30	GO:0000166,GO:0000902,GO:0003779,GO:0004550,GO:0005096,GO:0005096,GO:0005524,GO:0005525,GO:0005737,GO:0005886,GO:0005886,GO:0005886,GO:0006165,GO:0006183,GO:0006228,GO:0006241,GO:0007010,GO:0016020,GO:0043547,GO:0043547,GO:0007023
comp26751_c0_seq3.p1			
comp26753_c0_seq1.p1			
comp26754_c0_seq2.p1	sp|B9EYD3|PLA4_ORYSJ_Phospholipase_A1-II_4_OS=Oryza_sativa_subsp._japonica_GN=Os01g0652300_PE=2_SV=2	5.00E-19	GO:0005737,GO:0005737,GO:0005737,GO:0006629,GO:0006629,GO:0008970,GO:0016042,GO:0016787
comp26754_c1_seq1.p1	sp|Q3B8Q2|IF4A3_RAT_Eukaryotic_initiation_factor_4A-III_OS=Rattus_norvegicus_GN=Eif4a3_PE=1_SV=1	0	GO:0000166,GO:0000184,GO:0000184,GO:0000381,GO:0003676,GO:0003723,GO:0003729,GO:0004004,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005681,GO:0005737,GO:0005737,GO:0006200,GO:0006200,GO:0006364,GO:0006397,GO:0006417,GO:0006810,GO:0008026,GO:0008143,GO:0008380,GO:0016020,GO:0016607,GO:0016787,GO:0017148,GO:0035145,GO:0044822,GO:0045727,GO:0048701,GO:0048701,GO:0051028,GO:0071013
comp26755_c0_seq1.p1			
comp26756_c0_seq2.p1	sp|P53468|ACT1_OXYTR_Actin,_cytoplasmic_OS=Oxytricha_trifallax_PE=3_SV=1	3.00E-44	GO:0000166,GO:0005524,GO:0005737,GO:0005856,GO:0005856
comp26756_c0_seq3.p1	sp|P27131|ACT1_NAEFO_Actin-1_OS=Naegleria_fowleri_PE=2_SV=2	6.00E-76	GO:0000166,GO:0005524,GO:0005737,GO:0005856,GO:0005856
comp26756_c0_seq3.p10			
comp26756_c0_seq3.p2	sp|B2HDP8|OTSB_MYCMM_Trehalose-phosphate_phosphatase_OS=Mycobacterium_marinum_(strain_ATCC_BAA-535_/_M)_GN=otsB_PE=3_SV=1	2.00E-43	GO:0003824,GO:0004805,GO:0005992,GO:0005992,GO:0008152,GO:0016311,GO:0016787,GO:0046872
comp26756_c0_seq3.p8			
comp26757_c0_seq3.p1			
comp26757_c0_seq4.p1			
comp26758_c0_seq1.p1	sp|P01103|MYB_CHICK_Transcriptional_activator_Myb_OS=Gallus_gallus_GN=MYB_PE=2_SV=1	1.00E-37	GO:0003677,GO:0003677,GO:0003682,GO:0005515,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0006355,GO:0010468
comp26760_c0_seq1.p1			
comp26761_c0_seq1.p1			
comp26763_c0_seq1.p1	sp|Q51363|NADB_PSEAE_L-aspartate_oxidase_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=nadB_PE=3_SV=1	4.00E-91	GO:0005737,GO:0005737,GO:0005737,GO:0008734,GO:0008734,GO:0009435,GO:0009435,GO:0016491,GO:0016491,GO:0019363,GO:0044318,GO:0055114,GO:0055114
comp26764_c0_seq1.p1			
comp26765_c0_seq1.p1	sp|Q54KA7|SECG_DICDI_Ankyrin_repeat,_PH_and_SEC7_domain_containing_protein_secG_OS=Dictyostelium_discoideum_GN=secG_PE=2_SV=1	6.00E-30	GO:0005086,GO:0005764,GO:0005829,GO:0006935,GO:0030036,GO:0031154,GO:0031589,GO:0032012,GO:0043327,GO:0043547
comp26768_c0_seq1.p1	sp|Q5ZJF6|DDX10_CHICK_Probable_ATP-dependent_RNA_helicase_DDX10_OS=Gallus_gallus_GN=DDX10_PE=2_SV=1	1.00E-161	GO:0000166,GO:0003676,GO:0003723,GO:0004386,GO:0005524,GO:0005524,GO:0006200,GO:0008026,GO:0008152,GO:0008152,GO:0016787
comp26769_c0_seq1.p1			
comp26770_c0_seq1.p1	sp|Q5UP57|P4H_MIMIV_Putative_prolyl_4-hydroxylase_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L593_PE=1_SV=1	4.00E-13	GO:0004656,GO:0005506,GO:0016491,GO:0016491,GO:0016705,GO:0016706,GO:0019012,GO:0019012,GO:0019511,GO:0031418,GO:0031418,GO:0046872,GO:0051213,GO:0055114,GO:0055114
comp26771_c0_seq1.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	8.00E-49	
comp26771_c1_seq1.p1	sp|Q4V8A2|CDC27_RAT_Cell_division_cycle_protein_27_homolog_OS=Rattus_norvegicus_GN=Cdc27_PE=2_SV=1	1.00E-110	GO:0005634,GO:0005634,GO:0005634,GO:0005680,GO:0005680,GO:0005737,GO:0005813,GO:0005876,GO:0007091,GO:0016567,GO:0019903,GO:0070979,GO:0070979
comp26772_c0_seq2.p1	sp|C5D6U5|MENE_GEOSW_2-succinylbenzoate--CoA_ligase_OS=Geobacillus_sp._(strain_WCH70)_GN=menE_PE=3_SV=1	1.00E-43	GO:0000166,GO:0003824,GO:0005524,GO:0005524,GO:0008152,GO:0008756,GO:0008756,GO:0008756,GO:0009234,GO:0009234,GO:0009234,GO:0009234,GO:0016874
comp26772_c0_seq2.p2			
comp26773_c0_seq1.p2			
comp26774_c0_seq1.p2			
comp26774_c0_seq2.p1	sp|Q5QQ55|XYLT_CIOIN_Xylosyltransferase_OS=Ciona_intestinalis_GN=xt_PE=2_SV=1	4.00E-21	GO:0000139,GO:0005783,GO:0005789,GO:0005794,GO:0006024,GO:0008375,GO:0015012,GO:0016020,GO:0016020,GO:0016021,GO:0016740,GO:0016757,GO:0030158,GO:0030158,GO:0030206
comp26774_c0_seq2.p5			
comp26775_c0_seq1.p1			
comp26777_c0_seq1.p1			
comp26778_c0_seq1.p1	sp|Q9V3S9|BGM_DROME_Very_long-chain-fatty-acid--CoA_ligase_bubblegum_OS=Drosophila_melanogaster_GN=bgm_PE=2_SV=1	1.00E-26	GO:0000166,GO:0001676,GO:0003824,GO:0004467,GO:0004467,GO:0004467,GO:0005524,GO:0005575,GO:0006629,GO:0006631,GO:0008152,GO:0016874,GO:0034976
comp26779_c0_seq1.p1	sp|Q6LA54|YF48_SCHPO_Uncharacterized_WD_repeat-containing_protein_C3H5.08c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC3H5.08c_PE=1_SV=2	1.00E-45	GO:0003674,GO:0005634,GO:0005634,GO:0005634,GO:0005783,GO:0005783,GO:0005789,GO:0008150,GO:0043234,GO:0044732
comp26780_c0_seq1.p1			
comp26781_c0_seq1.p1			
comp26781_c0_seq5.p1	sp|Q6ZQ89|MARH6_MOUSE_E3_ubiquitin-protein_ligase_MARCH6_OS=Mus_musculus_GN=March6_PE=2_SV=2	2.00E-25	GO:0004842,GO:0005783,GO:0005789,GO:0008270,GO:0016020,GO:0016020,GO:0016021,GO:0016567,GO:0016874,GO:0019899,GO:0030176,GO:0030176,GO:0031624,GO:0046872,GO:0070936,GO:0070936
comp26781_c1_seq2.p1	sp|Q54CX6|3HIDH_DICDI_Probable_3-hydroxyisobutyrate_dehydrogenase,_mitochondrial_OS=Dictyostelium_discoideum_GN=hibA_PE=3_SV=1	4.00E-71	GO:0004616,GO:0005739,GO:0005739,GO:0006098,GO:0006574,GO:0008442,GO:0008442,GO:0009083,GO:0016491,GO:0016491,GO:0016616,GO:0044351,GO:0050662,GO:0051287,GO:0055114,GO:0055114
comp26783_c0_seq1.p1			
comp26784_c0_seq1.p1			
comp26787_c0_seq3.p1	sp|Q9NYQ2|HAOX2_MOUSE_Hydroxyacid_oxidase_2_OS=Mus_musculus_GN=Hao2_PE=2_SV=1	1.00E-47	GO:0003824,GO:0003973,GO:0003973,GO:0003973,GO:0005102,GO:0005739,GO:0005777,GO:0005777,GO:0005777,GO:0005777,GO:0010181,GO:0016491,GO:0016491,GO:0018924,GO:0019395,GO:0051260,GO:0052852,GO:0052853,GO:0052853,GO:0052854,GO:0055114,GO:0055114,GO:0070062
comp26787_c0_seq3.p2			
comp26787_c0_seq4.p1	sp|Q9UJM8|HAOX1_HUMAN_Hydroxyacid_oxidase_1_OS=Homo_sapiens_GN=HAO1_PE=1_SV=1	4.00E-76	GO:0001561,GO:0003824,GO:0003973,GO:0003973,GO:0003973,GO:0005102,GO:0005777,GO:0005777,GO:0005777,GO:0005782,GO:0005782,GO:0006979,GO:0008891,GO:0008891,GO:0008891,GO:0010181,GO:0010181,GO:0016491,GO:0016491,GO:0034641,GO:0044281,GO:0046296,GO:0046296,GO:0046487,GO:0047969,GO:0052852,GO:0052853,GO:0052854,GO:0055114,GO:0055114
comp26787_c0_seq4.p2			
comp2679_c0_seq1.p1	sp|P07018|MCP4_ECOLI_Methyl-accepting_chemotaxis_protein_IV_OS=Escherichia_coli_(strain_K12)_GN=tap_PE=1_SV=2	4.00E-63	GO:0004871,GO:0004871,GO:0004871,GO:0004888,GO:0004888,GO:0005886,GO:0005886,GO:0005886,GO:0005887,GO:0006935,GO:0006935,GO:0006935,GO:0007165,GO:0007165,GO:0016020,GO:0016020,GO:0016021,GO:0016021

comp26968_c0_seq2.p1	sp|P20425|KCY_DICDI_UMP-CMP_kinase_OS=Dictyostelium_discoideum_GN=pyrK_PE=1_SV=2	2.00E-31	[illegible]	[illegible]
comp26969_c0_seq1.p1	sp|Q54PF3|CSN5_DICDI_COP9_signalosome_complex_subunit_5_OS=Dictyostelium_discoideum_GN=csn5_PE=1_SV=1	3.00E-62	[illegible]	[illegible]
comp26970_c0_seq2.p1	sp|Q60HE9|MA2B1_MACFA_Lysosomal_alpha-mannosidase_OS=Macaca_fascicularis_GN=MAN2B1_PE=2_SV=1	2.00E-142	[illegible]	[illegible]
comp26970_c0_seq4.p1	sp|Q8VHC8|MA2B1_CAVPO_Lysosomal_alpha-mannosidase_OS=Cavia_porcellus_GN=MAN2B1_PE=1_SV=1	2.00E-87	[illegible]	[illegible]
comp26971_c0_seq1.p1				
comp26971_c0_seq2.p1				
comp26972_c0_seq2.p1				
comp26973_c0_seq1.p1				
comp26973_c0_seq1.p2				
comp26974_c0_seq1.p1	sp|Q98TZ8|FLOT2_DANRE_Flotillin-2a_OS=Danio_rerio_GN=flot2a_PE=2_SV=2	4.00E-59	[illegible]	[illegible]
comp26974_c0_seq2.p1	sp|Q98TZ8|FLOT2_DANRE_Flotillin-2a_OS=Danio_rerio_GN=flot2a_PE=2_SV=2	2.00E-63	[illegible]	[illegible]
comp26975_c0_seq1.p1	sp|Q640V9|TATD1_XENLA_Putative_deoxyribonuclease_TATDN1_OS=Xenopus_laevis_GN=tatdn1_PE=2_SV=1	9.00E-63	[illegible]	[illegible]
comp26975_c0_seq4.p1	sp|Q640V9|TATD1_XENLA_Putative_deoxyribonuclease_TATDN1_OS=Xenopus_laevis_GN=tatdn1_PE=2_SV=1	9.00E-114	[illegible]	[illegible]
comp26975_c0_seq6.p1	sp|Q640V9|TATD1_XENLA_Putative_deoxyribonuclease_TATDN1_OS=Xenopus_laevis_GN=tatdn1_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp26976_c0_seq1.p1				
comp26977_c0_seq4.p1	sp|Q54C25|GPN1_DICDI_GPN-loop_GTPase_1_homolog_OS=Dictyostelium_discoideum_GN=xab1_PE=3_SV=1	5.00E-37	[illegible]	[illegible]
comp26977_c0_seq5.p1	sp|Q54C25|GPN1_DICDI_GPN-loop_GTPase_1_homolog_OS=Dictyostelium_discoideum_GN=xab1_PE=3_SV=1	2.00E-105	[illegible]	[illegible]
comp26977_c0_seq5.p2	sp|B8HWY2|Y899_CYAP4_UPF0133_protein_Cyan7425_0899_OS=Cyanothece_sp._(strain_PCC_7425_/_ATCC_29141)_GN=Cyan7425_0899_PE=3_SV=1	2.00E-15	[illegible]	[illegible]
comp26978_c0_seq3.p1				
comp26979_c0_seq1.p1	sp|Q9UPE1|SRPK3_HUMAN_SRSF_protein_kinase_3_OS=Homo_sapiens_GN=SRPK3_PE=2_SV=2	2.00E-57	[illegible]	[illegible]
comp26980_c0_seq1.p1				
comp26980_c0_seq2.p1				
comp26980_c1_seq1.p1	sp|O94653|BMS1_SCHPO_Ribosome_biogenesis_protein_BMS1_homolog_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC31E1.06_PE=1_SV=2	1.00E-93	[illegible]	[illegible]
comp26981_c0_seq4.p1				
comp26981_c0_seq5.p1				
comp26983_c0_seq1.p1	sp|Q7XAB8|THF1_SOLTU_Protein_THYLAKOID_FORMATION1,_chloroplastic_OS=Solanum_tuberosum_GN=THF1_PE=2_SV=1	2.00E-29	[illegible]	[illegible]
comp26984_c0_seq2.p1	sp|P47943|IF4A_SCHPO_ATP-dependent_RNA_helicase_eIF4A_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=tif1_PE=1_SV=2	0	[illegible]	[illegible]
comp26985_c0_seq1.p1				
comp26985_c0_seq1.p2				
comp26985_c0_seq3.p3				
comp26986_c0_seq2.p1				
comp26986_c0_seq3.p1				
comp26987_c0_seq1.p1	sp|Q9H6K1|CF106_HUMAN_Uncharacterized_protein_C6orf106_OS=Homo_sapiens_GN=C6orf106_PE=1_SV=2	2.00E-17	[illegible]	[illegible]
comp26987_c0_seq1.p5				
comp26988_c0_seq2.p1				
comp26989_c0_seq2.p1	sp|P09960|LKHA4_HUMAN_Leukotriene_A-4_hydrolase_OS=Homo_sapiens_GN=LTA4H_PE=1_SV=2	3.00E-163	[illegible]	[illegible]
comp26990_c0_seq1.p1				
comp26991_c0_seq1.p1				
comp26993_c0_seq1.p1				
comp26993_c0_seq2.p1				
comp26994_c0_seq1.p1	sp|Q6JQN1|ACD10_HUMAN_Acyl-CoA_dehydrogenase_family_member_10_OS=Homo_sapiens_GN=ACAD10_PE=2_SV=1	3.00E-55	[illegible]	[illegible]
comp26995_c0_seq1.p1	sp|Q3J872|PYRC_NITOC_Dihydroorotase_OS=Nitrosococcus_oceani_(strain_ATCC_19707_/_NCIMB_11848)_GN=pyrC_PE=3_SV=1	3.00E-111	[illegible]	[illegible]
comp26995_c0_seq2.p1	sp|Q3J872|PYRC_NITOC_Dihydroorotase_OS=Nitrosococcus_oceani_(strain_ATCC_19707_/_NCIMB_11848)_GN=pyrC_PE=3_SV=1	3.00E-127	[illegible]	[illegible]
comp26995_c1_seq1.p1				
comp26996_c0_seq1.p1	sp|Q54VQ7|HDA22_DICDI_Type-2_histone_deacetylase_2_OS=Dictyostelium_discoideum_GN=hdaC_PE=2_SV=1	3.00E-43	[illegible]	[illegible]
comp26996_c0_seq2.p1	sp|Q54VQ7|HDA22_DICDI_Type-2_histone_deacetylase_2_OS=Dictyostelium_discoideum_GN=hdaC_PE=2_SV=1	4.00E-28	[illegible]	[illegible]
comp26997_c0_seq1.p1				
comp26997_c1_seq1.p1	sp|Q6NZS4|RTCB_DANRE_tRNA-splicing_ligase_RtcB_homolog_OS=Danio_rerio_GN=zgc:76871_PE=2_SV=1	0	[illegible]	[illegible]
comp26998_c0_seq1.p1				
comp26999_c0_seq1.p1	sp|P34113|RL3_DICDI_60S_ribosomal_protein_L3_OS=Dictyostelium_discoideum_GN=rpl3_PE=1_SV=2	4.00E-53	[illegible]	[illegible]
comp27000_c0_seq1.p1	sp|O15541|R113A_HUMAN_RING_finger_protein_113A_OS=Homo_sapiens_GN=RNF113A_PE=1_SV=1	2.00E-67	[illegible]	[illegible]
comp27000_c0_seq1.p2	sp|Q5RD67|S2544_PONAB_Solute_carrier_family_25_member_44_OS=Pongo_abelii_GN=SLC25A44_PE=2_SV=2	2.00E-56	[illegible]	[illegible]
comp27001_c0_seq1.p1				
comp27001_c0_seq2.p1				
comp27003_c0_seq3.p1	sp|O42916|ALE1_SCHPO_Lysophospholipid_acyltransferase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ale1_PE=1_SV=1	3.00E-59	[illegible]	[illegible]
comp27005_c0_seq1.p1	sp|Q641Z5|CHAC2_RAT_Cation_transport_regulator-like_protein_2_OS=Rattus_norvegicus_GN=Chac2_PE=2_SV=1	3.00E-25		
comp27008_c0_seq1.p1	sp|Q8HZK2|DUOX2_PIG_Dual_oxidase_2_OS=Sus_scrofa_GN=DUOX2_PE=1_SV=2	3.00E-16	[illegible]	[illegible]
comp27009_c0_seq1.p1	sp|Q8WVK2|SNR27_HUMAN_U4/U6.U5_small_nuclear_ribonucleoprotein_27_kDa_protein_OS=Homo_sapiens_GN=SNRNP27_PE=1_SV=1	2.00E-16	[illegible]	[illegible]
comp27009_c0_seq2.p1				
comp27009_c0_seq3.p1	sp|Q54PW5|DPH1_DICDI_Diphthamide_biosynthesis_protein_1_OS=Dictyostelium_discoideum_GN=dph1_PE=3_SV=1	3.00E-147	[illegible]	[illegible]
comp27009_c0_seq3.p2	sp|Q8WVK2|SNR27_HUMAN_U4/U6.U5_small_nuclear_ribonucleoprotein_27_kDa_protein_OS=Homo_sapiens_GN=SNRNP27_PE=1_SV=1	2.00E-16	[illegible]	[illegible]
comp27009_c0_seq4.p1	sp|Q54PW5|DPH1_DICDI_Diphthamide_biosynthesis_protein_1_OS=Dictyostelium_discoideum_GN=dph1_PE=3_SV=1	3.00E-147	[illegible]	[illegible]
comp27009_c0_seq4.p2				
comp27010_c0_seq1.p1	sp|Q552R1|DCAF7_DICDI_DDB1-_and_CUL4-associated_factor_7_homolog_OS=Dictyostelium_discoideum_GN=wdr68_PE=3_SV=2	2.00E-146	[illegible]	[illegible]
comp27011_c0_seq1.p1				
comp27012_c1_seq1.p1	sp|Q54NI7|MED31_DICDI_Putative_mediator_of_RNA_polymerase_II_transcription_subunit_31_OS=Dictyostelium_discoideum_GN=med31_PE=3_SV=1	8.00E-29	[illegible]	[illegible]
comp27012_c1_seq4.p1	sp|Q8VYB1|MED31_ARATH_Mediator_of_RNA_polymerase_II_transcription_subunit_31_OS=Arabidopsis_thaliana_GN=At5g19910_PE=2_SV=1	2.00E-22	[illegible]	[illegible]
comp27013_c0_seq3.p1	sp|Q8NCR3|CK065_HUMAN_Uncharacterized_protein_C11orf65_OS=Homo_sapiens_GN=C11orf65_PE=2_SV=1	4.00E-27		
comp27014_c0_seq1.p1				
comp27015_c0_seq1.p2				
comp27015_c0_seq2.p1				
comp27018_c0_seq2.p1				
comp27019_c0_seq1.p1	sp|A7P514|RBR_VITVI_Retinoblastoma-related_protein_OS=Vitis_vinifera_GN=RBR_PE=2_SV=1	2.00E-17	[illegible]	[illegible]
comp27019_c0_seq1.p2				
comp27019_c0_seq2.p1	sp|A7P514|RBR_VITVI_Retinoblastoma-related_protein_OS=Vitis_vinifera_GN=RBR_PE=2_SV=1	3.00E-17	[illegible]	[illegible]
comp27020_c0_seq1.p1	sp|Q9DBF7|CWC25_MOUSE_Pre-mRNA-splicing_factor_CWC25_homolog_OS=Mus_musculus_GN=Cwc25_PE=2_SV=2	1.00E-14	[illegible]	[illegible]
comp27020_c0_seq1.p5				
comp27021_c0_seq1.p1	sp|P14325|SYQ_DICDI_Probable_glutamine--tRNA_ligase_OS=Dictyostelium_discoideum_GN=glnS_PE=2_SV=2	1.00E-158	[illegible]	[illegible]
comp27023_c0_seq1.p1	sp|Q92BZ4|FOLD_LISIN_Bifunctional_protein_FolD_OS=Listeria_innocua_GN=folD_PE=3_SV=1	2.00E-87	[illegible]	[illegible]
comp27023_c0_seq2.p1	sp|Q92BZ4|FOLD_LISIN_Bifunctional_protein_FolD_OS=Listeria_innocua_GN=folD_PE=3_SV=1	1.00E-87	[illegible]	[illegible]
comp27023_c0_seq3.p1	sp|Q92BZ4|FOLD_LISIN_Bifunctional_protein_FolD_OS=Listeria_innocua_GN=folD_PE=3_SV=1	3.00E-31	[illegible]	[illegible]
comp27025_c0_seq1.p1	sp|Q5BGR2|MESA_EMENI_Protein_mesA_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=mesA_PE=1_SV=2	6.00E-26	[illegible]	[illegible]
comp27026_c0_seq1.p1	sp|Q84SN3|CDKF3_ORYSJ_Cyclin-dependent_kinase_F-3_OS=Oryza_sativa_subsp._japonica_GN=CDKF-3_PE=2_SV=1	1.00E-13	[illegible]	[illegible]
comp27027_c0_seq2.p1	sp|O23653|AK2_ARATH_Aspartokinase_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=AK2_PE=1_SV=1	1.00E-135	[illegible]	[illegible]
comp27029_c0_seq1.p1				
comp27030_c0_seq1.p1				
comp27030_c0_seq2.p1				
comp27032_c0_seq1.p1	sp|O74135|CKI3_SCHPO_Casein_kinase_I_homolog_3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=cki3_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp27032_c0_seq1.p2				
comp27033_c0_seq3.p1	sp|Q88BD4|ALGC_PSESM_Phosphomannomutase/phosphoglucomutase_OS=Pseudomonas_syringae_pv._tomato_(strain_DC3000)_GN=algC_PE=3_SV=1	8.00E-40	[illegible]	[illegible]
comp27035_c0_seq1.p1				
comp27036_c0_seq2.p1				
comp27036_c0_seq3.p1				
comp27038_c0_seq1.p2	sp|O65059|RS15_PICMA_40S_ribosomal_protein_S15_OS=Picea_mariana_GN=RPS15_PE=2_SV=1	1.00E-68	[illegible]	[illegible]
comp27039_c0_seq2.p1				
comp27040_c0_seq1.p1	sp|Q5I0D1|GLOD4_RAT_Glyoxalase_domain-containing_protein_4_OS=Rattus_norvegicus_GN=Glod4_PE=1_SV=1	5.00E-58	[illegible]	[illegible]
comp27041_c0_seq2.p1	sp|Q9LHN4|LPAT5_ARATH_Probable_1-acyl-sn-glycerol-3-phosphate_acyltransferase_5_OS=Arabidopsis_thaliana_GN=LPAT5_PE=2_SV=1	8.00E-29	[illegible]	[illegible]
comp27042_c0_seq1.p1				
comp27043_c0_seq1.p1	sp|Q15751|HERC1_HUMAN_Probable_E3_ubiquitin-protein_ligase_HERC1_OS=Homo_sapiens_GN=HERC1_PE=1_SV=2	3.00E-45	[illegible]	[illegible]
comp27043_c0_seq1.p2	sp|Q3SXD3|HDDC2_MOUSE_HD_domain-containing_protein_2_OS=Mus_musculus_GN=Hddc2_PE=2_SV=1	3.00E-48	[illegible]	[illegible]
comp27043_c0_seq2.p1	sp|Q15751|HERC1_HUMAN_Probable_E3_ubiquitin-protein_ligase_HERC1_OS=Homo_sapiens_GN=HERC1_PE=1_SV=2	3.00E-45	[illegible]	[illegible]
comp27043_c0_seq2.p4	sp|Q3SXD3|HDDC2_MOUSE_HD_domain-containing_protein_2_OS=Mus_musculus_GN=Hddc2_PE=2_SV=1	6.00E-32	[illegible]	[illegible]
comp27044_c0_seq1.p1				
comp27044_c0_seq2.p1				
comp27045_c0_seq2.p1	sp|Q5C9L6|CNMT_THLFG_(S)-coclaurine_N-methyltransferase_OS=Thalictrum_flavum_subsp._glaucum_PE=1_SV=1	5.00E-90	[illegible]	[illegible]
comp27046_c0_seq3.p2				
comp27046_c0_seq3.p3				
comp27047_c0_seq1.p1	sp|P16171|MERA_BACCE_Mercuric_reductase_OS=Bacillus_cereus_GN=merA_PE=1_SV=1	3.00E-80	[illegible]	[illegible]
comp27047_c0_seq1.p2				
comp27047_c0_seq4.p1	sp|Q6CAP3|IML1_YARLI_Vacuolar_membrane-associated_protein_IML1_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=IML1_PE=3_SV=1	3.00E-12	[illegible]	[illegible]
comp27048_c0_seq2.p1				
comp27048_c0_seq3.p2	sp|B2A1E8|ENGB_NATTJ_Probable_GTP-binding_protein_EngB_OS=Natranaerobius_thermophilus_(strain_ATCC_BAA-1301_/_DSM_18059_/_JW/NM-WN-LF)_GN=engB_PE=3_SV=1	1.00E-11	[illegible]	[illegible]
comp27048_c0_seq6.p1	sp|B2A1E8|ENGB_NATTJ_Probable_GTP-binding_protein_EngB_OS=Natranaerobius_thermophilus_(strain_ATCC_BAA-1301_/_DSM_18059_/_JW/NM-WN-LF)_GN=engB_PE=3_SV=1	1.00E-11	[illegible]	[illegible]
comp27048_c1_seq2.p1				
comp27049_c0_seq1.p1				
comp27050_c0_seq1.p1	sp|O75037|KI21B_HUMAN_Kinesin-like_protein_KIF21B_OS=Homo_sapiens_GN=KIF21B_PE=1_SV=2	2.00E-79	[illegible]	[illegible]
comp27051_c0_seq2.p1				
comp27053_c0_seq1.p1	sp|Q06952|GM4D1_VIBCH_Probable_GDP-mannose_4,6-dehydratase_OS=Vibrio_cholerae_GN=rfbD_PE=3_SV=1	5.00E-160	[illegible]	[illegible]
comp27055_c1_seq2.p1				
comp27055_c1_seq3.p2				
comp27056_c0_seq3.p1	sp|Q5FW12|TIPRL_XENTR_TIP41-like_protein_OS=Xenopus_tropicalis_GN=tiprl_PE=2_SV=1	5.00E-25	[illegible]	[illegible]
comp27056_c0_seq4.p1	sp|Q5FW12|TIPRL_XENTR_TIP41-like_protein_OS=Xenopus_tropicalis_GN=tiprl_PE=2_SV=1	3.00E-25	[illegible]	[illegible]
comp27057_c0_seq1.p1				
comp27058_c0_seq1.p1				
comp27058_c1_seq1.p2				
comp27059_c0_seq2.p1				
comp27059_c0_seq3.p1				
comp27060_c0_seq1.p2				
comp27060_c0_seq3.p1	sp|B4N9T4|SUR8_DROWI_Leucine-rich_repeat_protein_soc-2_homolog_OS=Drosophila_willistoni_GN=Sur-8_PE=3_SV=1	7.00E-22	GO:0000164,GO:0046579	[illegible]
comp27061_c0_seq1.p1				
comp27061_c0_seq2.p1	sp|Q9CQL0|MT21A_MOUSE_Methyltransferase-like_protein_21A_OS=Mus_musculus_GN=Mettl21A_PE=2_SV=1	3.00E-13	[illegible]	[illegible]
comp27061_c0_seq3.p2				
comp27062_c0_seq1.p2				
comp27062_c0_seq3.p1				
comp27063_c0_seq1.p1				
comp27064_c0_seq4.p1	sp|Q38868|CDPK9_ARATH_Calcium-dependent_protein_kinase_9_OS=Arabidopsis_thaliana_GN=CPK9_PE=1_SV=1	1.00E-59	[illegible]	[illegible]
comp27064_c0_seq4.p2				
comp27065_c0_seq1.p1				
comp27067_c0_seq1.p3				
comp27068_c0_seq1.p2				
comp27068_c0_seq2.p1				
comp27068_c0_seq3.p1				
comp27070_c0_seq1.p1				
comp27072_c0_seq2.p2	sp|O80513|CCU41_ARATH_Cyclin-U4-1_OS=Arabidopsis_thaliana_GN=CYCU4-1_PE=1_SV=1	2.00E-38	[illegible]	[illegible]
comp27073_c0_seq1.p1				
comp27073_c0_seq2.p1				
comp27074_c0_seq3.p1	sp|Q9CA86|PEX2_ARATH_Peroxisome_biogenesis_protein_2_OS=Arabidopsis_thaliana_GN=PEX2_PE=1_SV=1	8.00E-16	[illegible]	[illegible]
comp27074_c0_seq4.p2				
comp27074_c0_seq7.p1	sp|Q75JQ3|PEX2_DICDI_Peroxisome_biogenesis_factor_2_OS=Dictyostelium_discoideum_GN=pex2_PE=3_SV=1	7.00E-37	[illegible]	[illegible]
comp27075_c1_seq2.p1	sp|Q9JIM3|RAD26_MOUSE_Putative_DNA_repair_and_recombination_protein_RAD26-like_OS=Mus_musculus_GN=Rad26l_PE=2_SV=2	2.00E-22	[illegible]	[illegible]
comp27075_c1_seq3.p1	sp|Q9JIM3|RAD26_MOUSE_Putative_DNA_repair_and_recombination_protein_RAD26-like_OS=Mus_musculus_GN=Rad26l_PE=2_SV=2	5.00E-48	[illegible]	[illegible]
comp27075_c1_seq4.p1	sp|Q9JIM3|RAD26_MOUSE_Putative_DNA_repair_and_recombination_protein_RAD26-like_OS=Mus_musculus_GN=Rad26l_PE=2_SV=2	8.00E-48	[illegible]	[illegible]
comp27076_c0_seq1.p1	sp|Q31QE7|CLPS_SYNE7_ATP-dependent_Clp_protease_adapter_protein_ClpS_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=clpS_PE=3_SV=1	2.00E-11	GO:0006508,GO:0030163	[illegible]
comp27076_c0_seq1.p2				
comp27077_c0_seq1.p1				
comp27077_c0_seq1.p3				
comp27078_c0_seq1.p1	sp|Q9D8S9|BOLA1_MOUSE_BolA-like_protein_1_OS=Mus_musculus_GN=Bola1_PE=1_SV=1	7.00E-21	[illegible]	[illegible]
comp27078_c0_seq3.p1				
comp27078_c0_seq3.p2	sp|Q56585|BOLA_VIBAL_Protein_BolA_homolog_OS=Vibrio_alginolyticus_GN=bolA_PE=3_SV=1	1.00E-22	[illegible]	[illegible]
comp27079_c0_seq2.p1				
comp27079_c0_seq3.p1				
comp27079_c0_seq3.p2				
comp27079_c0_seq4.p1				
comp27080_c0_seq2.p1	sp|Q8RXW0|Y3761_ARATH_Uncharacterized_protein_At3g17611_OS=Arabidopsis_thaliana_GN=At3g17611_PE=2_SV=1	2.00E-33	[illegible]	[illegible]
comp27080_c0_seq2.p2	sp|Q54HH2|SRR_DICDI_Probable_serine_racemase_OS=Dictyostelium_discoideum_GN=srr_PE=3_SV=1	2.00E-79	[illegible]	[illegible]
comp27081_c0_seq1.p1	sp|Q54JC0|CMBB_DICDI_Calmodulin-binding_protein_CmbB_OS=Dictyostelium_discoideum_GN=cmbB_PE=1_SV=1	1.00E-18	[illegible]	[illegible]
comp27081_c0_seq2.p1	sp|Q54JC0|CMBB_DICDI_Calmodulin-binding_protein_CmbB_OS=Dictyostelium_discoideum_GN=cmbB_PE=1_SV=1	1.00E-18	[illegible]	[illegible]
comp27082_c0_seq1.p1	sp|P48625|FAD3E_SOYBN_Omega-3_fatty_acid_desaturase,_endoplasmic_reticulum_OS=Glycine_max_GN=FAD3_PE=2_SV=1	1.00E-59	[illegible]	[illegible]
comp27083_c0_seq1.p1	sp|Q8N9T8|KRI1_HUMAN_Protein_KRI1_homolog_OS=Homo_sapiens_GN=KRI1_PE=1_SV=2	1.00E-11	GO:0005730,GO:0044822	[illegible]
comp27083_c2_seq1.p1				
comp27083_c2_seq3.p1				
comp27083_c2_seq3.p4				
comp27084_c0_seq2.p2				
comp27085_c0_seq1.p1				
comp27085_c0_seq1.p2				
comp27085_c0_seq2.p1				
comp27086_c0_seq1.p1	sp|Q0IHH1|NAA30_XENLA_N-alpha-acetyltransferase_30_OS=Xenopus_laevis_GN=naa30_PE=2_SV=1	4.00E-51	[illegible]	[illegible]
comp27089_c0_seq2.p1	sp|P62311|LSM3_MOUSE_U6_snRNA-associated_Sm-like_protein_LSm3_OS=Mus_musculus_GN=Lsm3_PE=2_SV=2	2.00E-18	[illegible]	[illegible]
comp27090_c0_seq1.p1				
comp27090_c0_seq2.p1				
comp27090_c0_seq4.p1				
comp27091_c0_seq2.p1	sp|B4F6K2|GLO2_XENTR_Hydroxyacylglutathione_hydrolase,_mitochondrial_OS=Xenopus_tropicalis_GN=hagh_PE=2_SV=1	2.00E-85	[illegible]	[illegible]
comp27091_c0_seq2.p4				
comp27091_c0_seq3.p1				
comp27091_c0_seq3.p2	sp|B4F6K2|GLO2_XENTR_Hydroxyacylglutathione_hydrolase,_mitochondrial_OS=Xenopus_tropicalis_GN=hagh_PE=2_SV=1	2.00E-85	[illegible]	[illegible]
comp27091_c0_seq4.p1	sp|B4F6K2|GLO2_XENTR_Hydroxyacylglutathione_hydrolase,_mitochondrial_OS=Xenopus_tropicalis_GN=hagh_PE=2_SV=1	2.00E-85	[illegible]	[illegible]
comp27091_c0_seq4.p4				
comp27093_c1_seq1.p1				
comp27094_c0_seq3.p1				
comp27095_c0_seq1.p1				
comp27095_c0_seq2.p2				
comp27096_c0_seq1.p2				
comp27096_c0_seq2.p1				
comp27097_c0_seq1.p1	sp|Q7ZVZ7|F108C_DANRE_Abhydrolase_domain-containing_protein_FAM108C1_OS=Danio_rerio_GN=fam108c1_PE=2_SV=1	1.00E-46	[illegible]	[illegible]
comp27098_c0_seq1.p1	sp|Q9BRD0|BUD13_HUMAN_BUD13_homolog_OS=Homo_sapiens_GN=BUD13_PE=1_SV=1	2.00E-30	[illegible]	[illegible]
comp27098_c0_seq5.p1				
comp27098_c0_seq5.p4				
comp27099_c0_seq2.p1	sp|P84239|H3_URECA_Histone_H3_OS=Urechis_caupo_PE=1_SV=2	1.00E-87	[illegible]	[illegible]
comp27100_c0_seq1.p1	sp|Q8XHJ4|KPRS_CLOPE_Ribose-phosphate_pyrophosphokinase_OS=Clostridium_perfringens_GN=prs_PE=3_SV=1	8.00E-56	[illegible]	[illegible]
comp27100_c0_seq3.p1	sp|Q8XHJ4|KPRS_CLOPE_Ribose-phosphate_pyrophosphokinase_OS=Clostridium_perfringens_GN=prs_PE=3_SV=1	6.00E-61	[illegible]	[illegible]
comp27100_c0_seq3.p2				
comp27100_c0_seq5.p1				
comp27100_c0_seq5.p2	sp|Q6AJL7|KPRS_DESPS_Ribose-phosphate_pyrophosphokinase_OS=Desulfotalea_psychrophila_(strain_LSv54_/_DSM_12343)_GN=prs_PE=3_SV=1	6.00E-41	[illegible]	[illegible]
comp27100_c0_seq5.p4				
comp27102_c0_seq1.p1				
comp27102_c0_seq1.p2				
comp27102_c0_seq1.p8				
comp27103_c0_seq1.p1	sp|Q13733|AT1A4_HUMAN_Sodium/potassium-transporting_ATPase_subunit_alpha-4_OS=Homo_sapiens_GN=ATP1A4_PE=1_SV=3	1.00E-24	[illegible]	[illegible]
comp27103_c0_seq2.p1	sp|Q13733|AT1A4_HUMAN_Sodium/potassium-transporting_ATPase_subunit_alpha-4_OS=Homo_sapiens_GN=ATP1A4_PE=1_SV=3	1.00E-16	[illegible]	[illegible]
comp27103_c0_seq3.p1	sp|D2WKD8|AT1A2_PIG_Sodium/potassium-transporting_ATPase_subunit_alpha-2_OS=Sus_scrofa_GN=ATP1A2_PE=1_SV=1	0	[illegible]	[illegible]
comp27104_c0_seq1.p1	sp|Q54KZ8|EIF3M_DICDI_Eukaryotic_translation_initiation_factor_3_subunit_M_OS=Dictyostelium_discoideum_GN=eif3m_PE=1_SV=1	6.00E-52	[illegible]	[illegible]
comp27104_c0_seq1.p2	sp|Q32L63|VTA1_BOVIN_Vacuolar_protein_sorting-associated_protein_VTA1_homolog_OS=Bos_taurus_GN=VTA1_PE=2_SV=1	3.00E-26	[illegible]	[illegible]
comp27104_c0_seq2.p1	sp|Q54KZ8|EIF3M_DICDI_Eukaryotic_translation_initiation_factor_3_subunit_M_OS=Dictyostelium_discoideum_GN=eif3m_PE=1_SV=1	8.00E-52	[illegible]	[illegible]
comp27104_c0_seq2.p2	sp|Q32L63|VTA1_BOVIN_Vacuolar_protein_sorting-associated_protein_VTA1_homolog_OS=Bos_taurus_GN=VTA1_PE=2_SV=1	3.00E-26	[illegible]	[illegible]
comp27105_c0_seq1.p1	sp|Q68EH8|FAD1_DANRE_FAD_synthase_OS=Danio_rerio_GN=flad1_PE=2_SV=1	2.00E-33	[illegible]	[illegible]
comp27105_c0_seq2.p1	sp|Q03219|YM44_YEAST_Uncharacterized_protein_YMR178W_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YMR178W_PE=1_SV=1	1.00E-21	[illegible]	[illegible]
comp27105_c0_seq2.p3				
comp27105_c0_seq3.p1	sp|Q6ING7|FLAD1_XENLA_FAD_synthase_OS=Xenopus_laevis_GN=flad1_PE=2_SV=1	7.00E-32	[illegible]	[illegible]
comp27106_c0_seq1.p1				
comp27106_c0_seq3.p1				
comp27106_c0_seq4.p1				
comp27106_c0_seq5.p1				
comp27107_c0_seq2.p1				
comp27108_c0_seq1.p1				
comp27109_c0_seq1.p1	sp|Q9C6D2|MTK_ARATH_Methylthioribose_kinase_OS=Arabidopsis_thaliana_GN=MTK_PE=1_SV=1	4.00E-117	[illegible]	[illegible]
comp2711_c0_seq1.p1	sp|P15288|PEPD_ECOLI_Cytosol_non-specific_dipeptidase_OS=Escherichia_coli_(strain_K12)_GN=pepD_PE=1_SV=3	3.00E-102	[illegible]	[illegible]
comp27110_c0_seq1.p1	sp|Q6DW74|DGDG1_LOTJA_Digalactosyldiacylglycerol_synthase_1,_chloroplastic_OS=Lotus_japonicus_GN=DGD1_PE=2_SV=1	3.00E-119	[illegible]	[illegible]
comp27110_c0_seq3.p1				
comp27111_c0_seq1.p1	sp|P44740|Y510_HAEIN_UPF0066_protein_HI_0510_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=HI_0510_PE=1_SV=1	1.00E-26	[illegible]	[illegible]
comp27112_c0_seq1.p1	sp|P21868|CSK21_CHICK_Casein_kinase_II_subunit_alpha_OS=Gallus_gallus_GN=CSNK2A1_PE=2_SV=1	2.00E-72	[illegible]	[illegible]
comp27113_c0_seq1.p1	sp|P39623|SPSC_BACSU_Spore_coat_polysaccharide_biosynthesis_protein_spsC_OS=Bacillus_subtilis_GN=spsC_PE=3_SV=1	2.00E-33	[illegible]	[illegible]
comp27114_c0_seq3.p1				
comp27115_c0_seq2.p1				
comp27115_c0_seq4.p1				
comp27115_c0_seq7.p1				
comp27115_c0_seq8.p1				
comp27115_c0_seq9.p1				
comp27117_c0_seq2.p1				
comp27118_c0_seq2.p1	sp|Q02978|M2OM_HUMAN_Mitochondrial_2-oxoglutarate/malate_carrier_protein_OS=Homo_sapiens_GN=SLC25A11_PE=1_SV=3	4.00E-69	[illegible]	[illegible]
comp27119_c0_seq1.p1	sp|O48741|PORC_ARATH_Protochlorophyllide_reductase_C,_chloroplastic_OS=Arabidopsis_thaliana_GN=PORC_PE=1_SV=1	5.00E-93	[illegible]	[illegible]
comp27119_c0_seq1.p2				
comp27120_c0_seq2.p1				
comp27120_c0_seq2.p2	sp|O89116|VTI1A_MOUSE_Vesicle_transport_through_interaction_with_t-SNAREs_homolog_1A_OS=Mus_musculus_GN=Vti1a_PE=1_SV=1	1.00E-25	[illegible]	[illegible]
comp27120_c0_seq2.p3				
comp27120_c0_seq3.p1				
comp27120_c0_seq3.p2	sp|Q96AJ9|VTI1A_HUMAN_Vesicle_transport_through_interaction_with_t-SNAREs_homolog_1A_OS=Homo_sapiens_GN=VTI1A_PE=1_SV=2	4.00E-25	[illegible]	[illegible]
comp27121_c0_seq3.p1	sp|Q5RBN8|LIN54_PONAB_Protein_lin-54_homolog_OS=Pongo_abelii_GN=LIN54_PE=2_SV=1	1.00E-30	[illegible]	[illegible]
comp27122_c0_seq4.p1				
comp27122_c0_seq4.p2				
comp27123_c0_seq1.p1	sp|Q0DVX2|RH50_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_50_OS=Oryza_sativa_subsp._japonica_GN=Os03g0108600_PE=2_SV=2	6.00E-103	[illegible]	[illegible]
comp27124_c0_seq2.p1				
comp27124_c0_seq2.p2	sp|B3QBY0|RL3_RHOPT_50S_ribosomal_protein_L3_OS=Rhodopseudomonas_palustris_(strain_TIE-1)_GN=rplC_PE=3_SV=1	6.00E-68	[illegible]	[illegible]
comp27126_c0_seq2.p1				
comp27127_c0_seq1.p1	sp|Q39709|FCP_ISOGA_Fucoxanthin-chlorophyll_a-c_binding_protein,_chloroplastic_OS=Isochrysis_galbana_GN=FCP_PE=2_SV=1	4.00E-21	[illegible]	[illegible]
comp27130_c0_seq1.p1	sp|Q9MB58|F26_ARATH_6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase_OS=Arabidopsis_thaliana_GN=FKFBP_PE=1_SV=1	8.00E-38	[illegible]	[illegible]
comp27131_c0_seq1.p2				
comp27132_c0_seq1.p1	sp|Q9ESD7|DYSF_MOUSE_Dysferlin_OS=Mus_musculus_GN=Dysf_PE=1_SV=3	4.00E-18	[illegible]	[illegible]
comp27135_c0_seq1.p1	sp|Q75HE6|MTHR_ORYSJ_Probable_methylenetetrahydrofolate_reductase_OS=Oryza_sativa_subsp._japonica_GN=Os03g0815200_PE=2_SV=1	0	[illegible]	[illegible]
comp27135_c0_seq2.p1	sp|Q91YQ7|RMD5B_MOUSE_Protein_RMD5_homolog_B_OS=Mus_musculus_GN=Rmnd5b_PE=2_SV=1	5.00E-61	[illegible]	[illegible]
comp27136_c0_seq1.p2	sp|P49397|RS3A_ORYSJ_40S_ribosomal_protein_S3a_OS=Oryza_sativa_subsp._japonica_GN=RPS3A_PE=2_SV=2	3.00E-104	[illegible]	[illegible]
comp27136_c0_seq2.p1	sp|B4S616|GPMA_PROA2_2,3-bisphosphoglycerate-dependent_phosphoglycerate_mutase_OS=Prosthecochloris_aestuarii_(strain_DSM_271_/_SK_413)_GN=gpmA_PE=3_SV=1	9.00E-104	[illegible]	[illegible]
comp27136_c0_seq6.p1	sp|Q4QQW4|HDAC1_RAT_Histone_deacetylase_1_OS=Rattus_norvegicus_GN=Hdac1_PE=2_SV=1	0	[illegible]	[illegible]
comp27138_c0_seq3.p1				
comp27139_c0_seq4.p1	sp|Q2M3M2|SC5A9_HUMAN_Sodium/glucose_cotransporter_4_OS=Homo_sapiens_GN=SLC5A9_PE=2_SV=2	1.00E-14	[illegible]	[illegible]
comp27140_c0_seq1.p2				
comp27141_c0_seq1.p1				
comp27141_c0_seq2.p1				
comp27142_c0_seq3.p1	sp|P05303|EF1A2_DROME_Elongation_factor_1-alpha_2_OS=Drosophila_melanogaster_GN=Ef1alpha100E_PE=2_SV=2	2.00E-63	[illegible]	[illegible]
comp27143_c0_seq2.p1				
comp27145_c0_seq1.p1				
comp27145_c1_seq3.p1				
comp27145_c1_seq3.p2				
comp27146_c1_seq1.p1	sp|O13787|SEC62_SCHPO_Translocation_protein_sec62_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=sec62_PE=2_SV=1	3.00E-13	[illegible]	[illegible]
comp27146_c1_seq2.p1	sp|O13787|SEC62_SCHPO_Translocation_protein_sec62_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=sec62_PE=2_SV=1	1.00E-19	[illegible]	[illegible]
comp27147_c0_seq1.p1	sp|P54176|HLY3_BACCE_Hemolysin-3_OS=Bacillus_cereus_PE=3_SV=1	8.00E-28	[illegible]	[illegible]
comp27149_c0_seq1.p1	sp|P51563|TCR7_VIBAN_Tetracycline_resistance_protein,_class_G_OS=Vibrio_anguillarum_GN=tetA_PE=3_SV=1	2.00E-24	[illegible]	[illegible]
comp27150_c0_seq1.p1	sp|Q9HFF2|YL92_SCHPO_Uncharacterized_protein_C683.02c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC683.02c_PE=2_SV=1	1.00E-31	[illegible]	[illegible]
comp27150_c0_seq2.p1				
comp27151_c0_seq1.p1	sp|O44400|F37C4_CAEEL_Protein_F37C4.5_OS=Caenorhabditis_elegans_GN=F37C4.5_PE=1_SV=3	4.00E-26	GO:0005515,GO:0005515	[illegible]
comp27153_c0_seq1.p1	sp|Q8K0U4|HS12A_MOUSE_Heat_shock_70_kDa_protein_12A_OS=Mus_musculus_GN=Hspa12a_PE=1_SV=1	1.00E-37	[illegible]	[illegible]
comp27154_c0_seq1.p1	sp|P73056|YC64L_SYNY3_Uncharacterized_monothiol_glutaredoxin_ycf64-like_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr1846_PE=3_SV=1	6.00E-43	[illegible]	[illegible]
comp27155_c0_seq1.p4				
comp27156_c0_seq1.p1	sp|Q6P1R4|DUS1L_HUMAN_tRNA-dihydrouridine(16/17)_synthase_[NAD(P)(+)]-like_OS=Homo_sapiens_GN=DUS1L_PE=1_SV=1	3.00E-14	[illegible]	[illegible]
comp27156_c0_seq3.p1	sp|Q8K582|DUS1L_RAT_tRNA-dihydrouridine(16/17)_synthase_[NAD(P)(+)]-like_OS=Rattus_norvegicus_GN=Dus1l_PE=2_SV=1	2.00E-47	[illegible]	[illegible]
comp27156_c0_seq6.p1	sp|Q6P1R4|DUS1L_HUMAN_tRNA-dihydrouridine(16/17)_synthase_[NAD(P)(+)]-like_OS=Homo_sapiens_GN=DUS1L_PE=1_SV=1	5.00E-11	[illegible]	[illegible]
comp27157_c0_seq2.p1	sp|C4QW04|LCL3_PICPG_Probable_endonuclease_LCL3_OS=Pichia_pastoris_(strain_GS115_/_ATCC_20864)_GN=LCL3_PE=3_SV=1	8.00E-35	[illegible]	[illegible]
comp27158_c0_seq2.p1				
comp27158_c0_seq2.p3				
comp27159_c1_seq1.p1	sp|Q8ZD12|Y2781_YERPE_Uncharacterized_Nudix_hydrolase_YPO2781/y1614/YP_2383_OS=Yersinia_pestis_GN=YPO2781_PE=3_SV=1	3.00E-22	[illegible]	[illegible]
comp27161_c0_seq2.p1	sp|Q54KA7|SECG_DICDI_Ankyrin_repeat,_PH_and_SEC7_domain_containing_protein_secG_OS=Dictyostelium_discoideum_GN=secG_PE=2_SV=1	7.00E-24	[illegible]	[illegible]
comp27162_c0_seq2.p1				
comp27163_c0_seq2.p1	sp|O14249|CLD1_SCHPO_probable_cardiolipin-specific_deacylase,_mitochondrial_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC6G10.03c_PE=2_SV=1	2.00E-29	[illegible]	[illegible]
comp27164_c0_seq1.p1	sp|Q7NSP5|MINC_CHRVO_Probable_septum_site-determining_protein_MinC_OS=Chromobacterium_violaceum_(strain_ATCC_12472_/_DSM_30191_/_JCM_1249_/_NBRC_12614_/_NCIMB_9131_/_NCTC_9757)_GN=minC_PE=3_SV=1	6.00E-22	[illegible]	[illegible]
comp27164_c0_seq4.p1				
comp27166_c0_seq1.p1				
comp27166_c0_seq2.p1				
comp27168_c0_seq1.p1	sp|A7MN76|BGAL_CROS8_Beta-galactosidase_OS=Cronobacter_sakazakii_(strain_ATCC_BAA-894)_GN=lacZ_PE=3_SV=1	4.00E-109	[illegible]	[illegible]
comp27169_c0_seq1.p1				
comp27172_c0_seq3.p1				
comp27173_c0_seq2.p1				
comp27176_c0_seq1.p1				
comp27176_c0_seq3.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	3.00E-43		
comp27176_c0_seq4.p1				
comp27178_c0_seq1.p1				
comp27179_c0_seq1.p1				
comp27180_c0_seq4.p1				
comp27182_c0_seq1.p1				
comp27183_c0_seq2.p1	sp|Q54ZX5|PX24A_DICDI_PXMP2/4_family_protein_1_OS=Dictyostelium_discoideum_GN=DDB_G0277335_PE=3_SV=1	1.00E-17	[illegible]	[illegible]
comp27183_c0_seq2.p2	sp|A6QPH1|WIBG_BOVIN_Partner_of_Y14_and_mago_OS=Bos_taurus_GN=WIBG_PE=2_SV=1	5.00E-21	[illegible]	[illegible]
comp27188_c0_seq1.p1	sp|Q9ZVN2|Y1457_ARATH_Acyltransferase-like_protein_At1g54570,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g54570_PE=1_SV=1	2.00E-18	[illegible]	[illegible]
comp27188_c1_seq1.p1	sp|Q9ZVN2|Y1457_ARATH_Acyltransferase-like_protein_At1g54570,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g54570_PE=1_SV=1	2.00E-53	[illegible]	[illegible]
comp27188_c1_seq2.p1	sp|Q9ZVN2|Y1457_ARATH_Acyltransferase-like_protein_At1g54570,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g54570_PE=1_SV=1	3.00E-41	[illegible]	[illegible]
comp27190_c0_seq1.p1	sp|Q562D6|NAP1_MOUSE_Nef-associated_protein_1_OS=Mus_musculus_GN=Nap1_PE=2_SV=1	2.00E-14	[illegible]	[illegible]
comp27192_c1_seq4.p1	sp|Q7XK25|PCH2_ORYSJ_Pachytene_checkpoint_protein_2_homolog_OS=Oryza_sativa_subsp._japonica_GN=Os04g0479000_PE=3_SV=3	3.00E-120	[illegible]	[illegible]
comp27193_c0_seq1.p1				
comp27194_c0_seq2.p1				
comp27197_c0_seq1.p1	sp|Q50940|CAH_NEIGO_Carbonic_anhydrase_OS=Neisseria_gonorrhoeae_GN=cah_PE=1_SV=2	4.00E-16	[illegible]	[illegible]
comp27197_c0_seq3.p1	sp|Q50940|CAH_NEIGO_Carbonic_anhydrase_OS=Neisseria_gonorrhoeae_GN=cah_PE=1_SV=2	1.00E-11	[illegible]	[illegible]
comp27198_c0_seq1.p1	sp|Q5R814|PRP4B_PONAB_Serine/threonine-protein_kinase_PRP4_homolog_OS=Pongo_abelii_GN=PRPF4B_PE=2_SV=1	3.00E-29	[illegible]	[illegible]
comp27198_c0_seq2.p1	sp|Q5RKH1|PRP4B_RAT_Serine/threonine-protein_kinase_PRP4_homolog_OS=Rattus_norvegicus_GN=Prpf4b_PE=2_SV=1	3.00E-87	[illegible]	[illegible]
comp27199_c0_seq3.p2	sp|Q8VHT6|AS3MT_RAT_Arsenite_methyltransferase_OS=Rattus_norvegicus_GN=As3mt_PE=1_SV=1	3.00E-90	[illegible]	[illegible]
comp27199_c1_seq1.p1				
comp27200_c0_seq2.p1				
comp27200_c0_seq3.p1				
comp27201_c0_seq1.p1	sp|B2FQP3|ASPN_STRMK_Peptidyl-Asp_metalloendopeptidase_OS=Stenotrophomonas_maltophilia_(strain_K279a)_GN=Smlt0970_PE=3_SV=1	4.00E-12	[illegible]	[illegible]
comp27201_c0_seq3.p1	sp|Q8PC00|ASPN_XANCP_Peptidyl-Asp_metalloendopeptidase_OS=Xanthomonas_campestris_pv._campestris_GN=XCC0955_PE=3_SV=1	2.00E-12	[illegible]	[illegible]
comp27202_c0_seq2.p1				
comp27203_c0_seq4.p1				
comp27203_c0_seq4.p2				
comp27205_c0_seq1.p1				

comp27205_c0_seq3.p1	sp|Q92J08|FER2_RICCN_2Fe-2S_ferredoxin_OS=Rickettsia_conorii_(strain_ATCC_VR-613_/_Malish_7)_GN=fdxB_PE=3_SV=1	7.00E-28	GO:0009055,GO:0046872,GO:0051536,GO:0051536,GO:0051537,GO:0051537,GO:0055114
comp27206_c0_seq1.p1			
comp27210_c0_seq1.p1	sp|A9X1D0|SETD3_PAPAN_Histone-lysine_N-methyltransferase_setd3_OS=Papio_anubis_GN=SETD3_PE=3_SV=1	6.00E-26	GO:0000790,GO:0001102,GO:0003713,GO:0003713,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0008168,GO:0010452,GO:0010452,GO:0016568,GO:0016740,GO:0018022,GO:0018023,GO:0018024,GO:0018026,GO:0018027,GO:0032259,GO:0042800,GO:0045893,GO:0045944,GO:0046975,GO:0046975,GO:0051149,GO:0051568
comp27212_c0_seq1.p1			
comp27213_c0_seq1.p1			
comp27214_c0_seq1.p1	sp|P54278|PMS2_HUMAN_Mismatch_repair_endonuclease_PMS2_OS=Homo_sapiens_GN=PMS2_PE=1_SV=2	2.00E-80	GO:0003677,GO:0004518,GO:0004519,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005737,GO:0006200,GO:0006281,GO:0006281,GO:0006298,GO:0006298,GO:0006298,GO:0006974,GO:0006974,GO:0015630,GO:0016446,GO:0016446,GO:0016447,GO:0016787,GO:0016887,GO:0030983,GO:0032138,GO:0032300,GO:0032389,GO:0032389,GO:0042493,GO:0090305,GO:0090305,GO:0003697,GO:0032407
comp27214_c0_seq2.p1	sp|P14242|PMS1_YEAST_DNA_mismatch_repair_protein_PMS1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PMS1_PE=1_SV=3	2.00E-54	GO:0000710,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006200,GO:0006281,GO:0006298,GO:0006298,GO:0006974,GO:0016887,GO:0016887,GO:0030983,GO:0032300,GO:0032389,GO:0000404,GO:0003690,GO:0003697,GO:0032135,GO:0032139
comp27214_c0_seq2.p2			
comp27214_c0_seq3.p1	sp|P54279|PMS2_MOUSE_Mismatch_repair_endonuclease_PMS2_OS=Mus_musculus_GN=Pms2_PE=1_SV=1	2.00E-55	GO:0003697,GO:0004518,GO:0004519,GO:0005524,GO:0005634,GO:0005634,GO:0006200,GO:0006281,GO:0006281,GO:0006298,GO:0006298,GO:0006298,GO:0006298,GO:0006298,GO:0006298,GO:0006298,GO:0006298,GO:0006298,GO:0006974,GO:0006974,GO:0006974,GO:0007126,GO:0016446,GO:0016447,GO:0016787,GO:0016887,GO:0030983,GO:0032300,GO:0032389,GO:0090305,GO:0090305
comp27214_c0_seq3.p2			
comp27215_c0_seq4.p1			
comp27215_c0_seq4.p2	sp|Q5T2D3|OTUD3_HUMAN_OTU_domain-containing_protein_3_OS=Homo_sapiens_GN=OTUD3_PE=1_SV=1	2.00E-24	GO:0004843,GO:0006508,GO:0008233,GO:0008234,GO:0016787,GO:0035871,GO:0044313
comp27215_c0_seq4.p5			
comp27218_c0_seq2.p1	sp|Q8BWW4|LARP4_MOUSE_La-related_protein_4_OS=Mus_musculus_GN=Larp4_PE=1_SV=2	9.00E-25	GO:0003676,GO:0003723,GO:0007010,GO:0022604
comp27219_c0_seq1.p1	sp|O55767|VF179_IIV6_Uncharacterized_protein_179R_OS=Invertebrate_iridescent_virus_6_GN=IIV6-179R_PE=4_SV=1	2.00E-26	GO:0004672,GO:0006468,GO:0016772
comp27219_c0_seq1.p2	sp|O55767|VF179_IIV6_Uncharacterized_protein_179R_OS=Invertebrate_iridescent_virus_6_GN=IIV6-179R_PE=4_SV=1	1.00E-16	GO:0004672,GO:0006468,GO:0016772
comp27220_c0_seq1.p1	sp|Q1MTN8|YGC1_SCHPO_UPF0661_TPR_repeat-containing_protein_C16D10.01c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC16D10.01c_PE=3_SV=2	2.00E-29	GO:0003674,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0008150,GO:0043234
comp27220_c0_seq2.p1	sp|Q1MTN8|YGC1_SCHPO_UPF0661_TPR_repeat-containing_protein_C16D10.01c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC16D10.01c_PE=3_SV=2	3.00E-29	GO:0003674,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0008150,GO:0043234
comp27220_c0_seq6.p1	sp|Q1MTN8|YGC1_SCHPO_UPF0661_TPR_repeat-containing_protein_C16D10.01c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC16D10.01c_PE=3_SV=2	1.00E-17	GO:0003674,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0008150,GO:0043234
comp27222_c0_seq1.p1	sp|O67679|ENGB_AQUAE_Probable_GTP-binding_protein_EngB_OS=Aquifex_aeolicus_(strain_VF5)_GN=engB_PE=3_SV=1	2.00E-14	GO:0000166,GO:0000287,GO:0000917,GO:0000917,GO:0000917,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0006184,GO:0007049,GO:0046872,GO:0046872,GO:0051301
comp27223_c0_seq1.p1	sp|A1K5T6|Y1574_AZOSB_UPF0061_protein_azo1574_OS=Azoarcus_sp._(strain_BH72)_GN=azo1574_PE=3_SV=1	7.00E-33	
comp27223_c0_seq1.p2			
comp27224_c0_seq1.p1	sp|P11009|KCRS_CHICK_Creatine_kinase_S-type,_mitochondrial_OS=Gallus_gallus_GN=CKMT2_PE=1_SV=2	4.00E-89	GO:0000166,GO:0003824,GO:0004111,GO:0005524,GO:0005739,GO:0005743,GO:0005743,GO:0016020,GO:0016301,GO:0016301,GO:0016310,GO:0016740,GO:0016772
comp27224_c0_seq1.p4			
comp27226_c0_seq1.p1	sp|P84798|DPOD3_BOVIN_DNA_polymerase_delta_subunit_3_OS=Bos_taurus_GN=POLD3_PE=1_SV=2	5.00E-12	GO:0003887,GO:0003887,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0006260,GO:0006260,GO:0006260,GO:0016740,GO:0016779,GO:0071897,GO:0071897
comp27228_c0_seq1.p1			
comp27230_c0_seq1.p1			
comp27232_c0_seq2.p1	sp|Q8H0V6|AB3F_ARATH_ABC_transporter_F_family_member_3_OS=Arabidopsis_thaliana_GN=ABCF3_PE=2_SV=1	3.00E-80	GO:0000166,GO:0005215,GO:0005524,GO:0005524,GO:0005829,GO:0006094,GO:0006096,GO:0006200,GO:0006406,GO:0006606,GO:0006810,GO:0007010,GO:0009651,GO:0010498,GO:0016887,GO:0042742,GO:0046686,GO:0046686
comp27233_c1_seq2.p1	sp|Q6K687|C3H18_ORYSJ_Zinc_finger_CCCH_domain-containing_protein_18_OS=Oryza_sativa_subsp._japonica_GN=Os02g0793000_PE=2_SV=1	1.00E-15	GO:0003676,GO:0003676,GO:0003677,GO:0003677,GO:0008150,GO:0046872,GO:0046872,GO:0046872
comp27233_c1_seq3.p1			
comp27235_c0_seq1.p1			
comp27241_c1_seq1.p2			
comp27241_c1_seq1.p3			
comp27241_c1_seq2.p2			
comp27241_c1_seq2.p3			
comp27241_c1_seq3.p1			
comp27241_c1_seq4.p1			
comp27242_c0_seq1.p1			
comp27242_c0_seq3.p1			
comp27245_c1_seq1.p1			
comp27246_c0_seq2.p1	sp|Q99MJ9|DDX50_MOUSE_ATP-dependent_RNA_helicase_DDX50_OS=Mus_musculus_GN=Ddx50_PE=2_SV=1	5.00E-151	GO:0000166,GO:0003676,GO:0003723,GO:0003723,GO:0004386,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0005886,GO:0008150,GO:0008152,GO:0008152,GO:0008152,GO:0016020,GO:0016787,GO:0044822
comp27247_c0_seq2.p1			
comp27248_c0_seq1.p2			
comp27248_c0_seq2.p1			
comp27251_c0_seq1.p1			
comp27251_c0_seq2.p1			
comp27251_c0_seq3.p1			
comp27252_c0_seq1.p1	sp|Q54EY1|DTD_DICDI_D-tyrosyl-tRNA(Tyr)_deacylase_OS=Dictyostelium_discoideum_GN=dtd_PE=3_SV=1	7.00E-33	GO:0002161,GO:0005575,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006399,GO:0006450,GO:0016787,GO:0016788,GO:0019478,GO:0019478,GO:0051500,GO:0051500
comp27255_c0_seq1.p1			
comp27256_c0_seq3.p1	sp|Q9NW13|RBM28_HUMAN_RNA-binding_protein_28_OS=Homo_sapiens_GN=RBM28_PE=1_SV=3	2.00E-32	GO:0000166,GO:0003676,GO:0003723,GO:0005634,GO:0005681,GO:0005730,GO:0005730,GO:0006397,GO:0008380,GO:0044822,GO:0044822
comp27257_c0_seq1.p1			
comp27257_c0_seq1.p2			
comp27257_c0_seq2.p1			
comp27257_c0_seq3.p1			
comp27258_c0_seq1.p1			
comp27258_c0_seq2.p1			
comp27258_c0_seq3.p1			
comp27259_c0_seq2.p2			
comp27259_c0_seq2.p4			
comp27260_c0_seq1.p1			
comp27263_c1_seq2.p1	sp|P94479|YNBB_BACSU_Uncharacterized_protein_ynbB_OS=Bacillus_subtilis_GN=ynbB_PE=4_SV=2	1.00E-109	GO:0003824,GO:0008152,GO:0030170
comp27263_c1_seq3.p1	sp|P94479|YNBB_BACSU_Uncharacterized_protein_ynbB_OS=Bacillus_subtilis_GN=ynbB_PE=4_SV=2	5.00E-80	GO:0003824,GO:0008152,GO:0030170
comp27263_c1_seq3.p2			
comp27265_c0_seq2.p2			
comp27266_c0_seq1.p1	sp|Q9LDI3|CIPKO_ARATH_CBL-interacting_serine/threonine-protein_kinase_24_OS=Arabidopsis_thaliana_GN=CIPK24_PE=1_SV=1	2.00E-64	GO:0000166,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006468,GO:0007165,GO:0009651,GO:0009705,GO:0016301,GO:0016310,GO:0016740,GO:0016772
comp27267_c0_seq2.p1			
comp27267_c0_seq2.p2	sp|Q9ZVN4|Y1500_ARATH_Probable_tyrosine-protein_phosphatase_At1g05000_OS=Arabidopsis_thaliana_GN=At1g05000_PE=1_SV=1	3.00E-42	GO:0004721,GO:0004725,GO:0004725,GO:0016311,GO:0016787,GO:0016791,GO:0035335,GO:0035335
comp27267_c0_seq2.p5			
comp27267_c0_seq4.p2	sp|Q9ZVN4|Y1500_ARATH_Probable_tyrosine-protein_phosphatase_At1g05000_OS=Arabidopsis_thaliana_GN=At1g05000_PE=1_SV=1	3.00E-42	GO:0004721,GO:0004725,GO:0004725,GO:0016311,GO:0016787,GO:0016791,GO:0035335,GO:0035335
comp27267_c0_seq4.p4			
comp27269_c0_seq1.p1			
comp27269_c0_seq3.p1			
comp27269_c0_seq4.p1			
comp27271_c0_seq2.p1	sp|B6ISY6|CLPX_RHOCS_ATP-dependent_Clp_protease_ATP-binding_subunit_ClpX_OS=Rhodospirillum_centenum_(strain_ATCC_51521_/_SW)_GN=clpX_PE=3_SV=1	2.00E-97	GO:0000166,GO:0005524,GO:0005524,GO:0005524,GO:0006457,GO:0006457,GO:0008270,GO:0046872,GO:0046983,GO:0051082,GO:0051082
comp27272_c1_seq2.p1			
comp27273_c0_seq4.p1	sp|Q5URB9|YR840_MIMIV_Putative_ankyrin_repeat_protein_R840_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R840_PE=4_SV=1	1.00E-11	
comp27274_c0_seq1.p1			
comp27274_c0_seq4.p1	sp|Q54DD7|UNC50_DICDI_Protein_unc-50_homolog_OS=Dictyostelium_discoideum_GN=DDB_G0292320_PE=3_SV=1	7.00E-50	GO:0016020,GO:0016020,GO:0016021
comp27274_c0_seq4.p4			
comp27275_c0_seq1.p1			
comp27275_c0_seq2.p1			
comp27276_c0_seq2.p1			
comp27276_c0_seq3.p1			
comp27278_c0_seq1.p1			
comp27278_c1_seq3.p2	sp|Q1PFH8|CDPKJ_ARATH_Calcium-dependent_protein_kinase_19_OS=Arabidopsis_thaliana_GN=CPK19_PE=2_SV=1	7.00E-12	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005509,GO:0005524,GO:0005524,GO:0005886,GO:0006468,GO:0016020,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0046872
comp27278_c1_seq7.p1	sp|Q8ICR0|CDPK2_PLAF7_Calcium-dependent_protein_kinase_2_OS=Plasmodium_falciparum_(isolate_3D7)_GN=CPK2_PE=2_SV=3	7.00E-110	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005509,GO:0005524,GO:0005524,GO:0006468,GO:0006468,GO:0009931,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0046872
comp27281_c0_seq1.p1			
comp27282_c0_seq1.p1			
comp27283_c0_seq2.p1	sp|O52535|CAH_KLEPN_Carbonic_anhydrase_OS=Klebsiella_pneumoniae_GN=cah_PE=3_SV=1	3.00E-14	GO:0004089,GO:0004089,GO:0006730,GO:0008270,GO:0016829,GO:0042597,GO:0042597,GO:0046872
comp27283_c1_seq2.p1			
comp27284_c1_seq1.p1			
comp27284_c1_seq1.p2	sp|A1A4M4|TATD3_BOVIN_Putative_deoxyribonuclease_TATDN3_OS=Bos_taurus_GN=TATDN3_PE=2_SV=1	1.00E-54	GO:0000737,GO:0004518,GO:0004536,GO:0005634,GO:0005634,GO:0005739,GO:0006308,GO:0016787,GO:0016888,GO:0043229,GO:0046872,GO:0090305
comp27284_c1_seq2.p1	sp|A1A4M4|TATD3_BOVIN_Putative_deoxyribonuclease_TATDN3_OS=Bos_taurus_GN=TATDN3_PE=2_SV=1	1.00E-54	GO:0000737,GO:0004518,GO:0004536,GO:0005634,GO:0005634,GO:0005739,GO:0006308,GO:0016787,GO:0016888,GO:0043229,GO:0046872,GO:0090305
comp27284_c1_seq2.p3			
comp27285_c0_seq2.p1	sp|Q62651|ECH1_RAT_Delta(3,5)-Delta(2,4)-dienoyl-CoA_isomerase,_mitochondrial_OS=Rattus_norvegicus_GN=Ech1_PE=1_SV=2	1.00E-84	GO:0003824,GO:0005102,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005777,GO:0005777,GO:0006629,GO:0006631,GO:0006635,GO:0008152,GO:0016020,GO:0016853,GO:0046872,GO:0070062
comp27286_c0_seq1.p1			
comp27286_c0_seq3.p1			
comp27288_c0_seq3.p1			
comp27290_c0_seq2.p1			
comp27290_c0_seq2.p7			
comp27291_c0_seq1.p1			
comp27291_c0_seq1.p2	sp|B9LED5|URK_CHLSY_Uridine_kinase_OS=Chloroflexus_aurantiacus_(strain_ATCC_29364_/_DSM_637_/_Y-400-fl)_GN=udk_PE=3_SV=1	3.00E-64	GO:0000166,GO:0004849,GO:0004849,GO:0004849,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0008152,GO:0008655,GO:0016301,GO:0016301,GO:0016310,GO:0016740,GO:0016773,GO:0044206,GO:0044211
comp27291_c1_seq2.p1	sp|P05466|AROA_ARATH_3-phosphoshikimate_1-carboxyvinyltransferase,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g45300_PE=2_SV=3	1.00E-176	GO:0003824,GO:0003866,GO:0003866,GO:0003866,GO:0008652,GO:0009073,GO:0009423,GO:0009423,GO:0009507,GO:0009507,GO:0009536,GO:0009570,GO:0016740,GO:0016765,GO:0005829
comp27292_c0_seq1.p1	sp|A2AV36|ANM7_DANRE_Protein_arginine_N-methyltransferase_7_OS=Danio_rerio_GN=prmt7_PE=2_SV=1	2.00E-31	GO:0000387,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0005829,GO:0006349,GO:0006351,GO:0006355,GO:0006355,GO:0006479,GO:0008168,GO:0008168,GO:0008276,GO:0008469,GO:0008469,GO:0008757,GO:0016277,GO:0016568,GO:0016740,GO:0018216,GO:0019918,GO:0019919,GO:0030154,GO:0032259,GO:0034969,GO:0034969,GO:0035241,GO:0035242,GO:0035243,GO:0043046,GO:0043985,GO:0044020
comp27292_c0_seq4.p1			
comp27293_c1_seq1.p1	sp|P37742|RFBK7_ECOLX_Phosphomannomutase_OS=Escherichia_coli_GN=manB_PE=3_SV=1	2.00E-109	GO:0000287,GO:0004615,GO:0005975,GO:0009103,GO:0009243,GO:0009298,GO:0016853,GO:0016868,GO:0046872
comp27294_c0_seq1.p1	sp|Q70HW3|SAMC_HUMAN_S-adenosylmethionine_mitochondrial_carrier_protein_OS=Homo_sapiens_GN=SLC25A26_PE=2_SV=1	8.00E-17	GO:0000095,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0006810,GO:0015805,GO:0016020,GO:0016021,GO:1901962
comp27296_c0_seq1.p1			
comp27298_c0_seq1.p1			
comp27298_c0_seq2.p1	sp|Q3SZV5|POMP_BOVIN_Proteasome_maturation_protein_OS=Bos_taurus_GN=POMP_PE=2_SV=1	3.00E-16	GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005783,GO:0005829,GO:0016020,GO:0031090,GO:0043231,GO:0043248,GO:0043248
comp27298_c0_seq2.p2			
comp2730_c0_seq1.p1			
comp27301_c0_seq1.p1			
comp27301_c0_seq2.p1			
comp27301_c0_seq4.p1	sp|O44400|F37C4_CAEEL_Protein_F37C4.5_OS=Caenorhabditis_elegans_GN=F37C4.5_PE=1_SV=3	2.00E-17	GO:0005515,GO:0005515
comp27301_c0_seq4.p5			
comp27301_c0_seq5.p1			
comp27303_c0_seq1.p1			
comp27303_c0_seq2.p1			
comp27304_c1_seq1.p1	sp|Q8BUV8|GP107_MOUSE_Protein_GPR107_OS=Mus_musculus_GN=Gpr107_PE=2_SV=2	2.00E-71	GO:0003674,GO:0005575,GO:0005794,GO:0005794,GO:0008150,GO:0016020,GO:0016021,GO:0016021
comp27306_c0_seq2.p1			
comp27308_c0_seq2.p2			
comp27309_c0_seq1.p1	sp|P0C5K5|FH21B_ARATH_Formin-like_protein_21b_OS=Arabidopsis_thaliana_GN=FH21B_PE=2_SV=1	2.00E-18	GO:0005884,GO:0045010
comp27311_c0_seq1.p1	sp|O80944|AKRC8_ARATH_Aldo-keto_reductase_family_4_member_C8_OS=Arabidopsis_thaliana_GN=AKR4C8_PE=1_SV=2	5.00E-30	GO:0004033,GO:0004033,GO:0005829,GO:0009409,GO:0009409,GO:0009414,GO:0009414,GO:0009636,GO:0009651,GO:0009651,GO:0016229,GO:0016491,GO:0016491,GO:0046482,GO:0046686,GO:0055114,GO:0055114,GO:0055114,GO:0070401
comp27312_c0_seq1.p1			
comp27314_c0_seq2.p1			
comp27315_c0_seq1.p1	sp|A6QLU1|GPDM_BOVIN_Glycerol-3-phosphate_dehydrogenase,_mitochondrial_OS=Bos_taurus_GN=GPD2_PE=2_SV=1	4.00E-75	GO:0004368,GO:0004368,GO:0005509,GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0006072,GO:0006072,GO:0006094,GO:0009331,GO:0016491,GO:0016491,GO:0019563,GO:0035264,GO:0043010,GO:0046872,GO:0052590,GO:0052591,GO:0055114,GO:0055114
comp27315_c0_seq1.p2	sp|P90795|GPDM_CAEEL_Probable_glycerol-3-phosphate_dehydrogenase,_mitochondrial_OS=Caenorhabditis_elegans_GN=T25G3.4_PE=2_SV=2	1.00E-87	GO:0004368,GO:0004368,GO:0005509,GO:0005739,GO:0005739,GO:0006072,GO:0009331,GO:0016491,GO:0016491,GO:0019563,GO:0046872,GO:0052590,GO:0052591,GO:0055114,GO:0055114
comp27315_c0_seq2.p1	sp|P90795|GPDM_CAEEL_Probable_glycerol-3-phosphate_dehydrogenase,_mitochondrial_OS=Caenorhabditis_elegans_GN=T25G3.4_PE=2_SV=2	8.00E-176	GO:0004368,GO:0004368,GO:0005509,GO:0005739,GO:0005739,GO:0006072,GO:0009331,GO:0016491,GO:0016491,GO:0019563,GO:0046872,GO:0052590,GO:0052591,GO:0055114,GO:0055114
comp27316_c0_seq1.p1			
comp27317_c0_seq4.p1	sp|Q55G10|PNCB_DICDI_Nicotinate_phosphoribosyltransferase_OS=Dictyostelium_discoideum_GN=napt_PE=2_SV=1	3.00E-151	GO:0004514,GO:0004516,GO:0009435,GO:0009435,GO:0016740,GO:0016874,GO:0019358,GO:0019363
comp27317_c0_seq5.p1	sp|Q55G10|PNCB_DICDI_Nicotinate_phosphoribosyltransferase_OS=Dictyostelium_discoideum_GN=napt_PE=2_SV=1	0	GO:0004514,GO:0004516,GO:0009435,GO:0009435,GO:0016740,GO:0016874,GO:0019358,GO:0019363
comp27318_c0_seq1.p1			
comp27319_c0_seq2.p1			
comp27322_c0_seq1.p1	sp|Q5R9L3|G3BP2_PONAB_Ras_GTPase-activating_protein-binding_protein_2_OS=Pongo_abelii_GN=G3BP2_PE=2_SV=1	5.00E-13	GO:0000166,GO:0003676,GO:0003723,GO:0005622,GO:0005737,GO:0006810,GO:0006810,GO:0044822,GO:0051028
comp27322_c0_seq2.p1			
comp27323_c0_seq1.p1			
comp27323_c0_seq2.p1			
comp27324_c0_seq1.p1	sp|Q94IR2|CCD1_PHAVU_Carotenoid_9,10(9',10')-cleavage_dioxygenase_1_OS=Phaseolus_vulgaris_GN=CCD1_PE=1_SV=1	6.00E-52	GO:0016491,GO:0046872,GO:0051213,GO:0055114
comp27324_c0_seq1.p2	sp|Q94IR2|CCD1_PHAVU_Carotenoid_9,10(9',10')-cleavage_dioxygenase_1_OS=Phaseolus_vulgaris_GN=CCD1_PE=1_SV=1	6.00E-15	GO:0016491,GO:0046872,GO:0051213,GO:0055114
comp27324_c0_seq1.p3	sp|Q84KG5|CCD_CROSA_Carotenoid_9,10(9',10')-cleavage_dioxygenase_OS=Crocus_sativus_GN=CCD_PE=1_SV=1	4.00E-22	GO:0005737,GO:0005737,GO:0016491,GO:0046872,GO:0051213,GO:0055114
comp27325_c0_seq1.p1	sp|Q64237|DOPO_MOUSE_Dopamine_beta-hydroxylase_OS=Mus_musculus_GN=Dbh_PE=2_SV=1	2.00E-23	GO:0001816,GO:0001974,GO:0001974,GO:0001975,GO:0002443,GO:0003824,GO:0004497,GO:0004497,GO:0004500,GO:0005507,GO:0007613,GO:0007613,GO:0007626,GO:0008306,GO:0008542,GO:0016020,GO:0016021,GO:0016023,GO:0016491,GO:0016715,GO:0030658,GO:0031410,GO:0031418,GO:0034466,GO:0042127,GO:0042309,GO:0042420,GO:0042421,GO:0042421,GO:0042421,GO:0042423,GO:0042584,GO:0042593,GO:0042596,GO:0042711,GO:0045907,GO:0046872,GO:0048149,GO:0048265,GO:0050900,GO:0055114,GO:0055114,GO:2001236
comp27326_c0_seq1.p1	sp|A8MEV9|MNMA_ALKOO_tRNA-specific_2-thiouridylase_mnmA_OS=Alkaliphilus_oremlandii_(strain_OhILAs)_GN=mnmA_PE=3_SV=1	4.00E-75	GO:0000049,GO:0000166,GO:0003723,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006400,GO:0008033,GO:0008033,GO:0016740,GO:0016740,GO:0016783
comp27326_c0_seq2.p1	sp|B1HUL3|MNMA_LYSSC_tRNA-specific_2-thiouridylase_mnmA_OS=Lysinibacillus_sphaericus_(strain_C3-41)_GN=mnmA_PE=3_SV=1	5.00E-56	GO:0000049,GO:0000166,GO:0003723,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006400,GO:0008033,GO:0008033,GO:0016740,GO:0016740,GO:0016783
comp27329_c0_seq1.p2			
comp27329_c0_seq4.p1			
comp27330_c0_seq1.p1			
comp27332_c0_seq1.p1			
comp27333_c0_seq1.p2			
comp27334_c0_seq1.p1	sp|Q9Y713|EF1A_ASPOR_Elongation_factor_1-alpha_OS=Aspergillus_oryzae_(strain_ATCC_42149_/_RIB_40)_GN=tef1_PE=3_SV=1	5.00E-96	GO:0000166,GO:0003746,GO:0003746,GO:0003924,GO:0005525,GO:0005525,GO:0005575,GO:0005737,GO:0005737,GO:0005737,GO:0006184,GO:0006412,GO:0006414,GO:0006414,GO:0008150
comp27334_c0_seq1.p2	sp|Q27139|EF1A1_EUPCR_Elongation_factor_1-alpha_1_OS=Euplotes_crassus_GN=EFA1_PE=3_SV=1	1.00E-15	GO:0000166,GO:0003746,GO:0003746,GO:0003924,GO:0005525,GO:0005525,GO:0005737,GO:0005737,GO:0005737,GO:0006184,GO:0006412,GO:0006414,GO:0006414
comp27336_c0_seq1.p1	sp|Q54GB2|CTSL2_DICDI_CTD_small_phosphatase-like_protein_2_OS=Dictyostelium_discoideum_GN=ctdspl2_PE=3_SV=1	7.00E-46	GO:0004721,GO:0005575,GO:0008150,GO:0008152,GO:0016311,GO:0016311,GO:0016787,GO:0016791
comp27337_c0_seq2.p1	sp|O80934|Y2766_ARATH_Uncharacterized_protein_At2g37660,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g37660_PE=1_SV=2	7.00E-67	GO:0000272,GO:0005507,GO:0005982,GO:0006364,GO:0009409,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009570,GO:0009570,GO:0009570,GO:0009579,GO:0009664,GO:0009697,GO:0009814,GO:0015995,GO:0019288,GO:0019684,GO:0042742,GO:0042742,GO:0048046
comp27338_c0_seq2.p1			
comp27339_c2_seq1.p1			
comp27342_c0_seq1.p2			
comp27342_c0_seq2.p1	sp|Q9LK09|SYP32_ARATH_Syntaxin-32_OS=Arabidopsis_thaliana_GN=SYP32_PE=2_SV=1	2.00E-28	GO:0005484,GO:0005794,GO:0005794,GO:0006810,GO:0006886,GO:0015031,GO:0016020,GO:0016020,GO:0016021,GO:0016192
comp27342_c0_seq4.p1			
comp27343_c0_seq1.p1	sp|Q9N599|PSA4_CAEEL_Proteasome_subunit_alpha_type-4_OS=Caenorhabditis_elegans_GN=pas-3_PE=2_SV=2	1.00E-48	GO:0000502,GO:0004175,GO:0004298,GO:0004298,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005839,GO:0006508,GO:0006511,GO:0008233,GO:0016787,GO:0019773,GO:0051603
comp27343_c0_seq2.p1			
comp27343_c0_seq2.p2	sp|P52427|PSA4_SPIOL_Proteasome_subunit_alpha_type-4_OS=Spinacia_oleracea_GN=PAC1_PE=2_SV=1	4.00E-102	GO:0000502,GO:0004175,GO:0004298,GO:0004298,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005839,GO:0006508,GO:0006511,GO:0008233,GO:0016787,GO:0019773,GO:0051603
comp27346_c0_seq1.p1			
comp27347_c0_seq2.p2			
comp27351_c1_seq1.p1			
comp27354_c0_seq1.p1	sp|Q54V77|PYRG_DICDI_CTP_synthase_OS=Dictyostelium_discoideum_GN=ctps_PE=3_SV=1	0	GO:0000166,GO:0003883,GO:0003883,GO:0003883,GO:0005524,GO:0005575,GO:0006221,GO:0006221,GO:0006241,GO:0006541,GO:0008654,GO:0016874,GO:0019856,GO:0044210,GO:0044351
comp27354_c0_seq2.p1	sp|Q54V77|PYRG_DICDI_CTP_synthase_OS=Dictyostelium_discoideum_GN=ctps_PE=3_SV=1	4.00E-179	GO:0000166,GO:0003883,GO:0003883,GO:0003883,GO:0005524,GO:0005575,GO:0006221,GO:0006221,GO:0006241,GO:0006541,GO:0008654,GO:0016874,GO:0019856,GO:0044210,GO:0044351
comp27354_c1_seq2.p1	sp|P36428|SYA_ARATH_Alanine--tRNA_ligase_OS=Arabidopsis_thaliana_GN=ALATS_PE=1_SV=3	0	GO:0000049,GO:0000166,GO:0000166,GO:0003676,GO:0003723,GO:0004812,GO:0004813,GO:0004813,GO:0004813,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0005739,GO:0005739,GO:0005829,GO:0006094,GO:0006096,GO:0006406,GO:0006412,GO:0006419,GO:0006419,GO:0006499,GO:0008270,GO:0009507,GO:0009651,GO:0009909,GO:0010074,GO:0016874,GO:0016876,GO:0043039,GO:0046686,GO:0046686,GO:0046872,GO:0051604,GO:0070143
comp27354_c1_seq2.p3	sp|Q7ZXP9|PYG1B_XENLA_CTP_synthase_1-B_OS=Xenopus_laevis_GN=ctps-b_PE=2_SV=1	9.00E-24	GO:0000166,GO:0003883,GO:0003883,GO:0003883,GO:0005524,GO:0006221,GO:0006221,GO:0006241,GO:0006541,GO:0016874,GO:0044210
comp27356_c0_seq2.p1			
comp27359_c0_seq1.p1			
comp27359_c0_seq2.p1			
comp27360_c0_seq3.p1	sp|Q75K12|NT5D_DICDI_5'-nucleotidase_domain-containing_protein_DDB_G0275467_OS=Dictyostelium_discoideum_GN=DDB_G0275467_PE=3_SV=1	2.00E-95	GO:0003674,GO:0005575,GO:0008152,GO:0008253,GO:0016311,GO:0016787,GO:0046872
comp27360_c0_seq4.p1	sp|Q75K12|NT5D_DICDI_5'-nucleotidase_domain-containing_protein_DDB_G0275467_OS=Dictyostelium_discoideum_GN=DDB_G0275467_PE=3_SV=1	2.00E-97	GO:0003674,GO:0005575,GO:0008152,GO:0008253,GO:0016311,GO:0016787,GO:0046872
comp27361_c0_seq1.p1	sp|Q5RBD9|TBCE_PONAB_Tubulin-specific_chaperone_E_OS=Pongo_abelii_GN=TBCE_PE=2_SV=1	2.00E-58	GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0007023
comp27363_c0_seq1.p1			
comp27364_c0_seq1.p1			
comp27366_c0_seq1.p1			
comp27367_c0_seq1.p1			
comp27367_c0_seq2.p1			
comp27368_c1_seq1.p1			
comp27369_c0_seq4.p1			
comp27371_c0_seq4.p1			
comp27371_c0_seq5.p1			
comp27372_c0_seq1.p1			
comp27373_c0_seq1.p1			
comp27374_c0_seq1.p1			
comp27374_c0_seq1.p2			
comp27377_c0_seq1.p1	sp|P38117|ETFB_HUMAN_Electron_transfer_flavoprotein_subunit_beta_OS=Homo_sapiens_GN=ETFB_PE=1_SV=3	1.00E-98	GO:0005739,GO:0005739,GO:0005739,GO:0005759,GO:0005759,GO:0005759,GO:0005759,GO:0009055,GO:0009055,GO:0022904,GO:0022904,GO:0043231,GO:0044237,GO:0044281,GO:0055114,GO:0070062
comp27380_c1_seq1.p1			
comp27381_c0_seq1.p1			
comp27381_c0_seq2.p1			
comp27381_c0_seq3.p1			
comp27382_c0_seq2.p1	sp|P39981|AVT2_YEAST_Vacuolar_amino_acid_transporter_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=AVT2_PE=2_SV=1	3.00E-32	GO:0003674,GO:0005773,GO:0005774,GO:0005783,GO:0006810,GO:0006865,GO:0008150,GO:0016020,GO:0016021
comp27385_c0_seq1.p1	sp|P38023|RPOD1_SYNE7_RNA_polymerase_sigma_factor_rpoD1_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=rpoD1_PE=3_SV=1	3.00E-34	GO:0001123,GO:0003677,GO:0003677,GO:0003677,GO:0003700,GO:0005737,GO:0005737,GO:0005737,GO:0006351,GO:0006352,GO:0006355,GO:0006355,GO:0006355,GO:0010468,GO:0016987,GO:0016987,GO:0016987
comp27386_c0_seq2.p1			
comp27387_c0_seq3.p1	sp|P48037|ANXA6_RAT_Annexin_A6_OS=Rattus_norvegicus_GN=Anxa6_PE=1_SV=2	3.00E-41	GO:0005509,GO:0005544,GO:0005544,GO:0005544,GO:0005544,GO:0005737,GO:0005737,GO:0005737,GO:0016324,GO:0042470,GO:0043234,GO:0046903
comp27387_c1_seq1.p1			
comp27387_c2_seq1.p1	sp|Q99JG3|ANX13_MOUSE_Annexin_A13_OS=Mus_musculus_GN=Anxa13_PE=2_SV=3	4.00E-30	GO:0005509,GO:0005544,GO:0005544,GO:0005886,GO:0005886,GO:0008150,GO:0016020
comp27387_c3_seq1.p1			
comp27388_c0_seq1.p1	sp|Q54GS1|CL16A_DICDI_Protein_CLEC16A_homolog_OS=Dictyostelium_discoideum_GN=DDB_G0289943_PE=3_SV=1	2.00E-11	GO:0003674,GO:0005575,GO:0006914,GO:0008150
comp27388_c0_seq1.p4			
comp27388_c0_seq5.p1			
comp27388_c0_seq7.p1			
comp27388_c0_seq7.p4	sp|Q54GS1|CL16A_DICDI_Protein_CLEC16A_homolog_OS=Dictyostelium_discoideum_GN=DDB_G0289943_PE=3_SV=1	4.00E-11	GO:0003674,GO:0005575,GO:0006914,GO:0008150
comp27388_c0_seq7.p5			
comp27388_c0_seq8.p1			
comp27388_c0_seq8.p3	sp|Q54GS1|CL16A_DICDI_Protein_CLEC16A_homolog_OS=Dictyostelium_discoideum_GN=DDB_G0289943_PE=3_SV=1	4.00E-11	GO:0003674,GO:0005575,GO:0006914,GO:0008150
comp27388_c0_seq8.p4			
comp27388_c0_seq9.p1	sp|Q80U30|CL16A_MOUSE_Protein_CLEC16A_OS=Mus_musculus_GN=Clec16a_PE=2_SV=2	3.00E-12	GO:0005515,GO:0005575,GO:0005764,GO:0005765,GO:0005768,GO:0006914,GO:0008150,GO:0010008,GO:0016020
comp27388_c0_seq9.p3			
comp27390_c0_seq1.p1			
comp27391_c0_seq1.p1	sp|Q5F3X4|U5S1_CHICK_116_kDa_U5_small_nuclear_ribonucleoprotein_component_OS=Gallus_gallus_GN=EFTUD2_PE=2_SV=1	0	GO:0000166,GO:0003924,GO:0005525,GO:0005525,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005681,GO:0005737,GO:0006184,GO:0006397,GO:0008380,GO:0015030,GO:0016020,GO:0016607,GO:0044822,GO:0071013
comp27392_c0_seq1.p1			
comp27395_c0_seq2.p1	sp|O15488|GLYG2_HUMAN_Glycogenin-2_OS=Homo_sapiens_GN=GYG2_PE=1_SV=2	1.00E-40	GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0005975,GO:0005978,GO:0005978,GO:0005978,GO:0005978,GO:0005980,GO:0006006,GO:0008466,GO:0008466,GO:0008466,GO:0016740,GO:0016757,GO:0044281
comp27397_c0_seq1.p1	sp|Q944L7|Y1480_ARATH_Uncharacterized_protein_At1g18480_OS=Arabidopsis_thaliana_GN=At1g18480_PE=2_SV=1	5.00E-29	GO:0005829,GO:0008152,GO:0016787
comp27397_c1_seq1.p2			
comp27397_c1_seq2.p1			
comp27398_c0_seq2.p1	sp|Q10UW6|PEBB_TRIEI_Phycoerythrobilin:ferredoxin_oxidoreductase_OS=Trichodesmium_erythraeum_(strain_IMS101)_GN=pebB_PE=3_SV=1	5.00E-59	GO:0010024,GO:0016491,GO:0016636,GO:0050618,GO:0050618,GO:0050618,GO:0050897,GO:0055114,GO:0055114
comp27402_c0_seq1.p1			
comp27403_c0_seq1.p1			
comp27404_c0_seq1.p1			
comp27404_c0_seq2.p1			
comp27405_c0_seq1.p1			
comp27406_c1_seq1.p1			
comp27409_c0_seq1.p1	sp|Q39757|1433_FUCVE_14-3-3-like_protein_OS=Fucus_vesiculosus_PE=2_SV=1	4.00E-103	GO:0019904
comp27409_c0_seq2.p2	sp|Q39757|1433_FUCVE_14-3-3-like_protein_OS=Fucus_vesiculosus_PE=2_SV=1	9.00E-105	GO:0019904
comp27410_c0_seq1.p1	sp|O67012|SPOT_AQUAE_Guanosine-3',5'-bis(diphosphate)_3'-pyrophosphohydrolase_OS=Aquifex_aeolicus_(strain_VF5)_GN=spoT_PE=3_SV=1	1.00E-71	GO:0008152,GO:0008893,GO:0015969,GO:0015970,GO:0016597,GO:0016787
comp27411_c0_seq1.p1			
comp27412_c0_seq1.p1			
comp27413_c0_seq1.p1	sp|Q7RTR2|NLRC3_HUMAN_Protein_NLRC3_OS=Homo_sapiens_GN=NLRC3_PE=2_SV=2	5.00E-14	GO:0000166,GO:0003674,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0007249,GO:0031396,GO:0032088,GO:0032496,GO:0042110,GO:0043124,GO:0043124
comp27413_c0_seq1.p2			
comp27415_c0_seq4.p1	sp|Q52KD1|NTP7B_XENLA_Sodium/bile_acid_cotransporter_7-B_OS=Xenopus_laevis_GN=slc10a7-b_PE=2_SV=1	2.00E-18	GO:0006810,GO:0006811,GO:0006814,GO:0015293,GO:0016020,GO:0016020,GO:0016021,GO:0055085
comp27415_c0_seq4.p2			
comp27417_c0_seq1.p1			
comp27417_c0_seq1.p2	sp|Q9FM04|GDL88_ARATH_GDSL_esterase/lipase_At5g62930_OS=Arabidopsis_thaliana_GN=At5g62930_PE=2_SV=1	5.00E-35	GO:0005829,GO:0006629,GO:0006629,GO:0016042,GO:0016787,GO:0016787,GO:0016788
comp27419_c0_seq1.p1	sp|Q92609|TBCD5_HUMAN_TBC1_domain_family_member_5_OS=Homo_sapiens_GN=TBC1D5_PE=1_SV=1	1.00E-24	GO:0002092,GO:0005096,GO:0005097,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005776,GO:0010008,GO:0010508,GO:0030904,GO:0032313,GO:0032851,GO:0035612,GO:0042147,GO:0042594,GO:0043547,GO:1902017,GO:0030122,GO:0030904,GO:0070969
comp27419_c0_seq2.p1			
comp27421_c0_seq1.p1	sp|P96554|Y319_MYXXA_Uncharacterized_membrane_protein_STKORF319_OS=Myxococcus_xanthus_PE=3_SV=1	3.00E-61	GO:0005886,GO:0005886,GO:0016020,GO:0016021,GO:0016021
comp27422_c0_seq3.p3			
comp27423_c0_seq3.p1			
comp27423_c1_seq1.p1	sp|O96952|THIO_GEOCY_Thioredoxin_OS=Geodia_cydonium_GN=THIO_PE=3_SV=1	2.00E-25	GO:0005737,GO:0005737,GO:0006662,GO:0015035,GO:0045454,GO:0055114
comp27425_c0_seq1.p1	sp|Q8VY97|Y4213_ARATH_UPF0480_protein_At4g32130_OS=Arabidopsis_thaliana_GN=At4g32130_PE=1_SV=1	8.00E-25	GO:0005783,GO:0005783,GO:0005783,GO:0005789,GO:0006007,GO:0006888,GO:0008150,GO:0016020,GO:0016021,GO:0030246
comp27425_c1_seq1.p1			
comp27425_c1_seq2.p1			
comp27426_c0_seq2.p1			
comp27427_c0_seq3.p1	sp|O60341|KDM1A_HUMAN_Lysine-specific_histone_demethylase_1A_OS=Homo_sapiens_GN=KDM1A_PE=1_SV=2	3.00E-56	GO:0000122,GO:0000122,GO:0000122,GO:0000790,GO:0000790,GO:0000790,GO:0001085,GO:0001701,GO:0002039,GO:0003677,GO:0003682,GO:0003682,GO:0003700,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005654,GO:0005667,GO:0005667,GO:0006351,GO:0006355,GO:0006355,GO:0006357,GO:0006482,GO:0007275,GO:0007596,GO:0008134,GO:0008134,GO:0008283,GO:0010725,GO:0016491,GO:0016491,GO:0016491,GO:0016568,GO:0019899,GO:0019899,GO:0021983,GO:0030374,GO:0030851,GO:0032091,GO:0032451,GO:0032452,GO:0032453,GO:0032454,GO:0033169,GO:0034648,GO:0034720,GO:0034720,GO:0034720,GO:0043392,GO:0043426,GO:0043426,GO:0043433,GO:0043433,GO:0043518,GO:0044212,GO:0044212,GO:0045648,GO:0045654,GO:0045892,GO:0045944,GO:0045944,GO:0046886,GO:0050660,GO:0050660,GO:0050681,GO:0051091,GO:0051572,GO:0051573,GO:0055001,GO:0055001,GO:0055114,GO:0055114,GO:1902166,GO:2000179,GO:2000648
comp27427_c0_seq3.p2			
comp27428_c0_seq1.p1			
comp27428_c0_seq2.p1			
comp27430_c0_seq1.p1	sp|Q8ICR0|CDPK2_PLAF7_Calcium-dependent_protein_kinase_2_OS=Plasmodium_falciparum_(isolate_3D7)_GN=CPK2_PE=2_SV=3	2.00E-12	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005509,GO:0005524,GO:0005524,GO:0006468,GO:0006468,GO:0009931,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0046872
comp27430_c0_seq2.p1	sp|Q8ICR0|CDPK2_PLAF7_Calcium-dependent_protein_kinase_2_OS=Plasmodium_falciparum_(isolate_3D7)_GN=CPK2_PE=2_SV=3	2.00E-13	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005509,GO:0005524,GO:0005524,GO:0006468,GO:0006468,GO:0009931,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0046872
comp27430_c0_seq3.p1	sp|Q8ICR0|CDPK2_PLAF7_Calcium-dependent_protein_kinase_2_OS=Plasmodium_falciparum_(isolate_3D7)_GN=CPK2_PE=2_SV=3	1.00E-12	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005509,GO:0005524,GO:0005524,GO:0006468,GO:0006468,GO:0009931,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0046872
comp27431_c0_seq1.p1			
comp27431_c0_seq1.p3			
comp27434_c0_seq1.p1			
comp27435_c0_seq1.p1	sp|Q2VEQ7|DDH_HALME_D-2-hydroxyacid_dehydrogenase_OS=Haloferax_mediterranei_GN=ddh_PE=1_SV=1	4.00E-30	GO:0016491,GO:0016616,GO:0019752,GO:0031406,GO:0051287,GO:0055114,GO:0055114,GO:0070402,GO:0070404
comp27435_c0_seq2.p1	sp|Q2VEQ7|DDH_HALME_D-2-hydroxyacid_dehydrogenase_OS=Haloferax_mediterranei_GN=ddh_PE=1_SV=1	6.00E-33	GO:0016491,GO:0016616,GO:0019752,GO:0031406,GO:0051287,GO:0055114,GO:0055114,GO:0070402,GO:0070404
comp27435_c0_seq3.p1	sp|Q2VEQ7|DDH_HALME_D-2-hydroxyacid_dehydrogenase_OS=Haloferax_mediterranei_GN=ddh_PE=1_SV=1	3.00E-28	GO:0016491,GO:0016616,GO:0019752,GO:0031406,GO:0051287,GO:0055114,GO:0055114,GO:0070402,GO:0070404
comp27436_c0_seq2.p1	sp|Q8PC00|ASPN_XANCP_Peptidyl-Asp_metalloendopeptidase_OS=Xanthomonas_campestris_pv._campestris_GN=XCC0955_PE=3_SV=1	2.00E-15	GO:0006508,GO:0008233,GO:0008237,GO:0008237,GO:0016787,GO:0046872
comp27437_c0_seq1.p1			
comp27437_c0_seq2.p1			
comp27438_c0_seq3.p1			
comp27438_c0_seq5.p1			
comp27439_c0_seq1.p1			
comp27439_c0_seq2.p1			
comp27441_c0_seq5.p1	sp|O94469|DUR31_SCHPO_Probable_urea_active_transporter_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=dur3-1_PE=2_SV=1	6.00E-146	GO:0005215,GO:0005634,GO:0005886,GO:0006810,GO:0006810,GO:0015204,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0055085,GO:0071918
comp27441_c0_seq5.p2	sp|O94469|DUR31_SCHPO_Probable_urea_active_transporter_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=dur3-1_PE=2_SV=1	6.00E-146	GO:0005215,GO:0005634,GO:0005886,GO:0006810,GO:0006810,GO:0015204,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0055085,GO:0071918
comp27441_c0_seq8.p1	sp|O94469|DUR31_SCHPO_Probable_urea_active_transporter_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=dur3-1_PE=2_SV=1	4.00E-146	GO:0005215,GO:0005634,GO:0005886,GO:0006810,GO:0006810,GO:0015204,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0055085,GO:0071918
comp27441_c2_seq1.p1			
comp27441_c2_seq1.p2			
comp27442_c0_seq1.p1			
comp27444_c0_seq2.p1	sp|P28760|SODM_BACCA_Superoxide_dismutase_[Mn]_OS=Bacillus_caldotenax_GN=sodA_PE=3_SV=2	5.00E-43	GO:0004784,GO:0004784,GO:0006801,GO:0016491,GO:0019430,GO:0019430,GO:0046872,GO:0046872,GO:0055114,GO:0055114
comp27445_c0_seq1.p1			
comp27445_c0_seq1.p3			
comp27446_c0_seq1.p1			
comp27446_c1_seq3.p1			
comp27446_c1_seq4.p1			
comp27447_c0_seq3.p1	sp|Q9Y376|CAB39_HUMAN_Calcium-binding_protein_39_OS=Homo_sapiens_GN=CAB39_PE=1_SV=1	2.00E-87	GO:0004674,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0006468,GO:0007050,GO:0008286,GO:0010800,GO:0019900,GO:0023014,GO:0030295,GO:0032147,GO:0033138,GO:0035556,GO:0043234,GO:0043539,GO:0043539,GO:0051291,GO:0070062,GO:0070062,GO:0070062,GO:0070062,GO:0071476,GO:0071902,GO:0071902,GO:1901017,GO:1901380,GO:1902554,GO:2000681,GO:2000687
comp27447_c0_seq6.p1			
comp27447_c0_seq8.p1	sp|Q06138|CAB39_MOUSE_Calcium-binding_protein_39_OS=Mus_musculus_GN=Cab39_PE=1_SV=2	9.00E-71	GO:0004674,GO:0004674,GO:0005509,GO:0005737,GO:0005737,GO:0005737,GO:0006468,GO:0018105,GO:0018107,GO:0019900,GO:0023014,GO:0030295,GO:0030295,GO:0032147,GO:0035556,GO:0043234,GO:0043539,GO:0051291,GO:0070062,GO:0071902
comp27447_c0_seq8.p2			
comp27450_c0_seq1.p1			
comp27451_c1_seq7.p1	sp|Q1ZXG8|D1060_DICDI_Probable_tyrosine-protein_phosphatase_DG1060_OS=Dictyostelium_discoideum_GN=DG1060_PE=3_SV=1	2.00E-13	GO:0003674,GO:0004721,GO:0004725,GO:0004725,GO:0005575,GO:0005737,GO:0005737,GO:0008150,GO:0008152,GO:0016311,GO:0016787,GO:0035335,GO:0035335
comp27451_c1_seq7.p3			
comp27452_c0_seq1.p1			
comp27452_c1_seq1.p1			
comp27454_c1_seq1.p1			
comp27454_c2_seq1.p1	sp|Q9SIC9|PP178_ARATH_Pentatricopeptide_repeat-containing_protein_At2g31400,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g31400_PE=2_SV=1	1.00E-15	GO:0003677,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0010019,GO:0031930
comp27455_c0_seq1.p1			
comp27455_c0_seq4.p1			
comp27456_c0_seq1.p1			
comp27458_c0_seq1.p1	sp|Q9UW24|PIK1A_CANAL_Phosphatidylinositol_4-kinase_PIK1a_OS=Candida_albicans_(strain_SC5314_/_ATCC_MYA-2876)_GN=PIKA_PE=3_SV=1	3.00E-33	GO:0000166,GO:0004430,GO:0004430,GO:0005524,GO:0005634,GO:0005634,GO:0006661,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016773,GO:0044011,GO:0046854,GO:0048015
comp27458_c0_seq3.p1	sp|Q9FMJ0|P4KB1_ARATH_Phosphatidylinositol_4-kinase_beta_1_OS=Arabidopsis_thaliana_GN=PI4KBETA1_PE=1_SV=1	2.00E-51	GO:0004430,GO:0004430,GO:0004430,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005794,GO:0005794,GO:0005829,GO:0005886,GO:0005886,GO:0005886,GO:0006661,GO:0007275,GO:0009860,GO:0016020,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016773,GO:0017137,GO:0030659,GO:0030659,GO:0031410,GO:0035619,GO:0043424,GO:0046854,GO:0048015,GO:0048768
comp27460_c0_seq1.p1			
comp27463_c0_seq1.p1	sp|Q9KJ21|SDMT_ECTHL_Sarcosine/dimethylglycine_N-methyltransferase_OS=Ectothiorhodospira_halochloris_PE=1_SV=1	9.00E-28	GO:0008152,GO:0008168,GO:0008168,GO:0016740,GO:0019286,GO:0019286,GO:0032259,GO:0032259,GO:0052729,GO:0052729,GO:0052730,GO:0052730
comp27464_c0_seq1.p1	sp|Q6TDU7|CASC1_HUMAN_Cancer_susceptibility_candidate_protein_1_OS=Homo_sapiens_GN=CASC1_PE=2_SV=2	8.00E-18	
comp27464_c0_seq2.p1	sp|Q6TDU7|CASC1_HUMAN_Cancer_susceptibility_candidate_protein_1_OS=Homo_sapiens_GN=CASC1_PE=2_SV=2	6.00E-18	
comp27464_c0_seq3.p1	sp|Q6TDU7|CASC1_HUMAN_Cancer_susceptibility_candidate_protein_1_OS=Homo_sapiens_GN=CASC1_PE=2_SV=2	3.00E-16	
comp27464_c0_seq4.p1	sp|Q6TDU7|CASC1_HUMAN_Cancer_susceptibility_candidate_protein_1_OS=Homo_sapiens_GN=CASC1_PE=2_SV=2	3.00E-16	
comp27466_c0_seq2.p1	sp|Q96IV6|CE004_HUMAN_Uncharacterized_protein_C5orf4_OS=Homo_sapiens_GN=C5orf4_PE=1_SV=1	3.00E-12	GO:0005506,GO:0006633,GO:0016020,GO:0016020,GO:0016021,GO:0016491,GO:0055114
comp27468_c0_seq1.p1	sp|P87121|TAF2_SCHPO_Transcription_initiation_factor_TFIID_subunit_2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=taf2_PE=2_SV=3	2.00E-13	GO:0000790,GO:0000991,GO:0005634,GO:0005634,GO:0005634,GO:0005669,GO:0005737,GO:0005737,GO:0005829,GO:0006351,GO:0006355,GO:0006357,GO:0006367,GO:0006508,GO:0008237,GO:0008270,GO:0032153
comp27469_c0_seq1.p1	sp|Q21122|F26_CAEEL_Probable_6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase_OS=Caenorhabditis_elegans_GN=K02B2.1_PE=3_SV=2	1.00E-51	GO:0000166,GO:0003824,GO:0003824,GO:0003873,GO:0003873,GO:0004331,GO:0004331,GO:0005524,GO:0005524,GO:0006000,GO:0006003,GO:0008152,GO:0008152,GO:0016301,GO:0016310,GO:0016311,GO:0016311,GO:0016740,GO:0016787,GO:0046835,GO:0046835
comp27471_c0_seq1.p1	sp|Q924L9|FOLC_CRIGR_Folylpolyglutamate_synthase,_mitochondrial_OS=Cricetulus_griseus_GN=FPGS_PE=2_SV=1	1.00E-44	GO:0000166,GO:0004326,GO:0004326,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005739,GO:0005743,GO:0005743,GO:0005759,GO:0006730,GO:0009058,GO:0009396,GO:0016020,GO:0016874,GO:0016874,GO:0046901
comp27471_c0_seq1.p2	sp|Q54CY5|FOLC_DICDI_Putative_folylpolyglutamate_synthase_OS=Dictyostelium_discoideum_GN=folC_PE=3_SV=1	4.00E-20	GO:0000166,GO:0004326,GO:0004326,GO:0005524,GO:0005524,GO:0005575,GO:0006730,GO:0009058,GO:0009396,GO:0016874,GO:0016874,GO:0046901
comp27471_c0_seq1.p4			
comp27471_c0_seq3.p1	sp|Q924L9|FOLC_CRIGR_Folylpolyglutamate_synthase,_mitochondrial_OS=Cricetulus_griseus_GN=FPGS_PE=2_SV=1	2.00E-52	GO:0000166,GO:0004326,GO:0004326,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005739,GO:0005743,GO:0005743,GO:0005759,GO:0006730,GO:0009058,GO:0009396,GO:0016020,GO:0016874,GO:0016874,GO:0046901
comp27471_c0_seq5.p1	sp|Q924L9|FOLC_CRIGR_Folylpolyglutamate_synthase,_mitochondrial_OS=Cricetulus_griseus_GN=FPGS_PE=2_SV=1	1.00E-41	GO:0000166,GO:0004326,GO:0004326,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005739,GO:0005743,GO:0005743,GO:0005759,GO:0006730,GO:0009058,GO:0009396,GO:0016020,GO:0016874,GO:0016874,GO:0046901
comp27471_c0_seq5.p2	sp|Q54CY5|FOLC_DICDI_Putative_folylpolyglutamate_synthase_OS=Dictyostelium_discoideum_GN=folC_PE=3_SV=1	4.00E-20	GO:0000166,GO:0004326,GO:0004326,GO:0005524,GO:0005524,GO:0005575,GO:0006730,GO:0009058,GO:0009396,GO:0016874,GO:0016874,GO:0046901
comp27471_c0_seq6.p1	sp|Q924L9|FOLC_CRIGR_Folylpolyglutamate_synthase,_mitochondrial_OS=Cricetulus_griseus_GN=FPGS_PE=2_SV=1	1.00E-55	GO:0000166,GO:0004326,GO:0004326,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005739,GO:0005743,GO:0005743,GO:0005759,GO:0006730,GO:0009058,GO:0009396,GO:0016020,GO:0016874,GO:0016874,GO:0046901
comp27471_c0_seq6.p5			
comp27472_c0_seq2.p1	sp|Q9GTN7|TAGA_DICDI_Serine_protease/ABC_transporter_B_family_protein_tagA_OS=Dictyostelium_discoideum_GN=tagA_PE=1_SV=2	2.00E-17	GO:0000166,GO:0004252,GO:0005524,GO:0005524,GO:0006200,GO:0006508,GO:0006508,GO:0006810,GO:0006810,GO:0006810,GO:0008233,GO:0008236,GO:0008236,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016021,GO:0016787,GO:0016887,GO:0030154,GO:0042626,GO:0042626,GO:0042626,GO:0045595,GO:0045595,GO:0055085,GO:0055085
comp27473_c0_seq3.p1	sp|Q75K28|NCSA_DICDI_Calcium-binding_protein_NCSA_OS=Dictyostelium_discoideum_GN=ncsA_PE=1_SV=2	2.00E-15	GO:0005509,GO:0005509,GO:0005575,GO:0007275,GO:0030587,GO:0046872
comp27473_c1_seq1.p2			
comp27474_c0_seq3.p1			
comp27474_c0_seq4.p1			
comp27475_c0_seq2.p1	sp|Q8GUM5|NICA_ARATH_Nicastrin_OS=Arabidopsis_thaliana_GN=At3g52640/At3g52650_PE=2_SV=1	2.00E-18	GO:0007219,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016485
comp27476_c0_seq1.p1			
comp27476_c0_seq1.p2			
comp27476_c0_seq2.p1			
comp27476_c0_seq2.p2			
comp27478_c0_seq1.p1	sp|O05218|YWRD_BACSU_Putative_gamma-glutamyltransferase_ywrD_OS=Bacillus_subtilis_GN=ywrD_PE=1_SV=1	3.00E-67	GO:0003840,GO:0003840,GO:0006508,GO:0006749,GO:0008233,GO:0016740,GO:0016746,GO:0016787,GO:0036374
comp27478_c0_seq6.p1	sp|O05218|YWRD_BACSU_Putative_gamma-glutamyltransferase_ywrD_OS=Bacillus_subtilis_GN=ywrD_PE=1_SV=1	1.00E-67	GO:0003840,GO:0003840,GO:0006508,GO:0006749,GO:0008233,GO:0016740,GO:0016746,GO:0016787,GO:0036374
comp27481_c0_seq2.p1	sp|Q32KJ8|ARSI_RAT_Arylsulfatase_I_OS=Rattus_norvegicus_GN=Arsi_PE=2_SV=1	4.00E-67	GO:0003824,GO:0005576,GO:0005576,GO:0005783,GO:0005783,GO:0008152,GO:0008484,GO:0016787,GO:0046872
comp27483_c0_seq1.p1	sp|Q7PC88|AB31G_ARATH_ABC_transporter_G_family_member_31_OS=Arabidopsis_thaliana_GN=ABCG31_PE=2_SV=1	5.00E-180	GO:0000166,GO:0005524,GO:0005524,GO:0006200,GO:0006810,GO:0006855,GO:0009506,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016887
comp27484_c0_seq2.p1			
comp27484_c0_seq4.p1			
comp27484_c0_seq6.p1			
comp27485_c0_seq1.p1			
comp27488_c0_seq2.p1			
comp27490_c0_seq4.p1			
comp27490_c0_seq6.p1			
comp27491_c0_seq1.p1	sp|Q6QI44|NAA25_RAT_N-alpha-acetyltransferase_25,_NatB_auxiliary_subunit_OS=Rattus_norvegicus_GN=Naa25_PE=2_SV=1	6.00E-44	GO:0005737,GO:0005737,GO:0005737
comp27495_c0_seq1.p1	sp|Q54FR4|PX24D_DICDI_PXMP2/4_family_protein_4_OS=Dictyostelium_discoideum_GN=DDB_G0290631_PE=3_SV=1	1.00E-13	GO:0003674,GO:0008150,GO:0016020,GO:0016021,GO:0016021
comp27496_c0_seq2.p1			
comp27499_c0_seq3.p1			
comp27503_c0_seq1.p1	sp|Q9FFI2|ATG5_ARATH_Autophagy_protein_5_OS=Arabidopsis_thaliana_GN=ATG5_PE=2_SV=1	4.00E-19	GO:0000045,GO:0000422,GO:0005737,GO:0005737,GO:0005737,GO:0006501,GO:0006810,GO:0006914,GO:0006914,GO:0006914,GO:0006995,GO:0010150,GO:0010150,GO:0015031,GO:0034045,GO:0034274,GO:0042594,GO:0044804,GO:0050832,GO:0019776
comp27504_c0_seq1.p1			
comp27504_c0_seq2.p1			
comp27506_c0_seq1.p1	sp|P35915|HMGCL_CHICK_Hydroxymethylglutaryl-CoA_lyase_OS=Gallus_gallus_GN=HMGCL_PE=1_SV=1	2.00E-88	GO:0003824,GO:0004419,GO:0004419,GO:0004419,GO:0004419,GO:0005739,GO:0005759,GO:0005777,GO:0005777,GO:0016829,GO:0046872,GO:0046872,GO:0046951
comp27507_c1_seq1.p1			
comp27507_c1_seq2.p1	sp|O82251|TI202_ARATH_Protein_TIC_20-II,_chloroplastic_OS=Arabidopsis_thaliana_GN=TIC20-II_PE=2_SV=1	5.00E-15	GO:0005739,GO:0006810,GO:0009507,GO:0009507,GO:0009507,GO:0009528,GO:0009536,GO:0009536,GO:0009536,GO:0009706,GO:0009706,GO:0009941,GO:0009941,GO:0009941,GO:0010207,GO:0015031,GO:0016020,GO:0016021
comp27508_c0_seq1.p1			
comp27509_c0_seq1.p1			
comp27510_c0_seq2.p1			
comp27511_c0_seq2.p1			
comp27512_c0_seq2.p1			
comp27515_c0_seq1.p1			
comp27515_c0_seq2.p1	sp|Q9ASX5|Y5520_ARATH_Uncharacterized_aarF_domain-containing_protein_kinase_At5g05200,_chloroplastic_OS=Arabidopsis_thaliana_GN=At5g05200_PE=1_SV=1	7.00E-131	GO:0000023,GO:0000166,GO:0005524,GO:0009507,GO:0009507,GO:0009536,GO:0010287,GO:0010287,GO:0010287,GO:0015996,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0019252,GO:0043085
comp27515_c0_seq2.p2			
comp27516_c0_seq2.p1			
comp27516_c0_seq2.p3			
comp27516_c0_seq3.p1			

comp27518_c0_seq1.p1		
comp27518_c0_seq1.p3	sp|Q9FHX2|MFL1_ARATH_Protein_MITOFERRINLIKE_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=MFL1_PE=2_SV=1	7.00E-21
comp27518_c0_seq2.p1	sp|Q9FHX2|MFL1_ARATH_Protein_MITOFERRINLIKE_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=MFL1_PE=2_SV=1	2.00E-27
comp27519_c0_seq1.p1		
comp27520_c1_seq1.p1	sp|Q3AET6|GCSH_CARHZ_Glycine_cleavage_system_H_protein_OS=Carboxydothermus_hydrogenoformans_(strain_Z-2901_/_DSM_6008)_GN=gcvH_PE=3_SV=1	2.00E-40
comp27520_c1_seq2.p2		
comp27520_c1_seq3.p1		
comp27521_c0_seq1.p1		
comp27521_c0_seq2.p1		
comp27522_c0_seq1.p1		
comp27522_c0_seq4.p1		
comp27523_c0_seq1.p1	sp|Q84UI5|MPK1_ORYSJ_Mitogen-activated_protein_kinase_1_OS=Oryza_sativa_subsp._japonica_GN=MPK1_PE=1_SV=1	6.00E-89
comp27524_c0_seq1.p1	sp|O94477|MYO52_SCHPO_Myosin-52_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=myo52_PE=1_SV=1	5.00E-19
comp27524_c1_seq1.p1	sp|P19524|MYO2_YEAST_Myosin-2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=MYO2_PE=1_SV=1	3.00E-56
comp27524_c2_seq1.p1	sp|Q02440|MYO5A_CHICK_Unconventional_myosin-Va_OS=Gallus_gallus_GN=MYO5A_PE=1_SV=1	1.00E-35
comp27525_c0_seq1.p1		
comp27525_c0_seq2.p1		
comp27526_c1_seq2.p1		
comp27527_c0_seq3.p1	sp|Q4UJ75|A20A4_HUMAN_Ankyrin_repeat_domain-containing_protein_20A4_OS=Homo_sapiens_GN=ANKRD20A4_PE=2_SV=1	3.00E-16
comp27529_c0_seq1.p1	sp|P87362|BLMH_CHICK_Bleomycin_hydrolase_OS=Gallus_gallus_GN=BLMH_PE=1_SV=1	1.00E-120
comp27529_c0_seq3.p1	sp|P87362|BLMH_CHICK_Bleomycin_hydrolase_OS=Gallus_gallus_GN=BLMH_PE=1_SV=1	2.00E-92
comp27529_c1_seq1.p1		
comp2753_c0_seq1.p1	sp|P25535|VISC_ECOLI_Protein_visC_OS=Escherichia_coli_(strain_K12)_GN=visC_PE=3_SV=2	1.00E-63
comp27530_c1_seq1.p1	sp|Q6P829|NOSIP_XENTR_Nitric_oxide_synthase-interacting_protein_OS=Xenopus_tropicalis_GN=nosip_PE=2_SV=1	5.00E-34
comp27534_c0_seq1.p1		
comp27534_c0_seq2.p3		
comp27535_c0_seq3.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	2.00E-13
comp27536_c0_seq2.p1		
comp27536_c0_seq4.p1		
comp27536_c0_seq5.p1		
comp27537_c0_seq2.p1	sp|Q562C4|MET7B_RAT_Methyltransferase-like_protein_7B_OS=Rattus_norvegicus_GN=Mettl7b_PE=1_SV=1	1.00E-14
comp27537_c0_seq2.p2		
comp27537_c0_seq3.p1	sp|Q562C4|MET7B_RAT_Methyltransferase-like_protein_7B_OS=Rattus_norvegicus_GN=Mettl7b_PE=1_SV=1	1.00E-14
comp27537_c0_seq3.p2		
comp27538_c0_seq1.p1	sp|P0AFP0|YADS_ECOLI_UPF0126_inner_membrane_protein_yadS_OS=Escherichia_coli_(strain_K12)_GN=yadS_PE=1_SV=1	8.00E-19
comp27539_c0_seq1.p2		
comp27539_c0_seq1.p4		
comp27539_c0_seq3.p1		
comp27540_c0_seq1.p1		
comp27541_c0_seq1.p1	sp|Q94C49|ZDH18_ARATH_Probable_S-acyltransferase_At4g22750_OS=Arabidopsis_thaliana_GN=At4g22750_PE=2_SV=1	3.00E-15
comp27542_c0_seq1.p2		
comp27543_c0_seq1.p1		
comp27544_c0_seq2.p1		
comp27545_c0_seq1.p1	sp|Q92538|GBF1_HUMAN_Golgi-specific_brefeldin_A-resistance_guanine_nucleotide_exchange_factor_1_OS=Homo_sapiens_GN=GBF1_PE=1_SV=2	2.00E-53
comp27547_c0_seq1.p1		
comp27547_c0_seq2.p1		
comp27548_c0_seq1.p1	sp|Q9XF67|PDPK1_ARATH_3-phosphoinositide-dependent_protein_kinase_1_OS=Arabidopsis_thaliana_GN=PDK1_PE=1_SV=1	1.00E-49
comp27548_c0_seq2.p1	sp|Q9XF67|PDPK1_ARATH_3-phosphoinositide-dependent_protein_kinase_1_OS=Arabidopsis_thaliana_GN=PDK1_PE=1_SV=1	5.00E-52
comp27549_c0_seq1.p1	sp|Q9WTV7|RNF12_MOUSE_E3_ubiquitin-protein_ligase_RLIM_OS=Mus_musculus_GN=Rlim_PE=1_SV=2	3.00E-11
comp27549_c0_seq1.p4		
comp27550_c0_seq3.p1		
comp27550_c0_seq4.p1		
comp27552_c0_seq2.p1		
comp27553_c0_seq1.p1		
comp27555_c0_seq2.p1	sp|Q8BTW8|CK5P1_MOUSE_CDK5_regulatory_subunit-associated_protein_1_OS=Mus_musculus_GN=Cdk5rap1_PE=2_SV=2	7.00E-102
comp27557_c1_seq1.p1	sp|Q8C6G8|WDR26_MOUSE_WD_repeat-containing_protein_26_OS=Mus_musculus_GN=Wdr26_PE=1_SV=3	2.00E-35
comp27559_c0_seq4.p1		
comp27560_c0_seq3.p1	sp|Q9STG6|DUT_ARATH_Deoxyuridine_5'-triphosphate_nucleotidohydrolase_OS=Arabidopsis_thaliana_GN=DUT_PE=1_SV=1	3.00E-54
comp27560_c0_seq3.p2	sp|Q9USK1|YJ2B_SCHPO_Uncharacterized_bolA-like_protein_C4B3.11c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC4B3.11c_PE=2_SV=1	1.00E-15
comp27560_c0_seq5.p1		
comp27560_c0_seq5.p2	sp|Q9STG6|DUT_ARATH_Deoxyuridine_5'-triphosphate_nucleotidohydrolase_OS=Arabidopsis_thaliana_GN=DUT_PE=1_SV=1	2.00E-55
comp27561_c0_seq1.p1		
comp27562_c0_seq1.p2		
comp27562_c0_seq2.p1		
comp27563_c0_seq1.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	2.00E-22
comp27563_c0_seq2.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	2.00E-22
comp27564_c0_seq1.p1	sp|Q8TB61|S35B2_HUMAN_Adenosine_3'-phospho_5'-phosphosulfate_transporter_1_OS=Homo_sapiens_GN=SLC35B2_PE=1_SV=1	3.00E-74
comp27564_c0_seq1.p2	sp|Q5RDY2|TM9S4_PONAB_Transmembrane_9_superfamily_member_4_OS=Pongo_abelii_GN=TM9SF4_PE=2_SV=1	1.00E-42
comp27564_c1_seq2.p1	sp|Q55FP0|PHG1A_DICDI_Putative_phagocytic_receptor_1a_OS=Dictyostelium_discoideum_GN=phg1a_PE=2_SV=1	1.00E-86
comp27565_c0_seq1.p1	sp|Q9Y7X4|YGRG_SCHPO_Uncharacterized_membrane_protein_C365.16_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC365.16_PE=2_SV=1	1.00E-19
comp27565_c0_seq1.p5		
comp27566_c0_seq3.p1	sp|Q5L025|IOLA1_GEOKA_Methylmalonate_semialdehyde_dehydrogenase_[acylating]_1_OS=Geobacillus_kaustophilus_(strain_HTA426)_GN=iolA1_PE=3_SV=1	1.00E-101
comp27567_c0_seq2.p1	sp|Q8R3Q0|TMM66_MOUSE_Transmembrane_protein_66_OS=Mus_musculus_GN=Tmem66_PE=2_SV=2	3.00E-17
comp27567_c1_seq1.p1		
comp27568_c0_seq2.p1	sp|Q6VBB2|HFA2B_ORYSJ_Heat_stress_transcription_factor_A-2b_OS=Oryza_sativa_subsp._japonica_GN=HSFA2B_PE=2_SV=1	2.00E-22
comp27569_c0_seq1.p1		
comp27569_c0_seq2.p1	sp|C1DJG1|ARGA_AZOVD_Amino-acid_acetyltransferase_OS=Azotobacter_vinelandii_(strain_DJ_/_ATCC_BAA-1303)_GN=argA_PE=3_SV=1	1.00E-72
comp27570_c0_seq1.p2		
comp27575_c0_seq1.p1	sp|Q0P5L5|SUMF1_BOVIN_Sulfatase-modifying_factor_1_OS=Bos_taurus_GN=SUMF1_PE=2_SV=1	2.00E-60
comp27575_c0_seq2.p2	sp|Q8R0F3|SUMF1_MOUSE_Sulfatase-modifying_factor_1_OS=Mus_musculus_GN=Sumf1_PE=1_SV=2	1.00E-36
comp27576_c0_seq2.p1		
comp27578_c0_seq1.p1		
comp27580_c0_seq1.p1		
comp27582_c0_seq1.p2	sp|Q5RAZ9|RL36_PONAB_60S_ribosomal_protein_L36_OS=Pongo_abelii_GN=RPL36_PE=3_SV=3	8.00E-45
comp27583_c0_seq1.p1		
comp27583_c0_seq4.p1		
comp27583_c0_seq4.p2		
comp27583_c0_seq6.p1		
comp27584_c0_seq1.p1		
comp27585_c0_seq1.p1	sp|Q0WVW7|RQL5_ARATH_ATP-dependent_DNA_helicase_Q-like_5_OS=Arabidopsis_thaliana_GN=RECQL5_PE=2_SV=2	2.00E-72
comp27586_c0_seq1.p1		
comp27586_c0_seq3.p1		
comp27587_c0_seq2.p1		
comp27587_c0_seq3.p1	sp|Q9LRB7|EL5_ORYSJ_E3_ubiquitin-protein_ligase_EL5_OS=Oryza_sativa_subsp._japonica_GN=EL5.1_PE=1_SV=1	1.00E-14
comp27588_c0_seq1.p1	sp|Q55GS4|CDK10_DICDI_Probable_cyclin-dependent_kinase_10_OS=Dictyostelium_discoideum_GN=cdk10_PE=2_SV=1	3.00E-118
comp27589_c0_seq2.p1		
comp27589_c0_seq3.p1	sp|Q0TK29|RIHA_ECOL5_Pyrimidine-specific_ribonucleoside_hydrolase_RihA_OS=Escherichia_coli_O6:K15:H31_(strain_536_/_UPEC)_GN=rihA_PE=3_SV=1	1.00E-20
comp27589_c0_seq4.p2		
comp27589_c0_seq5.p1	sp|Q0TK29|RIHA_ECOL5_Pyrimidine-specific_ribonucleoside_hydrolase_RihA_OS=Escherichia_coli_O6:K15:H31_(strain_536_/_UPEC)_GN=rihA_PE=3_SV=1	2.00E-18
comp27591_c0_seq2.p2		
comp27593_c0_seq2.p1	sp|P15043|RECQ_ECOLI_ATP-dependent_DNA_helicase_recQ_OS=Escherichia_coli_(strain_K12)_GN=recQ_PE=1_SV=5	4.00E-62
comp27594_c0_seq2.p1		
comp27595_c0_seq1.p1	sp|Q54DA8|STIP1_DICDI_Protein_STIP1_homolog_OS=Dictyostelium_discoideum_GN=sti1_PE=3_SV=1	6.00E-14
comp27598_c0_seq1.p1	sp|Q9M2S6|SDIR1_ARATH_E3_ubiquitin-protein_ligase_SDIR1_OS=Arabidopsis_thaliana_GN=SDIR1_PE=1_SV=1	4.00E-17
comp27599_c0_seq1.p1	sp|Q5QQ53|XYLT_DROPS_Xylosyltransferase_oxt_OS=Drosophila_pseudoobscura_pseudoobscura_GN=oxt_PE=2_SV=1	6.00E-16
comp27599_c0_seq2.p1	sp|Q5QQ53|XYLT_DROPS_Xylosyltransferase_oxt_OS=Drosophila_pseudoobscura_pseudoobscura_GN=oxt_PE=2_SV=1	6.00E-16
comp27600_c0_seq2.p2		
comp27601_c0_seq3.p1	sp|P97346|NXN_MOUSE_Nucleoredoxin_OS=Mus_musculus_GN=Nxn_PE=1_SV=1	4.00E-73
comp27601_c0_seq3.p3		
comp27602_c0_seq1.p1		
comp27602_c0_seq2.p1		
comp27604_c1_seq3.p1		
comp27605_c0_seq1.p1		
comp27609_c0_seq2.p2	sp|Q8VBT1|TXLNB_MOUSE_Beta-taxilin_OS=Mus_musculus_GN=Txlnb_PE=2_SV=2	3.00E-11
comp27609_c0_seq8.p2		
comp27610_c0_seq1.p1		
comp27610_c0_seq2.p1		
comp27611_c0_seq1.p2		
comp27611_c0_seq2.p1	sp|Q8K274|KT3K_MOUSE_Ketosamine-3-kinase_OS=Mus_musculus_GN=Fn3krp_PE=2_SV=2	8.00E-50
comp27612_c0_seq1.p1		
comp27612_c0_seq1.p2	sp|Q9SR70|FK164_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP16-4,_chloroplastic_OS=Arabidopsis_thaliana_GN=FKBP16-4_PE=1_SV=1	3.00E-20
comp27612_c0_seq5.p1	sp|Q9SR70|FK164_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP16-4,_chloroplastic_OS=Arabidopsis_thaliana_GN=FKBP16-4_PE=1_SV=1	3.00E-20
comp27612_c0_seq6.p1		
comp27612_c0_seq6.p2	sp|Q9SR70|FK164_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP16-4,_chloroplastic_OS=Arabidopsis_thaliana_GN=FKBP16-4_PE=1_SV=1	3.00E-20
comp27613_c0_seq1.p1		
comp27613_c0_seq2.p1	sp|Q84NP7|AMPD_ORYSJ_Probable_AMP_deaminase_OS=Oryza_sativa_subsp._japonica_GN=AMPD_PE=2_SV=1	0
comp27616_c0_seq2.p1	sp|O09452|G3PA_GUITH_Glyceraldehyde-3-phosphate_dehydrogenase,_chloroplastic_OS=Guillardia_theta_GN=GAPC1_PE=2_SV=1	4.00E-157
comp27616_c0_seq3.p1	sp|O09452|G3PA_GUITH_Glyceraldehyde-3-phosphate_dehydrogenase,_chloroplastic_OS=Guillardia_theta_GN=GAPC1_PE=2_SV=1	1.00E-12
comp27617_c0_seq2.p1	sp|Q9CZT4|RPC5_MOUSE_DNA-directed_RNA_polymerase_III_subunit_RPC5_OS=Mus_musculus_GN=Polr3e_PE=1_SV=2	5.00E-16
comp27617_c0_seq3.p1	sp|Q9CZT4|RPC5_MOUSE_DNA-directed_RNA_polymerase_III_subunit_RPC5_OS=Mus_musculus_GN=Polr3e_PE=1_SV=2	8.00E-16
comp27618_c0_seq1.p1		
comp27618_c1_seq1.p1		
comp27619_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	2.00E-19
comp27621_c1_seq1.p1	sp|Q8NBN7|RDH13_HUMAN_Retinol_dehydrogenase_13_OS=Homo_sapiens_GN=RDH13_PE=1_SV=2	2.00E-16
comp27621_c2_seq1.p1	sp|Q9ERI6|RDH14_MOUSE_Retinol_dehydrogenase_14_OS=Mus_musculus_GN=Rdh14_PE=1_SV=1	5.00E-16
comp27622_c0_seq1.p1	sp|Q8AVP1|RPF1_XENLA_Ribosome_production_factor_1_OS=Xenopus_laevis_GN=rpf1_PE=2_SV=1	4.00E-19
comp27622_c0_seq2.p1	sp|Q0DYP5|C3H17_ORYSJ_Zinc_finger_CCCH_domain-containing_protein_17_OS=Oryza_sativa_subsp._japonica_GN=Os02g0677700_PE=2_SV=2	6.00E-17
comp27622_c0_seq2.p2	sp|Q8AVP1|RPF1_XENLA_Ribosome_production_factor_1_OS=Xenopus_laevis_GN=rpf1_PE=2_SV=1	1.00E-102
comp27624_c0_seq1.p1		
comp27624_c0_seq1.p3	sp|Q8KFI4|PHS_CHLTE_Putative_pterin-4-alpha-carbinolamine_dehydratase_OS=Chlorobium_tepidum_(strain_ATCC_49652_/_DSM_12025_/_TLS)_GN=CT0342_PE=3_SV=1	1.00E-18
comp27625_c0_seq2.p1	sp|A5UY94|PDXS_ROSS1_Pyridoxal_biosynthesis_lyase_pdxS_OS=Roseiflexus_sp._(strain_RS-1)_GN=pdxS_PE=3_SV=1	7.00E-137
comp27625_c0_seq3.p1	sp|Q8L940|PDX13_ARATH_Pyridoxal_biosynthesis_protein_PDX1.3_OS=Arabidopsis_thaliana_GN=PDX13_PE=1_SV=2	7.00E-34
comp27625_c0_seq4.p1	sp|A5UY94|PDXS_ROSS1_Pyridoxal_biosynthesis_lyase_pdxS_OS=Roseiflexus_sp._(strain_RS-1)_GN=pdxS_PE=3_SV=1	1.00E-110
comp27625_c0_seq5.p1	sp|A5UY94|PDXS_ROSS1_Pyridoxal_biosynthesis_lyase_pdxS_OS=Roseiflexus_sp._(strain_RS-1)_GN=pdxS_PE=3_SV=1	7.00E-137
comp27626_c0_seq1.p2	sp|P45335|Y1706_HAEIN_Uncharacterized_transporter_HI_1706_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=HI_1706_PE=3_SV=1	1.00E-29
comp27627_c0_seq1.p1		
comp27630_c0_seq1.p1		
comp27631_c0_seq1.p1	sp|Q9DC53|CPNE8_MOUSE_Copine-8_OS=Mus_musculus_GN=Cpne8_PE=2_SV=2	2.00E-93
comp27631_c0_seq1.p2	sp|P59108|CPNE2_MOUSE_Copine-2_OS=Mus_musculus_GN=Cpne2_PE=2_SV=1	4.00E-21
comp27632_c0_seq1.p1		
comp27633_c0_seq1.p1		
comp27634_c0_seq1.p1	sp|P38811|TRA1_YEAST_Transcription-associated_protein_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TRA1_PE=1_SV=1	3.00E-37
comp27634_c0_seq1.p2		
comp27635_c0_seq1.p1		
comp27636_c0_seq1.p1	sp|Q3AF51|OBG_CARHZ_GTPase_obg_OS=Carboxydothermus_hydrogenoformans_(strain_Z-2901_/_DSM_6008)_GN=obg_PE=3_SV=1	2.00E-99
comp27636_c0_seq2.p1	sp|Q3AF51|OBG_CARHZ_GTPase_obg_OS=Carboxydothermus_hydrogenoformans_(strain_Z-2901_/_DSM_6008)_GN=obg_PE=3_SV=1	8.00E-79
comp27637_c0_seq1.p1	sp|Q9FIT7|PP442_ARATH_Pentatricopeptide_repeat-containing_protein_At5g61990,_mitochondrial_OS=Arabidopsis_thaliana_GN=At5g61990_PE=2_SV=1	3.00E-31
comp27640_c0_seq1.p1		
comp27640_c0_seq2.p1		
comp27641_c0_seq1.p1		
comp27641_c0_seq1.p2		
comp27641_c0_seq1.p3		
comp27641_c0_seq2.p1		
comp27641_c0_seq2.p2		
comp27641_c0_seq3.p1		
comp27642_c0_seq2.p1	sp|Q2JM21|UVRC_SYNJB_UvrABC_system_protein_C_OS=Synechococcus_sp._(strain_JA-2-3B'a(2-13))_GN=uvrC_PE=3_SV=1	9.00E-62
comp27644_c0_seq1.p1	sp|Q5REA7|FADS2_PONAB_Fatty_acid_desaturase_2_OS=Pongo_abelii_GN=FADS2_PE=2_SV=1	3.00E-51
comp27646_c0_seq1.p2		
comp27648_c0_seq1.p1		
comp27648_c0_seq2.p1		
comp27648_c1_seq1.p1		
comp27651_c0_seq1.p1		
comp27652_c0_seq1.p1		
comp27653_c0_seq2.p1		
comp27654_c0_seq1.p1	sp|Q9SZ67|WRK19_ARATH_Probable_WRKY_transcription_factor_19_OS=Arabidopsis_thaliana_GN=WRKY19_PE=2_SV=1	2.00E-13
comp27654_c0_seq1.p2		
comp27658_c0_seq1.p1	sp|Q13889|TF2H3_HUMAN_General_transcription_factor_IIH_subunit_3_OS=Homo_sapiens_GN=GTF2H3_PE=1_SV=2	1.00E-51
comp27659_c0_seq1.p2	sp|Q52629|BGAL_PYRWO_Beta-galactosidase_OS=Pyrococcus_woesei_PE=1_SV=1	1.00E-21
comp27659_c0_seq2.p1	sp|Q08638|BGLA_THEMA_Beta-glucosidase_A_OS=Thermotoga_maritima_GN=bglA_PE=1_SV=1	5.00E-69
comp27660_c0_seq2.p1	sp|Q5ZKN3|PHTF2_CHICK_Putative_homeodomain_transcription_factor_2_OS=Gallus_gallus_GN=PHTF2_PE=2_SV=1	1.00E-51
comp27661_c0_seq1.p1	sp|Q55BK0|UFD1_DICDI_Ubiquitin_fusion_degradation_protein_1_homolog_OS=Dictyostelium_discoideum_GN=ufd1_PE=3_SV=1	4.00E-65
comp27663_c0_seq1.p1		
comp27663_c0_seq2.p1		
comp27665_c0_seq1.p1		
comp27669_c0_seq2.p1	sp|Q8L6Z7|EXO1_ARATH_Exonuclease_1_OS=Arabidopsis_thaliana_GN=EXO1_PE=2_SV=2	1.00E-83
comp27669_c0_seq2.p3		
comp27670_c0_seq1.p1	sp|Q54QG0|PGFB_DICDI_Bifunctional_glycosyltransferase_pgtA_OS=Dictyostelium_discoideum_GN=pgtA_PE=1_SV=1	1.00E-14
comp27671_c0_seq2.p1	sp|Q09225|NRF6_CAEEL_Nose_resistant_to_fluoxetine_protein_6_OS=Caenorhabditis_elegans_GN=nrf-6_PE=1_SV=3	6.00E-34
comp27671_c0_seq4.p1	sp|Q09225|NRF6_CAEEL_Nose_resistant_to_fluoxetine_protein_6_OS=Caenorhabditis_elegans_GN=nrf-6_PE=1_SV=3	6.00E-34
comp27673_c0_seq1.p1		
comp27673_c0_seq3.p1		
comp27676_c0_seq2.p1		
comp27677_c0_seq1.p1		
comp27677_c0_seq2.p1		
comp27679_c0_seq2.p1	sp|Q5ZK63|TCP4_CHICK_Activated_RNA_polymerase_II_transcriptional_coactivator_p15_OS=Gallus_gallus_GN=SUB1_PE=2_SV=1	5.00E-12
comp2768_c0_seq1.p2	sp|P23877|FEPG_ECOLI_Ferric_enterobactin_transport_system_permease_protein_fepG_OS=Escherichia_coli_(strain_K12)_GN=fepG_PE=1_SV=2	5.00E-39
comp27680_c0_seq2.p1		
comp27682_c0_seq3.p1	sp|Q55BN8|NEK2_DICDI_Probable_serine/threonine-protein_kinase_nek2_OS=Dictyostelium_discoideum_GN=nek2_PE=1_SV=1	3.00E-78
comp27683_c0_seq1.p1		
comp27683_c1_seq1.p1	sp|Q6PID8|KLD10_HUMAN_Kelch_domain-containing_protein_10_OS=Homo_sapiens_GN=KLHDC10_PE=2_SV=1	7.00E-16
comp27684_c0_seq2.p1	sp|Q9M1I1|FB304_ARATH_F-box_protein_At3g54460_OS=Arabidopsis_thaliana_GN=At3g54460_PE=2_SV=1	1.00E-35
comp27685_c0_seq1.p1	sp|Q54TH9|GACY_DICDI_Rho_GTPase-activating_protein_gacY_OS=Dictyostelium_discoideum_GN=gacY_PE=3_SV=1	3.00E-24
comp27685_c0_seq1.p2		
comp27688_c0_seq2.p1		
comp27689_c0_seq1.p1		
comp27690_c0_seq1.p1		
comp27690_c0_seq1.p2		
comp27691_c0_seq4.p1		
comp27693_c0_seq1.p1	sp|P54567|YQKD_BACSU_Uncharacterized_protein_yqkD_OS=Bacillus_subtilis_GN=yqkD_PE=4_SV=1	2.00E-16
comp27693_c0_seq2.p1	sp|P54567|YQKD_BACSU_Uncharacterized_protein_yqkD_OS=Bacillus_subtilis_GN=yqkD_PE=4_SV=1	2.00E-16
comp27694_c0_seq2.p1		
comp27695_c0_seq1.p1	sp|Q6ZFT5|KPRS4_ORYSJ_Ribose-phosphate_pyrophosphokinase_4_OS=Oryza_sativa_subsp._japonica_GN=Os02g0714600_PE=2_SV=1	1.00E-66
comp27695_c0_seq2.p1	sp|Q6ZFT5|KPRS4_ORYSJ_Ribose-phosphate_pyrophosphokinase_4_OS=Oryza_sativa_subsp._japonica_GN=Os02g0714600_PE=2_SV=1	3.00E-67
comp27696_c0_seq1.p2	sp|P27592|EF1A_ONCVO_Elongation_factor_1-alpha_OS=Onchocerca_volvulus_PE=2_SV=1	5.00E-98
comp27696_c0_seq2.p1	sp|P02993|EF1A_ARTSA_Elongation_factor_1-alpha_OS=Artemia_salina_PE=1_SV=2	0
comp27697_c0_seq2.p1		
comp27698_c0_seq1.p2	sp|Q54JC0|CMBB_DICDI_Calmodulin-binding_protein_CmbB_OS=Dictyostelium_discoideum_GN=cmbB_PE=1_SV=1	2.00E-18
comp27699_c0_seq1.p1	sp|B1H3H9|PTSS1_XENTR_Phosphatidylserine_synthase_1_OS=Xenopus_tropicalis_GN=ptdss1_PE=2_SV=1	1.00E-48
comp27699_c0_seq2.p1		
comp27699_c0_seq4.p1	sp|B1H3H9|PTSS1_XENTR_Phosphatidylserine_synthase_1_OS=Xenopus_tropicalis_GN=ptdss1_PE=2_SV=1	1.00E-48
comp27699_c0_seq5.p1		
comp27699_c0_seq7.p1		
comp27701_c0_seq1.p2	sp|Q9LNF4|P2C13_ARATH_Probable_protein_phosphatase_2C_13_OS=Arabidopsis_thaliana_GN=At1g48040_PE=2_SV=2	4.00E-38
comp27701_c0_seq2.p1	sp|Q9LNF4|P2C13_ARATH_Probable_protein_phosphatase_2C_13_OS=Arabidopsis_thaliana_GN=At1g48040_PE=2_SV=2	1.00E-36
comp27702_c0_seq1.p1	sp|Q95LL3|TB22B_MACFA_TBC1_domain_family_member_22B_OS=Macaca_fascicularis_GN=TBC1D22B_PE=2_SV=1	7.00E-102
comp27705_c0_seq1.p1		
comp27706_c0_seq3.p1		
comp27707_c0_seq1.p1		
comp27708_c0_seq3.p2		
comp27709_c0_seq2.p1		
comp27710_c0_seq1.p1		
comp27711_c0_seq1.p1	sp|P28178|PK2_DICDI_Protein_kinase_2_OS=Dictyostelium_discoideum_GN=pkgB_PE=1_SV=1	3.00E-101
comp27711_c1_seq1.p1		
comp27712_c0_seq1.p1		
comp27712_c0_seq1.p2	sp|P51612|XPC_MOUSE_DNA_repair_protein_complementing_XP-C_cells_homolog_OS=Mus_musculus_GN=Xpc_PE=1_SV=2	8.00E-35
comp27712_c0_seq4.p1	sp|Q01831|XPC_HUMAN_DNA_repair_protein_complementing_XP-C_cells_OS=Homo_sapiens_GN=XPC_PE=1_SV=4	1.00E-38
comp27713_c0_seq1.p1		
comp27713_c0_seq1.p2	sp|P27133|COROA_DICDI_Coronin-A_OS=Dictyostelium_discoideum_GN=corA_PE=1_SV=2	4.00E-118
comp27714_c0_seq1.p1	sp|Q4V8C2|ZW10_RAT_Centromere/kinetochore_protein_zw10_homolog_OS=Rattus_norvegicus_GN=Zw10_PE=2_SV=3	1.00E-26
comp27717_c0_seq2.p1	sp|Q9M350|GCP4_ARATH_Gamma-tubulin_complex_component_4_homolog_OS=Arabidopsis_thaliana_GN=At3g53760_PE=2_SV=2	5.00E-37
comp27718_c0_seq1.p1		
comp27720_c0_seq2.p1		
comp27721_c0_seq2.p1		
comp27721_c0_seq3.p1		
comp27722_c0_seq2.p1	sp|Q9HU55|GLRX_PSEAE_Glutaredoxin_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=grx_PE=3_SV=1	8.00E-13
comp27723_c0_seq1.p1		
comp27724_c0_seq2.p1	sp|O06476|YFMR_BACSU_Uncharacterized_ABC_transporter_ATP-binding_protein_YfmR_OS=Bacillus_subtilis_GN=yfmR_PE=3_SV=1	9.00E-133
comp27725_c0_seq1.p1	sp|Q8C9X6|EPC1_MOUSE_Enhancer_of_polycomb_homolog_1_OS=Mus_musculus_GN=Epc1_PE=2_SV=1	6.00E-15
comp27725_c0_seq1.p2		
comp27725_c0_seq1.p4		
comp27726_c0_seq1.p1		
comp27729_c0_seq1.p1	sp|O43102|CBF5_ASPFU_Centromere/microtubule-binding_protein_cbf5_OS=Neosartorya_fumigata_(strain_ATCC_MYA-4609_/_Af293_/_CBS_101355_/_FGSC_A1100)_GN=cbf5_PE=2_SV=1	0
comp27731_c0_seq1.p1	sp|Q55DE2|SDA1_DICDI_Protein_SDA1_homolog_OS=Dictyostelium_discoideum_GN=sdad1_PE=3_SV=1	4.00E-51
comp27731_c0_seq2.p1	sp|Q80UZ2|SDA1_MOUSE_Protein_SDA1_homolog_OS=Mus_musculus_GN=Sdad1_PE=1_SV=1	7.00E-16
comp27731_c0_seq4.p1	sp|Q55DE2|SDA1_DICDI_Protein_SDA1_homolog_OS=Dictyostelium_discoideum_GN=sdad1_PE=3_SV=1	3.00E-59
comp27735_c0_seq1.p2		
comp27736_c0_seq1.p1	sp|A9UMG5|IMPTB_XENTR_Protein_IMPACT-B_OS=Xenopus_tropicalis_GN=impact-B_PE=2_SV=1	2.00E-42
comp27736_c0_seq2.p1		
comp27737_c0_seq2.p2		
comp27738_c0_seq5.p1		
comp27740_c0_seq1.p1		
comp27740_c0_seq4.p1		
comp27741_c0_seq1.p1		
comp27742_c0_seq1.p1		
comp27745_c0_seq3.p1		
comp27745_c0_seq4.p2		
comp27746_c0_seq2.p1	sp|Q767L0|ABCF1_PIG_ATP-binding_cassette_sub-family_F_member_1_OS=Sus_scrofa_GN=ABCF1_PE=3_SV=1	3.00E-125
comp27746_c0_seq3.p1	sp|Q8NE71|ABCF1_HUMAN_ATP-binding_cassette_sub-family_F_member_1_OS=Homo_sapiens_GN=ABCF1_PE=1_SV=2	8.00E-144
comp27747_c0_seq1.p1		
comp27749_c0_seq1.p1	sp|O48963|PHOT1_ARATH_Phototropin-1_OS=Arabidopsis_thaliana_GN=PHOT1_PE=1_SV=1	4.00E-29
comp27749_c0_seq2.p1	sp|Q9ST27|PHOT2_ORYSJ_Phototropin-2_OS=Oryza_sativa_subsp._japonica_GN=PHOT2_PE=1_SV=1	2.00E-29
comp27749_c0_seq4.p1	sp|Q9ST27|PHOT2_ORYSJ_Phototropin-2_OS=Oryza_sativa_subsp._japonica_GN=PHOT2_PE=1_SV=1	4.00E-18
comp27751_c1_seq1.p1		
comp27753_c0_seq1.p2		
comp27753_c0_seq1.p3		
comp27753_c0_seq1.p4		
comp27754_c0_seq2.p1	sp|Q68EX9|CHID1_XENLA_Chitinase_domain-containing_protein_1_OS=Xenopus_laevis_GN=chid1_PE=2_SV=1	2.00E-56
comp27755_c0_seq2.p1		
comp27755_c0_seq4.p1		
comp27756_c0_seq1.p1		
comp27756_c0_seq3.p1		
comp27756_c0_seq5.p1		
comp27758_c0_seq1.p1		
comp27760_c0_seq2.p1		
comp27760_c0_seq2.p2		
comp27760_c0_seq5.p1		
comp27760_c0_seq5.p2		
comp27765_c0_seq1.p1		
comp27765_c1_seq1.p1	sp|Q7T2E3|KC1DA_DANRE_Casein_kinase_I_isoform_delta-A_OS=Danio_rerio_GN=csnk1da_PE=2_SV=1	1.00E-114
comp27767_c0_seq2.p1		
comp27767_c0_seq3.p1		
comp27770_c0_seq2.p1		
comp27772_c0_seq2.p1		
comp27773_c0_seq1.p1		
comp27778_c0_seq3.p1	sp|Q7UJ69|ILVD_RHOBA_Dihydroxy-acid_dehydratase_OS=Rhodopirellula_baltica_(strain_SH1)_GN=ilvD_PE=3_SV=2	0
comp27781_c0_seq1.p1		
comp27782_c1_seq2.p2	sp|Q9ESG8|ZDH16_MOUSE_Probable_palmitoyltransferase_ZDHHC16_OS=Mus_musculus_GN=Zdhhc16_PE=1_SV=2	3.00E-23
comp27785_c0_seq1.p1		
comp27785_c0_seq2.p1		
comp27786_c0_seq3.p1		
comp27788_c0_seq2.p1	sp|Q5N643|SYR_SYNP6_Arginine--tRNA_ligase_OS=Synechococcus_sp._(strain_ATCC_27144_/_PCC_6301_/_SAUG_1402/1)_GN=argS_PE=3_SV=1	0
comp27789_c0_seq1.p1		
comp27791_c0_seq1.p1	sp|Q8KJ24|CH60_CLOBO_60_kDa_chaperonin_OS=Clostridium_botulinum_GN=groL_PE=3_SV=1	6.00E-169
comp27792_c0_seq1.p3	sp|P42825|DNAJ2_ARATH_Chaperone_protein_dnaJ_2_OS=Arabidopsis_thaliana_GN=ATJ2_PE=1_SV=2	2.00E-41
comp27793_c0_seq1.p1		
comp27795_c0_seq4.p1	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	3.00E-15
comp27798_c0_seq2.p1	sp|Q05609|CTR1_ARATH_Serine/threonine-protein_kinase_CTR1_OS=Arabidopsis_thaliana_GN=CTR1_PE=1_SV=1	1.00E-43
comp27799_c0_seq1.p1		
comp27800_c0_seq3.p1	sp|Q8BH16|FBXL2_MOUSE_F-box/LRR-repeat_protein_2_OS=Mus_musculus_GN=Fbxl2_PE=2_SV=1	1.00E-33
comp27801_c0_seq2.p1		
comp27802_c0_seq1.p1	sp|Q39069|CCB13_ARATH_Cyclin-B1-3_OS=Arabidopsis_thaliana_GN=CYCB1-3_PE=2_SV=2	9.00E-60
comp27802_c0_seq2.p1	sp|Q39069|CCB13_ARATH_Cyclin-B1-3_OS=Arabidopsis_thaliana_GN=CYCB1-3_PE=2_SV=2	2.00E-59
comp27803_c0_seq1.p1	sp|Q08BM0|RG9D3_DANRE_RNA_(guanine-9-)-methyltransferase_domain-containing_protein_3_OS=Danio_rerio_GN=rg9mtd3_PE=2_SV=1	4.00E-17
comp27803_c0_seq2.p1	sp|Q08BM0|RG9D3_DANRE_RNA_(guanine-9-)-methyltransferase_domain-containing_protein_3_OS=Danio_rerio_GN=rg9mtd3_PE=2_SV=1	4.00E-16
comp27804_c0_seq1.p1		
comp27804_c0_seq1.p2		
comp27804_c0_seq2.p1		
comp27805_c0_seq4.p1		
comp27805_c0_seq4.p3		
comp27806_c0_seq1.p1	sp|Q5UP39|YR873_MIMIV_Putative_ankyrin_repeat_protein_R873_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R873_PE=4_SV=1	7.00E-18

comp27809_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	3.00E-14
comp27812_c0_seq1.p1	sp|Q6NLC1|AB2D_ARATH_ABC_transporter_D_family_member_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=ABCC2_PE=1_SV=1	1.00E-136
comp27817_c0_seq2.p1	sp|Q2HJI8|RAB8B_BOVIN_Ras-related_protein_Rab-8B_OS=Bos_taurus_GN=RAB8B_PE=2_SV=1	9.00E-75
comp27818_c0_seq1.p1		
comp27818_c0_seq1.p3		
comp27819_c0_seq1.p1	sp|Q9FZ36|M3K2_ARATH_Mitogen-activated_protein_kinase_kinase_kinase_2_OS=Arabidopsis_thaliana_GN=ANP2_PE=2_SV=1	2.00E-18
comp27819_c0_seq4.p1		
comp27821_c0_seq1.p1		
comp27821_c0_seq1.p2		
comp27821_c0_seq1.p4		
comp27822_c0_seq1.p1		
comp27824_c0_seq1.p1	sp|Q9WUB4|DCTN6_MOUSE_Dynactin_subunit_6_OS=Mus_musculus_GN=Dctn6_PE=1_SV=1	3.00E-21
comp27824_c0_seq2.p1	sp|Q148G7|DCTN6_BOVIN_Dynactin_subunit_6_OS=Bos_taurus_GN=DCTN6_PE=2_SV=1	4.00E-16
comp27826_c0_seq1.p1	sp|Q8T126|FNKC_DICDI_Probable_inactive_serine/threonine-protein_kinase_fnkC_OS=Dictyostelium_discoideum_GN=fnkC_PE=3_SV=1	2.00E-11
comp27827_c0_seq1.p1		
comp27827_c0_seq2.p1		
comp27828_c0_seq1.p1	sp|Q5RE33|REEP5_PONAB_Receptor_expression-enhancing_protein_5_OS=Pongo_abelii_GN=REEP5_PE=2_SV=1	2.00E-33
comp27828_c0_seq2.p1	sp|Q5RE33|REEP5_PONAB_Receptor_expression-enhancing_protein_5_OS=Pongo_abelii_GN=REEP5_PE=2_SV=1	2.00E-33
comp27830_c0_seq1.p1		
comp27830_c1_seq2.p1		
comp27830_c1_seq3.p1		
comp27830_c1_seq4.p1		
comp27831_c0_seq1.p1	sp|Q95TN1|U533_DROME_UPF0533_protein_CG4953_OS=Drosophila_melanogaster_GN=CG4953_PE=2_SV=1	2.00E-16
comp27832_c1_seq1.p1		
comp27833_c0_seq2.p1		
comp27835_c0_seq2.p1	sp|Q58097|AAT2_METJA_Probable_aspartate_aminotransferase_2_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ0684_PE=1_SV=2	1.00E-53
comp27836_c0_seq1.p1		
comp27838_c0_seq1.p2	sp|Q9LK16|AMT15_ARATH_Putative_ammonium_transporter_1_member_5_OS=Arabidopsis_thaliana_GN=AMT1-5_PE=3_SV=1	4.00E-95
comp27838_c1_seq2.p1		
comp27840_c0_seq1.p1	sp|Q9X248|FABG_THEMA_3-oxoacyl-[acyl-carrier-protein]_reductase_FabG_OS=Thermotoga_maritima_GN=fabG_PE=3_SV=1	1.00E-38
comp27841_c0_seq1.p1		
comp27842_c0_seq2.p1		
comp27842_c0_seq3.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	4.00E-16
comp27842_c0_seq6.p1		
comp27843_c0_seq2.p1	sp|Q7QG28|TWF_ANOGA_Twinfilin_OS=Anopheles_gambiae_GN=twf_PE=3_SV=2	3.00E-19
comp27844_c0_seq2.p1		
comp27845_c0_seq1.p1		
comp27845_c0_seq2.p1	sp|A0PJE2|DHR12_HUMAN_Dehydrogenase/reductase_SDR_family_member_12_OS=Homo_sapiens_GN=DHRS12_PE=2_SV=2	2.00E-33
comp27847_c0_seq3.p1	sp|Q8JFW1|ASND1_DANRE_Asparagine_synthetase_domain-containing_protein_1_OS=Danio_rerio_GN=asnsd1_PE=2_SV=1	5.00E-23
comp27849_c0_seq3.p1	sp|Q8NEE6|FXL13_HUMAN_F-box/LRR-repeat_protein_13_OS=Homo_sapiens_GN=FBXL13_PE=2_SV=3	1.00E-12
comp27849_c0_seq4.p1		
comp27850_c0_seq1.p1		
comp27850_c0_seq4.p1		
comp27850_c0_seq4.p5		
comp27851_c0_seq2.p1		
comp27851_c0_seq4.p1		
comp27853_c0_seq1.p1		
comp27854_c0_seq1.p1	sp|P66006|STHA_MYCTU_Probable_soluble_pyridine_nucleotide_transhydrogenase_OS=Mycobacterium_tuberculosis_GN=sthA_PE=3_SV=1	9.00E-123
comp27855_c0_seq1.p1		
comp27860_c0_seq2.p1		
comp27865_c0_seq2.p1	sp|O81916|YC22_ARATH_Uncharacterized_calcium-binding_protein_At1g02270_OS=Arabidopsis_thaliana_GN=At1g02270_PE=2_SV=2	2.00E-56
comp27867_c0_seq1.p1	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	7.00E-14
comp27868_c0_seq2.p1	sp|Q80ZX8|SPAG1_MOUSE_Sperm-associated_antigen_1_OS=Mus_musculus_GN=Spag1_PE=1_SV=1	2.00E-33
comp27868_c0_seq2.p2		
comp27868_c0_seq3.p1	sp|Q80ZX8|SPAG1_MOUSE_Sperm-associated_antigen_1_OS=Mus_musculus_GN=Spag1_PE=1_SV=1	2.00E-33
comp27868_c0_seq3.p2		
comp27869_c0_seq1.p1		
comp27870_c0_seq1.p1		
comp27870_c0_seq1.p5		
comp27870_c0_seq3.p1		
comp27870_c0_seq3.p5		
comp27871_c0_seq3.p1		
comp27872_c0_seq2.p2		
comp27872_c0_seq3.p2		
comp27875_c0_seq1.p1	sp|Q10MX1|P2C32_ORYSJ_Probable_protein_phosphatase_2C_32_OS=Oryza_sativa_subsp._japonica_GN=Os03g0292100_PE=2_SV=1	3.00E-11
comp27878_c0_seq2.p1	sp|Q91ZN1|COR1A_RAT_Coronin-1A_OS=Rattus_norvegicus_GN=Coro1a_PE=1_SV=3	5.00E-54
comp27878_c0_seq3.p1		
comp27879_c0_seq1.p1		
comp27881_c0_seq1.p1		
comp27882_c0_seq1.p1	sp|O02414|DYL1_ANTCR_Dynein_light_chain_LC6,_flagellar_outer_arm_OS=Anthocidaris_crassispina_PE=3_SV=1	4.00E-19
comp27882_c0_seq4.p1	sp|O02414|DYL1_ANTCR_Dynein_light_chain_LC6,_flagellar_outer_arm_OS=Anthocidaris_crassispina_PE=3_SV=1	4.00E-19
comp27884_c0_seq1.p1		
comp27888_c0_seq2.p2		
comp27890_c0_seq2.p1		
comp27891_c0_seq1.p1		
comp27893_c0_seq1.p1	sp|Q54CV5|BUB1_DICDI_Probable_inactive_serine/threonine-protein_kinase_bub1_OS=Dictyostelium_discoideum_GN=bub1_PE=3_SV=1	6.00E-23
comp27893_c1_seq1.p1	sp|Q9D6J3|CCD94_MOUSE_Coiled-coil_domain-containing_protein_94_OS=Mus_musculus_GN=Ccdc94_PE=1_SV=1	2.00E-53
comp27895_c0_seq3.p2		
comp27895_c0_seq5.p1		
comp27897_c1_seq1.p2		
comp27900_c0_seq1.p1		
comp27901_c0_seq4.p1		
comp27901_c0_seq4.p2		
comp27903_c0_seq1.p1		
comp27903_c0_seq1.p9		
comp27904_c0_seq1.p1		
comp27904_c0_seq3.p1	sp|Q9DBH0|WWP2_MOUSE_NEDD4-like_E3_ubiquitin-protein_ligase_WWP2_OS=Mus_musculus_GN=Wwp2_PE=1_SV=1	3.00E-21
comp27907_c0_seq2.p1	sp|P16929|ACSA_NEUCR_Acetyl-coenzyme_A_synthetase_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=acu-5_PE=2_SV=2	0
comp27908_c0_seq2.p1		
comp27909_c0_seq1.p1		
comp27912_c0_seq1.p2		
comp27912_c0_seq4.p1		
comp27912_c0_seq4.p2		
comp27914_c0_seq3.p1	sp|P73456|FTSZ_SYNY3_Cell_division_protein_FtsZ_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=ftsZ_PE=1_SV=1	2.00E-81
comp27914_c0_seq4.p1	sp|P45482|FTSZ_NOSS1_Cell_division_protein_FtsZ_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=ftsZ_PE=3_SV=2	4.00E-80
comp27915_c0_seq2.p1		
comp27915_c1_seq1.p1		
comp27915_c1_seq2.p1		
comp27916_c0_seq1.p1		
comp27918_c0_seq2.p1		
comp27918_c0_seq5.p1		
comp27920_c0_seq2.p1	sp|Q5F361|TBCK_CHICK_TBC_domain-containing_protein_kinase-like_protein_OS=Gallus_gallus_GN=TBCK_PE=2_SV=2	8.00E-11
comp27921_c0_seq2.p1		
comp27921_c0_seq3.p1		
comp27922_c0_seq1.p1		
comp27922_c0_seq2.p1		
comp27922_c0_seq3.p1	sp|Q9JHI2|ADAT1_MOUSE_tRNA-specific_adenosine_deaminase_1_OS=Mus_musculus_GN=Adat1_PE=2_SV=1	8.00E-16
comp27927_c0_seq1.p1	sp|Q8BXZ1|TMX3_MOUSE_Protein_disulfide-isomerase_TMX3_OS=Mus_musculus_GN=Tmx3_PE=1_SV=2	7.00E-11
comp27927_c0_seq4.p1	sp|Q54VN2|COQ5_DICDI_2-methoxy-6-polyprenyl-1,4-benzoquinol_methylase,_mitochondrial_OS=Dictyostelium_discoideum_GN=coq5_PE=3_SV=1	2.00E-84
comp27928_c0_seq1.p1		
comp27928_c0_seq2.p1		
comp27930_c0_seq2.p1	sp|Q7Z406|MYH14_HUMAN_Myosin-14_OS=Homo_sapiens_GN=MYH14_PE=1_SV=2	2.00E-12
comp27930_c0_seq5.p1		
comp27930_c0_seq5.p2		
comp27930_c0_seq6.p1		
comp27932_c0_seq1.p1		
comp27934_c0_seq2.p1		
comp27934_c0_seq2.p2		
comp27934_c0_seq3.p1		
comp27934_c0_seq3.p2		
comp27937_c0_seq1.p1		
comp27937_c0_seq2.p1	sp|Q8N371|KDM8_HUMAN_Lysine-specific_demethylase_8_OS=Homo_sapiens_GN=JMJD5_PE=1_SV=1	1.00E-61
comp27937_c0_seq2.p2	sp|P66264|RL34_XYLFT_50S_ribosomal_protein_L34_OS=Xylella_fastidiosa_(strain_Temecula1_/_ATCC_700964)_GN=rpmH_PE=3_SV=1	2.00E-11
comp27937_c0_seq3.p1	sp|Q8N371|KDM8_HUMAN_Lysine-specific_demethylase_8_OS=Homo_sapiens_GN=JMJD5_PE=1_SV=1	2.00E-55
comp27937_c0_seq3.p3	sp|P66264|RL34_XYLFT_50S_ribosomal_protein_L34_OS=Xylella_fastidiosa_(strain_Temecula1_/_ATCC_700964)_GN=rpmH_PE=3_SV=1	2.00E-11
comp27937_c0_seq4.p1	sp|A8E534|KDM8_DANRE_Lysine-specific_demethylase_8_OS=Danio_rerio_GN=jmjd5_PE=2_SV=1	3.00E-45
comp27937_c0_seq4.p2	sp|P66264|RL34_XYLFT_50S_ribosomal_protein_L34_OS=Xylella_fastidiosa_(strain_Temecula1_/_ATCC_700964)_GN=rpmH_PE=3_SV=1	2.00E-11
comp27939_c0_seq2.p1	sp|O24412|PSD7_ARATH_Probable_26S_proteasome_non-ATPase_regulatory_subunit_7_OS=Arabidopsis_thaliana_GN=RPN8_PE=2_SV=1	2.00E-107
comp27942_c0_seq2.p1	sp|P35066|H2A_TRYCR_Histone_H2A_OS=Trypanosoma_cruzi_PE=3_SV=2	7.00E-28
comp27943_c0_seq1.p1	sp|P85107|TGS1_RAT_Trimethylguanosine_synthase_OS=Rattus_norvegicus_GN=Tgs1_PE=1_SV=1	3.00E-63
comp27948_c0_seq5.p1		
comp27949_c0_seq1.p1		
comp27950_c0_seq1.p1		
comp27952_c1_seq5.p1		
comp27954_c0_seq1.p1	sp|P54464|YQEY_BACSU_Uncharacterized_protein_yqeY_OS=Bacillus_subtilis_GN=yqeY_PE=1_SV=1	3.00E-21
comp27954_c0_seq2.p1	sp|P54464|YQEY_BACSU_Uncharacterized_protein_yqeY_OS=Bacillus_subtilis_GN=yqeY_PE=1_SV=1	3.00E-14
comp27954_c0_seq3.p1	sp|P54464|YQEY_BACSU_Uncharacterized_protein_yqeY_OS=Bacillus_subtilis_GN=yqeY_PE=1_SV=1	3.00E-14
comp27955_c0_seq1.p1	sp|P19468|GSH1_RAT_Glutamate--cysteine_ligase_catalytic_subunit_OS=Rattus_norvegicus_GN=Gclc_PE=1_SV=2	2.00E-133
comp27955_c0_seq2.p1	sp|P19468|GSH1_RAT_Glutamate--cysteine_ligase_catalytic_subunit_OS=Rattus_norvegicus_GN=Gclc_PE=1_SV=2	4.00E-159
comp27956_c0_seq2.p1	sp|O49939|TLP40_SPIOL_Peptidyl-prolyl_cis-trans_isomerase,_chloroplastic_OS=Spinacia_oleracea_GN=TLP40_PE=1_SV=1	4.00E-33
comp27956_c0_seq3.p1	sp|O49939|TLP40_SPIOL_Peptidyl-prolyl_cis-trans_isomerase,_chloroplastic_OS=Spinacia_oleracea_GN=TLP40_PE=1_SV=1	3.00E-27
comp27956_c0_seq4.p1	sp|O49939|TLP40_SPIOL_Peptidyl-prolyl_cis-trans_isomerase,_chloroplastic_OS=Spinacia_oleracea_GN=TLP40_PE=1_SV=1	1.00E-28
comp27956_c0_seq5.p1	sp|O49939|TLP40_SPIOL_Peptidyl-prolyl_cis-trans_isomerase,_chloroplastic_OS=Spinacia_oleracea_GN=TLP40_PE=1_SV=1	4.00E-34
comp27957_c0_seq1.p1		
comp27957_c0_seq5.p1		
comp27959_c0_seq2.p1		
comp27960_c0_seq1.p1	sp|Q54CW7|RTPR_DICDI_Probable_adenosylcobalamin-dependent_ribonucleoside-triphosphate_reductase_OS=Dictyostelium_discoideum_GN=rtpR_PE=3_SV=1	2.00E-42
comp27960_c0_seq10.p1	sp|Q54CW7|RTPR_DICDI_Probable_adenosylcobalamin-dependent_ribonucleoside-triphosphate_reductase_OS=Dictyostelium_discoideum_GN=rtpR_PE=3_SV=1	0
comp27960_c0_seq10.p2		
comp27960_c0_seq11.p1	sp|Q54CW7|RTPR_DICDI_Probable_adenosylcobalamin-dependent_ribonucleoside-triphosphate_reductase_OS=Dictyostelium_discoideum_GN=rtpR_PE=3_SV=1	0
comp27960_c0_seq11.p2		
comp27960_c0_seq13.p1	sp|Q54CW7|RTPR_DICDI_Probable_adenosylcobalamin-dependent_ribonucleoside-triphosphate_reductase_OS=Dictyostelium_discoideum_GN=rtpR_PE=3_SV=1	4.00E-178
comp27960_c0_seq5.p1	sp|Q54CW7|RTPR_DICDI_Probable_adenosylcobalamin-dependent_ribonucleoside-triphosphate_reductase_OS=Dictyostelium_discoideum_GN=rtpR_PE=3_SV=1	0
comp27960_c0_seq7.p1	sp|Q54CW7|RTPR_DICDI_Probable_adenosylcobalamin-dependent_ribonucleoside-triphosphate_reductase_OS=Dictyostelium_discoideum_GN=rtpR_PE=3_SV=1	0
comp27960_c0_seq8.p2	sp|Q54CW7|RTPR_DICDI_Probable_adenosylcobalamin-dependent_ribonucleoside-triphosphate_reductase_OS=Dictyostelium_discoideum_GN=rtpR_PE=3_SV=1	2.00E-42
comp27963_c0_seq1.p1	sp|Q8N3C0|ASCC3_HUMAN_Activating_signal_cointegrator_1_complex_subunit_3_OS=Homo_sapiens_GN=ASCC3_PE=1_SV=3	0
comp27963_c0_seq2.p1	sp|F1LPQ2|ASCC3_RAT_Activating_signal_cointegrator_1_complex_subunit_3_OS=Rattus_norvegicus_GN=Ascc3_PE=3_SV=1	0
comp27966_c0_seq1.p1		
comp27966_c0_seq2.p1		
comp27968_c0_seq1.p1		
comp27968_c0_seq3.p1		
comp27968_c0_seq3.p5		
comp27970_c0_seq1.p1		
comp27970_c0_seq2.p1		
comp27971_c0_seq1.p1	sp|Q69VR7|PPT1_ORYSJ_Phosphoenolpyruvate/phosphate_translocator_1,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=PPT1_PE=2_SV=1	1.00E-14
comp27971_c0_seq3.p1		
comp27971_c0_seq4.p1		
comp27971_c1_seq1.p1		
comp27972_c0_seq1.p1	sp|Q32KJ8|ARSI_RAT_Arylsulfatase_I_OS=Rattus_norvegicus_GN=Arsi_PE=2_SV=1	8.00E-62
comp27972_c0_seq2.p2		
comp27974_c0_seq2.p1	sp|O81304|PAP11_ARATH_Probable_plastid-lipid-associated_protein_11,_chloroplastic_OS=Arabidopsis_thaliana_GN=PAP11_PE=2_SV=1	3.00E-29
comp27975_c0_seq1.p1		
comp27976_c0_seq1.p1		
comp27976_c0_seq2.p1	sp|P20593|MX_PERFL_Interferon-induced_GTP-binding_protein_Mx_(Fragment)_OS=Perca_fluviatilis_GN=mx_PE=2_SV=1	5.00E-57
comp27976_c1_seq1.p1	sp|Q6TN15|MX_SINCH_Interferon-induced_GTP-binding_protein_Mx_OS=Siniperca_chuatsi_GN=mx_PE=2_SV=1	3.00E-18
comp27976_c1_seq2.p1	sp|Q6TN15|MX_SINCH_Interferon-induced_GTP-binding_protein_Mx_OS=Siniperca_chuatsi_GN=mx_PE=2_SV=1	5.00E-18
comp27979_c0_seq2.p1		
comp27980_c0_seq1.p1	sp|O42634|DMC1_SCHPO_Meiotic_recombination_protein_dmc1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=dmc1_PE=1_SV=2	4.00E-114
comp27981_c0_seq1.p1		
comp27981_c0_seq3.p1		
comp27981_c0_seq5.p1		
comp27982_c0_seq3.p1		
comp27984_c0_seq1.p2		
comp27985_c0_seq2.p1		
comp27987_c0_seq1.p1	sp|Q6PQZ1|AQP1_PIG_Aquaporin-1_OS=Sus_scrofa_GN=AQP1_PE=2_SV=3	7.00E-45
comp27989_c0_seq1.p1	sp|Q08CM4|LIN54_DANRE_Protein_lin-54_homolog_OS=Danio_rerio_GN=lin54_PE=1_SV=1	4.00E-28
comp27992_c0_seq1.p1		
comp27992_c0_seq2.p1		
comp27993_c0_seq2.p1	sp|Q3UFB2|BCD1_MOUSE_Box_C/D_snoRNA_protein_1_OS=Mus_musculus_GN=Znhit6_PE=2_SV=2	2.00E-16
comp27993_c0_seq3.p1		
comp27993_c0_seq4.p1		
comp27995_c0_seq1.p1		
comp27995_c0_seq3.p2		
comp27996_c0_seq1.p1		
comp27996_c0_seq2.p1	sp|Q8LBH4|SPX1_ARATH_SPX_domain-containing_protein_1_OS=Arabidopsis_thaliana_GN=SPX1_PE=2_SV=2	4.00E-22
comp27997_c1_seq5.p1	sp|Q8RY79|TYDC1_ARATH_Tyrosine_decarboxylase_1_OS=Arabidopsis_thaliana_GN=ELI5_PE=2_SV=1	9.00E-132
comp27998_c0_seq2.p4		
comp27998_c0_seq3.p1	sp|Q9CW42|MOSC1_MOUSE_MOSC_domain-containing_protein_1,_mitochondrial_OS=Mus_musculus_GN=Marc1_PE=1_SV=2	1.00E-36
comp28001_c1_seq2.p1		
comp28001_c1_seq3.p1		
comp28003_c0_seq1.p1	sp|Q7TXK5|FAA29_MYCBO_Long-chain-fatty-acid--AMP_ligase_FadD29_OS=Mycobacterium_bovis_GN=fadD29_PE=3_SV=1	2.00E-44
comp28004_c0_seq1.p1		
comp28005_c0_seq3.p1		
comp28009_c0_seq3.p1	sp|Q24799|MYPH_ECHGR_Myophilin_OS=Echinococcus_granulosus_PE=2_SV=1	2.00E-19
comp28010_c0_seq1.p1	sp|Q05001|NCPR_CATRO_NADPH--cytochrome_P450_reductase_OS=Catharanthus_roseus_GN=CPR_PE=2_SV=1	8.00E-42
comp28011_c0_seq1.p1		
comp28011_c0_seq2.p1		
comp28012_c0_seq2.p1		
comp28012_c0_seq4.p1		
comp28013_c0_seq1.p1	sp|Q9C927|PPA5_ARATH_Purple_acid_phosphatase_5_OS=Arabidopsis_thaliana_GN=PAP5_PE=2_SV=1	3.00E-27
comp28013_c0_seq1.p2	sp|Q9LJU7|PPA18_ARATH_Purple_acid_phosphatase_18_OS=Arabidopsis_thaliana_GN=PAP18_PE=2_SV=1	2.00E-27
comp28013_c0_seq2.p1	sp|Q9LJU7|PPA18_ARATH_Purple_acid_phosphatase_18_OS=Arabidopsis_thaliana_GN=PAP18_PE=2_SV=1	3.00E-41
comp28015_c1_seq1.p1	sp|Q9VCA5|SYFB_DROME_Probable_phenylalanine--tRNA_ligase_beta_subunit_OS=Drosophila_melanogaster_GN=CG5706_PE=2_SV=1	0
comp28017_c0_seq1.p1		
comp28018_c0_seq1.p1	sp|Q8VZC9|VPS25_ARATH_Vacuolar_protein_sorting-associated_protein_25_OS=Arabidopsis_thaliana_GN=VPS25_PE=1_SV=1	6.00E-39
comp28018_c0_seq4.p1	sp|Q8VZC9|VPS25_ARATH_Vacuolar_protein_sorting-associated_protein_25_OS=Arabidopsis_thaliana_GN=VPS25_PE=1_SV=1	6.00E-39
comp28023_c0_seq1.p2		
comp28023_c0_seq2.p2		
comp28026_c0_seq1.p1		
comp28026_c0_seq1.p2		
comp28028_c0_seq4.p1		
comp28029_c0_seq1.p1		
comp28030_c0_seq1.p1	sp|Q99288|DET1_YEAST_Putative_phosphoglycerate_mutase_DET1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=DET1_PE=1_SV=1	8.00E-29
comp28031_c0_seq1.p1	sp|P55133|RELA_PHOAS_GTP_pyrophosphokinase_OS=Photobacterium_angustum_(strain_S14_/_CCUG_15956)_GN=relA_PE=3_SV=1	2.00E-16
comp28032_c0_seq1.p1	sp|P29993|ITPR_DROME_Inositol_1,4,5-trisphosphate_receptor_OS=Drosophila_melanogaster_GN=Itp-r83A_PE=2_SV=3	1.00E-21
comp28033_c0_seq1.p1		
comp28033_c0_seq3.p1	sp|Q8SKU2|TIC62_PEA_Protein_TIC_62,_chloroplastic_OS=Pisum_sativum_GN=TIC62_PE=1_SV=1	2.00E-49
comp28039_c0_seq1.p1		
comp28039_c0_seq2.p1		
comp28042_c0_seq1.p1		
comp28045_c0_seq1.p1		
comp28045_c0_seq2.p1	sp|Q02817|MUC2_HUMAN_Mucin-2_OS=Homo_sapiens_GN=MUC2_PE=1_SV=2	3.00E-20
comp28045_c0_seq4.p2		
comp28045_c0_seq5.p1		
comp28045_c0_seq6.p2		
comp28046_c0_seq1.p1		
comp28046_c0_seq2.p1		
comp28046_c0_seq3.p1		
comp28047_c0_seq2.p1		
comp28050_c0_seq1.p1		
comp28050_c0_seq4.p1		
comp28054_c0_seq2.p1		
comp28055_c0_seq1.p1	sp|Q9FPT1|UBP12_ARATH_Ubiquitin_carboxyl-terminal_hydrolase_12_OS=Arabidopsis_thaliana_GN=UBP12_PE=1_SV=2	3.00E-124
comp28056_c0_seq1.p1		
comp28056_c0_seq1.p2	sp|P31106|MIP_LEGMI_Outer_membrane_protein_MIP_OS=Legionella_micdadei_GN=mip_PE=3_SV=1	2.00E-33
comp2806_c0_seq1.p2		
comp28062_c0_seq3.p1		
comp28064_c0_seq1.p1		
comp28065_c0_seq2.p1	sp|Q7T3E4|DBR1_DANRE_Lariat_debranching_enzyme_OS=Danio_rerio_GN=dbr1_PE=1_SV=1	5.00E-117
comp28068_c0_seq1.p1	sp|Q55GU0|Y9955_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0267514_OS=Dictyostelium_discoideum_GN=DDB_G0267514_PE=3_SV=1	9.00E-17
comp28068_c0_seq1.p5		
comp28068_c0_seq2.p1	sp|Q55GU0|Y9955_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0267514_OS=Dictyostelium_discoideum_GN=DDB_G0267514_PE=3_SV=1	2.00E-30
comp28069_c0_seq1.p1		
comp28070_c0_seq1.p1		
comp28070_c0_seq2.p2		
comp28070_c0_seq4.p1		
comp28071_c0_seq6.p1		
comp28071_c0_seq7.p1		
comp28073_c0_seq1.p1	sp|Q54II8|U553_DICDI_UPF0553_protein_OS=Dictyostelium_discoideum_GN=DDB_G0288723_PE=3_SV=1	1.00E-74
comp28074_c0_seq1.p1		
comp28074_c0_seq2.p1		
comp28075_c0_seq1.p1	sp|Q9P6U9|DED1_NEUCR_ATP-dependent_RNA_helicase_ded-1_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=ded-1_PE=3_SV=1	1.00E-179
comp28076_c0_seq1.p1	sp|Q9C0G6|DYH6_HUMAN_Dynein_heavy_chain_6,_axonemal_OS=Homo_sapiens_GN=DNAH6_PE=1_SV=3	0
comp28076_c0_seq1.p2	sp|Q9C0G6|DYH6_HUMAN_Dynein_heavy_chain_6,_axonemal_OS=Homo_sapiens_GN=DNAH6_PE=1_SV=3	5.00E-90
comp28076_c0_seq2.p1	sp|Q9C0G6|DYH6_HUMAN_Dynein_heavy_chain_6,_axonemal_OS=Homo_sapiens_GN=DNAH6_PE=1_SV=3	0
comp28076_c0_seq2.p2	sp|Q9C0G6|DYH6_HUMAN_Dynein_heavy_chain_6,_axonemal_OS=Homo_sapiens_GN=DNAH6_PE=1_SV=3	1.00E-63
comp28076_c0_seq2.p3	sp|Q9C0G6|DYH6_HUMAN_Dynein_heavy_chain_6,_axonemal_OS=Homo_sapiens_GN=DNAH6_PE=1_SV=3	5.00E-90
comp28077_c0_seq1.p1		
comp28078_c0_seq1.p1		
comp28079_c0_seq1.p1		
comp28079_c0_seq2.p1		
comp28080_c0_seq2.p1		
comp28080_c0_seq3.p1		
comp28080_c0_seq4.p1		
comp28081_c0_seq2.p1		
comp28083_c0_seq3.p1		
comp28088_c0_seq1.p1		
comp28088_c0_seq1.p2		
comp28088_c0_seq1.p3		
comp28088_c0_seq2.p1		
comp28088_c0_seq2.p2		
comp28088_c0_seq2.p3		
comp28089_c1_seq1.p1		
comp28089_c1_seq1.p2		
comp28089_c2_seq1.p1	sp|P51819|HSP83_IPONI_Heat_shock_protein_83_OS=Ipomoea_nil_GN=HSP83A_PE=2_SV=1	0
comp28090_c0_seq2.p1	sp|Q05609|CTR1_ARATH_Serine/threonine-protein_kinase_CTR1_OS=Arabidopsis_thaliana_GN=CTR1_PE=1_SV=1	3.00E-25
comp28090_c0_seq3.p1	sp|Q05609|CTR1_ARATH_Serine/threonine-protein_kinase_CTR1_OS=Arabidopsis_thaliana_GN=CTR1_PE=1_SV=1	1.00E-31
comp28090_c0_seq4.p1	sp|Q05609|CTR1_ARATH_Serine/threonine-protein_kinase_CTR1_OS=Arabidopsis_thaliana_GN=CTR1_PE=1_SV=1	7.00E-49
comp28091_c0_seq1.p1	sp|Q10717|CYSP2_MAIZE_Cysteine_proteinase_2_OS=Zea_mays_GN=CCP2_PE=2_SV=1	2.00E-102
comp28091_c0_seq1.p2		
comp28091_c0_seq3.p1	sp|Q10717|CYSP2_MAIZE_Cysteine_proteinase_2_OS=Zea_mays_GN=CCP2_PE=2_SV=1	2.00E-102
comp28091_c0_seq3.p2		
comp28092_c0_seq3.p1		
comp28092_c0_seq4.p2		
comp28093_c0_seq1.p1	sp|Q9ULJ7|ANR50_HUMAN_Ankyrin_repeat_domain-containing_protein_50_OS=Homo_sapiens_GN=ANKRD50_PE=1_SV=4	2.00E-18
comp28093_c0_seq1.p2	sp|Q562D6|NAP1_MOUSE_Nef-associated_protein_1_OS=Mus_musculus_GN=Nap1_PE=2_SV=2	2.00E-30
comp28094_c0_seq1.p1	sp|Q1HR79|TCTP_AEDAE_Translationally-controlled_tumor_protein_homolog_OS=Aedes_aegypti_GN=Tctp_PE=2_SV=1	3.00E-75
comp28095_c0_seq1.p1		
comp28097_c0_seq4.p1		
comp28097_c0_seq4.p2		
comp28098_c0_seq2.p1		
comp28098_c0_seq4.p1		
comp28099_c0_seq1.p1		
comp28101_c0_seq1.p1		
comp28101_c0_seq2.p1		
comp28102_c0_seq2.p1	sp|O24308|TOP2_PEA_DNA_topoisomerase_2_OS=Pisum_sativum_GN=TOP2_PE=2_SV=1	0
comp28102_c0_seq4.p1	sp|O24308|TOP2_PEA_DNA_topoisomerase_2_OS=Pisum_sativum_GN=TOP2_PE=2_SV=1	4.00E-15
comp28103_c1_seq1.p1		
comp28103_c1_seq1.p3		
comp28104_c1_seq1.p1	sp|Q6PCJ1|DCTN1_XENLA_Dynactin_subunit_1_OS=Xenopus_laevis_GN=dctn1_PE=2_SV=1	3.00E-17
comp28105_c0_seq2.p1	sp|Q94KU6|PAP2_BRACM_Plastid_lipid-associated_protein_2,_chloroplastic_OS=Brassica_campestris_GN=PAP2_PE=1_SV=1	3.00E-14
comp28106_c0_seq3.p1	sp|Q9MA55|ACBP4_ARATH_Acyl-CoA-binding_domain-containing_protein_4_OS=Arabidopsis_thaliana_GN=ACBP4_PE=1_SV=1	9.00E-22
comp28107_c0_seq1.p1	sp|Q9FYC2|PAO_ARATH_Pheophorbide_a_oxygenase,_chloroplastic_OS=Arabidopsis_thaliana_GN=PAO_PE=1_SV=1	1.00E-52
comp28107_c0_seq1.p4		
comp28107_c0_seq3.p1	sp|Q9FYC2|PAO_ARATH_Pheophorbide_a_oxygenase,_chloroplastic_OS=Arabidopsis_thaliana_GN=PAO_PE=1_SV=1	9.00E-61
comp28108_c0_seq3.p1	sp|Q42877|RPB2_SOLLC_DNA-directed_RNA_polymerase_II_subunit_RPB2_OS=Solanum_lycopersicum_GN=RPB2_PE=2_SV=1	0
comp28111_c0_seq1.p1		
comp28112_c0_seq1.p1		
comp28113_c0_seq1.p1		
comp28113_c0_seq2.p1	sp|Q557G3|TPPC1_DICDI_Trafficking_protein_particle_complex_subunit_1_OS=Dictyostelium_discoideum_GN=trappc1-1_PE=3_SV=1	2.00E-35
comp28113_c0_seq3.p1	sp|Q557G3|TPPC1_DICDI_Trafficking_protein_particle_complex_subunit_1_OS=Dictyostelium_discoideum_GN=trappc1-1_PE=3_SV=1	2.00E-28
comp28114_c0_seq2.p1	sp|Q54WW7|Y0010_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0279405_OS=Dictyostelium_discoideum_GN=DDB_G0279405_PE=3_SV=1	4.00E-30
comp28115_c0_seq1.p1	sp|A7Z794|MAF_BACA2_Septum_formation_protein_Maf_OS=Bacillus_amyloliquefaciens_(strain_FZB42)_GN=maf_PE=3_SV=1	1.00E-30
comp28115_c0_seq2.p2	sp|Q0SR36|Y2112_CLOPS_Maf-like_protein_CPR_2112_OS=Clostridium_perfringens_(strain_SM101_/_Type_A)_GN=CPR_2112_PE=3_SV=1	2.00E-26
comp28115_c0_seq3.p1	sp|Q0SR36|Y2112_CLOPS_Maf-like_protein_CPR_2112_OS=Clostridium_perfringens_(strain_SM101_/_Type_A)_GN=CPR_2112_PE=3_SV=1	2.00E-42
comp28115_c0_seq5.p1	sp|Q0SR36|Y2112_CLOPS_Maf-like_protein_CPR_2112_OS=Clostridium_perfringens_(strain_SM101_/_Type_A)_GN=CPR_2112_PE=3_SV=1	1.00E-24
comp28115_c0_seq6.p1	sp|Q0SR36|Y2112_CLOPS_Maf-like_protein_CPR_2112_OS=Clostridium_perfringens_(strain_SM101_/_Type_A)_GN=CPR_2112_PE=3_SV=1	3.00E-32
comp28115_c0_seq7.p1	sp|O95671|ASML_HUMAN_N-acetylserotonin_O-methyltransferase-like_protein_OS=Homo_sapiens_GN=ASMTL_PE=1_SV=3	9.00E-35
comp28115_c0_seq9.p1	sp|Q0SR36|Y2112_CLOPS_Maf-like_protein_CPR_2112_OS=Clostridium_perfringens_(strain_SM101_/_Type_A)_GN=CPR_2112_PE=3_SV=1	3.00E-38
comp28116_c0_seq1.p1	sp|Q28256|GP1BA_CANFA_Platelet_glycoprotein_Ib_alpha_chain_OS=Canis_familiaris_GN=GP1BA_PE=2_SV=2	6.00E-12
comp28117_c0_seq1.p1	sp|P50567|H2A_CHLRE_Histone_H2A_OS=Chlamydomonas_reinhardtii_GN=H2A-II_PE=3_SV=1	7.00E-56
comp28118_c0_seq2.p1		
comp28119_c0_seq2.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	1.00E-16
comp28119_c0_seq2.p2		
comp28119_c0_seq5.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	4.00E-16
comp28119_c0_seq6.p1		
comp28120_c0_seq2.p1		
comp28120_c0_seq2.p2		
comp28121_c0_seq1.p1	sp|P41753|HSP70_ACHKL_Heat_shock_70_kDa_protein_OS=Achlya_klebsiana_GN=HSP70_PE=2_SV=1	0
comp28121_c0_seq2.p1	sp|P49118|BIP_SOLLC_Luminal-binding_protein_OS=Solanum_lycopersicum_PE=2_SV=1	0
comp28123_c0_seq2.p1		
comp28124_c0_seq2.p1		

comp28125_c1_seq1.p1		
comp28126_c0_seq3.p1		
comp28127_c0_seq3.p1		
comp28127_c0_seq4.p1		
comp28127_c0_seq5.p1		
comp28128_c0_seq1.p1		
comp28128_c0_seq4.p1		
comp28128_c0_seq5.p1		
comp28128_c0_seq6.p1		
comp28129_c0_seq2.p1	sp|O80585|MTHR2_ARATH_Methylenetetrahydrofolate_reductase_2_OS=Arabidopsis_thaliana_GN=MTHFR2_PE=1_SV=2	7.00E-104
comp28130_c0_seq1.p1		
comp28130_c0_seq3.p1		
comp28131_c0_seq1.p1	sp|P51158|RAB28_RAT_Ras-related_protein_Rab-28_OS=Rattus_norvegicus_GN=Rab28_PE=2_SV=1	1.00E-68
comp28131_c0_seq3.p2	sp|P51157|RAB28_HUMAN_Ras-related_protein_Rab-28_OS=Homo_sapiens_GN=RAB28_PE=1_SV=2	3.00E-27
comp28132_c0_seq1.p1	sp|Q05609|CTR1_ARATH_Serine/threonine-protein_kinase_CTR1_OS=Arabidopsis_thaliana_GN=CTR1_PE=1_SV=1	8.00E-33
comp28133_c1_seq2.p1	sp|Q0J3D9|COPA3_ORYSJ_Coatomer_subunit_alpha-3_OS=Oryza_sativa_subsp._japonica_GN=Os09g0127800_PE=2_SV=1	0
comp28136_c0_seq1.p1	sp|Q02427|RBP1_DROME_RNA-binding_protein_1_OS=Drosophila_melanogaster_GN=Rbp1_PE=2_SV=3	9.00E-12
comp28139_c0_seq1.p1		
comp28140_c0_seq2.p1		
comp28141_c0_seq1.p2		
comp28143_c0_seq1.p1	sp|Q80YD1|SUV3_MOUSE_ATP-dependent_RNA_helicase_SUPV3L1,_mitochondrial_OS=Mus_musculus_GN=Supv3l1_PE=2_SV=1	2.00E-100
comp28145_c0_seq2.p1		
comp28147_c0_seq2.p1		
comp28148_c0_seq1.p1	sp|Q6DHU4|PR38A_DANRE_Pre-mRNA-splicing_factor_38A_OS=Danio_rerio_GN=prpf38a_PE=2_SV=1	4.00E-57
comp28150_c1_seq1.p1		
comp28150_c1_seq2.p1	sp|Q2QNF7|DAPF_ORYSJ_Diaminopimelate_epimerase,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=DAPF_PE=2_SV=1	6.00E-111
comp28150_c1_seq3.p1		
comp28150_c1_seq4.p1	sp|Q2QNF7|DAPF_ORYSJ_Diaminopimelate_epimerase,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=DAPF_PE=2_SV=1	3.00E-27
comp28151_c0_seq1.p1		
comp28155_c0_seq5.p1		
comp28156_c0_seq2.p1	sp|P35055|HEM6_SOYBN_Coproporphyrinogen-III_oxidase,_chloroplastic_OS=Glycine_max_GN=CPX_PE=2_SV=1	4.00E-128
comp28157_c0_seq3.p1		
comp28158_c0_seq1.p1	sp|P74594|Y1563_SYNY3_Uncharacterized_protein_slr1563_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr1563_PE=3_SV=1	8.00E-74
comp28159_c0_seq1.p1		
comp28160_c0_seq1.p1		
comp28160_c0_seq3.p1		
comp28161_c0_seq1.p1	sp|Q86C65|TOR_DICDI_Target_of_rapamycin_OS=Dictyostelium_discoideum_GN=tor_PE=1_SV=1	0
comp28162_c0_seq1.p1	sp|Q2TBU3|GOSR1_BOVIN_Golgi_SNAP_receptor_complex_member_1_OS=Bos_taurus_GN=GOSR1_PE=2_SV=1	7.00E-22
comp28163_c0_seq1.p1	sp|Q9LR78|BSU1_ARATH_Serine/threonine-protein_phosphatase_BSU1_OS=Arabidopsis_thaliana_GN=BSU1_PE=2_SV=2	8.00E-39
comp28163_c0_seq1.p2		
comp28163_c0_seq2.p1	sp|Q9SHS7|BSL3_ARATH_Serine/threonine-protein_phosphatase_BSL3_OS=Arabidopsis_thaliana_GN=BSL3_PE=1_SV=2	7.00E-28
comp28163_c0_seq2.p2		
comp28163_c0_seq4.p1	sp|Q9LR78|BSU1_ARATH_Serine/threonine-protein_phosphatase_BSU1_OS=Arabidopsis_thaliana_GN=BSU1_PE=2_SV=2	2.00E-41
comp28163_c0_seq4.p3		
comp28164_c0_seq3.p1		
comp28165_c0_seq1.p1		
comp28166_c0_seq3.p1	sp|Q8WXX0|DYH7_HUMAN_Dynein_heavy_chain_7,_axonemal_OS=Homo_sapiens_GN=DNAH7_PE=1_SV=2	0
comp28167_c0_seq1.p1		
comp28167_c0_seq3.p2		
comp28168_c0_seq1.p1		
comp28168_c1_seq1.p1		
comp28170_c0_seq2.p1		
comp28171_c0_seq1.p1		
comp28171_c1_seq1.p1		
comp28171_c1_seq2.p1		
comp28172_c0_seq1.p1		
comp28172_c0_seq1.p2		
comp28173_c0_seq1.p1	sp|Q6IWH7|ANO7_HUMAN_Anoctamin-7_OS=Homo_sapiens_GN=ANO7_PE=1_SV=2	1.00E-50
comp28173_c0_seq2.p1	sp|Q6IWH7|ANO7_HUMAN_Anoctamin-7_OS=Homo_sapiens_GN=ANO7_PE=1_SV=2	3.00E-54
comp28176_c0_seq2.p1		
comp28178_c0_seq1.p1	sp|Q9Z118|PTBP3_RAT_Polypyrimidine_tract-binding_protein_3_OS=Rattus_norvegicus_GN=Ptbp3_PE=2_SV=1	1.00E-14
comp28178_c0_seq2.p1	sp|Q9Z118|PTBP3_RAT_Polypyrimidine_tract-binding_protein_3_OS=Rattus_norvegicus_GN=Ptbp3_PE=2_SV=1	3.00E-15
comp28178_c0_seq3.p3	sp|Q9FGL9|PTBP2_ARATH_Polypyrimidine_tract-binding_protein_homolog_2_OS=Arabidopsis_thaliana_GN=At5g53180_PE=2_SV=1	1.00E-11
comp28181_c0_seq2.p1	sp|Q8N136|WDR69_HUMAN_Outer_row_dynein_assembly_protein_16_homolog_OS=Homo_sapiens_GN=WDR69_PE=1_SV=1	1.00E-21
comp28182_c0_seq1.p1		
comp28183_c0_seq1.p1	sp|Q5EE05|ABHD5_PIG_1-acylglycerol-3-phosphate_O-acyltransferase_ABHD5_OS=Sus_scrofa_GN=ABHD5_PE=2_SV=1	4.00E-49
comp28184_c0_seq2.p1		
comp28185_c0_seq1.p1	sp|Q39493|DSK1_CYLFU_Diatom_spindle_kinesin_1_OS=Cylindrotheca_fusiformis_GN=DSK1_PE=2_SV=1	1.00E-14
comp28187_c0_seq1.p1		
comp28187_c0_seq3.p1	sp|Q0III6|DNJB6_BOVIN_DnaJ_homolog_subfamily_B_member_6_OS=Bos_taurus_GN=DNAJB6_PE=2_SV=1	6.00E-20
comp28188_c0_seq1.p2		
comp28188_c0_seq2.p1	sp|Q9LMM2|FRO1_ARATH_Probable_ferric_reduction_oxidase_1_OS=Arabidopsis_thaliana_GN=FRO1_PE=2_SV=1	9.00E-16
comp28190_c0_seq2.p1	sp|Q8VDD9|PHIP_MOUSE_PH-interacting_protein_OS=Mus_musculus_GN=Phip_PE=1_SV=2	6.00E-28
comp28191_c0_seq1.p1	sp|Q75JN1|IFKC_DICDI_Probable_serine/threonine-protein_kinase_ifkC_OS=Dictyostelium_discoideum_GN=ifkC_PE=3_SV=1	3.00E-18
comp28192_c0_seq1.p1		
comp28192_c0_seq5.p1		
comp28193_c0_seq1.p2		
comp28193_c0_seq2.p1		
comp28193_c0_seq3.p2		
comp28194_c0_seq2.p1	sp|Q45632|MALA_GEOSE_Maltose_permease_OS=Geobacillus_stearothermophilus_GN=malA_PE=3_SV=1	7.00E-21
comp28194_c0_seq4.p1	sp|Q45632|MALA_GEOSE_Maltose_permease_OS=Geobacillus_stearothermophilus_GN=malA_PE=3_SV=1	1.00E-11
comp28194_c0_seq4.p2	sp|A1DWM3|MFSD6_PIG_Major_facilitator_superfamily_domain-containing_protein_6_OS=Sus_scrofa_GN=MFSD6_PE=2_SV=1	5.00E-14
comp28196_c0_seq1.p1		
comp28198_c0_seq3.p1		
comp28198_c0_seq4.p1	sp|O16299|FIGL1_CAEEL_Fidgetin-like_protein_1_OS=Caenorhabditis_elegans_GN=figl-1_PE=1_SV=1	2.00E-46
comp28198_c0_seq4.p2	sp|P50199|GNO_GLUOX_Gluconate_5-dehydrogenase_OS=Gluconobacter_oxydans_(strain_621H)_GN=gno_PE=1_SV=1	1.00E-30
comp28198_c0_seq5.p1	sp|Q5ZK92|SPAST_CHICK_Spastin_OS=Gallus_gallus_GN=SPAST_PE=2_SV=1	6.00E-42
comp28198_c0_seq5.p2	sp|P50199|GNO_GLUOX_Gluconate_5-dehydrogenase_OS=Gluconobacter_oxydans_(strain_621H)_GN=gno_PE=1_SV=1	1.00E-30
comp28199_c0_seq1.p1	sp|Q4R3Y4|S27A4_MACFA_Long-chain_fatty_acid_transport_protein_4_OS=Macaca_fascicularis_GN=SLC27A4_PE=2_SV=1	3.00E-137
comp28199_c0_seq1.p2		
comp28200_c0_seq2.p1		
comp28200_c0_seq3.p1		
comp28201_c0_seq5.p1	sp|Q54GC1|DGAT2_DICDI_Diacylglycerol_O-acyltransferase_2_OS=Dictyostelium_discoideum_GN=dgat2_PE=3_SV=1	3.00E-26
comp28201_c0_seq9.p1	sp|Q54GC1|DGAT2_DICDI_Diacylglycerol_O-acyltransferase_2_OS=Dictyostelium_discoideum_GN=dgat2_PE=3_SV=1	2.00E-26
comp28202_c1_seq2.p1		
comp28204_c1_seq2.p1		
comp28205_c0_seq1.p1		
comp28207_c0_seq1.p1	sp|Q54LN4|GGHA_DICDI_Gamma-glutamyl_hydrolase_A_OS=Dictyostelium_discoideum_GN=gghA_PE=3_SV=1	8.00E-36
comp28209_c0_seq1.p1		
comp28209_c0_seq2.p1		
comp28211_c0_seq2.p1	sp|Q8RY73|DOM3Z_ARATH_Protein_Dom3z_homolog,_chloroplastic_OS=Arabidopsis_thaliana_GN=At4g17620_PE=1_SV=1	2.00E-41
comp28211_c1_seq1.p1		
comp28213_c0_seq3.p1		
comp28214_c0_seq1.p1		
comp28214_c0_seq1.p2		
comp28214_c0_seq2.p1		
comp28216_c0_seq2.p1		
comp28216_c0_seq4.p1		
comp28217_c0_seq1.p1	sp|A1A5H6|CNOT1_DANRE_CCR4-NOT_transcription_complex_subunit_1_OS=Danio_rerio_GN=cnot1_PE=2_SV=1	3.00E-38
comp28217_c0_seq2.p1	sp|A1A5H6|CNOT1_DANRE_CCR4-NOT_transcription_complex_subunit_1_OS=Danio_rerio_GN=cnot1_PE=2_SV=1	3.00E-38
comp28218_c0_seq1.p1		
comp28218_c0_seq4.p1		
comp28219_c0_seq1.p1		
comp28219_c0_seq4.p1		
comp28220_c0_seq2.p1		
comp28220_c0_seq2.p2		
comp28222_c0_seq5.p1		
comp28222_c0_seq6.p1	sp|Q54PR9|CF60_DICDI_Counting_factor_60_OS=Dictyostelium_discoideum_GN=cf60_PE=1_SV=1	9.00E-19
comp28224_c0_seq1.p1		
comp28224_c0_seq3.p1		
comp28225_c1_seq2.p1	sp|A8HAL1|UBP16_DANRE_Ubiquitin_carboxyl-terminal_hydrolase_16_OS=Danio_rerio_GN=usp16_PE=3_SV=1	1.00E-31
comp28225_c1_seq2.p3		
comp28229_c0_seq2.p1		
comp28230_c0_seq1.p1	sp|Q5PQP5|SLX1_RAT_Structure-specific_endonuclease_subunit_SLX1_OS=Rattus_norvegicus_GN=Slx1b_PE=2_SV=1	3.00E-48
comp28230_c0_seq1.p2	sp|B9EB94|FMT_MACCJ_Methionyl-tRNA_formyltransferase_OS=Macrococcus_caseolyticus_(strain_JCSC5402)_GN=fmt_PE=3_SV=1	1.00E-44
comp28232_c0_seq2.p1	sp|P59470|RPC2_MOUSE_DNA-directed_RNA_polymerase_III_subunit_RPC2_OS=Mus_musculus_GN=Polr3b_PE=2_SV=2	0
comp28233_c0_seq1.p1		
comp28235_c0_seq1.p1	sp|P00582|DPO1_ECOLI_DNA_polymerase_I_OS=Escherichia_coli_(strain_K12)_GN=polA_PE=1_SV=1	1.00E-59
comp28235_c0_seq3.p1	sp|P00582|DPO1_ECOLI_DNA_polymerase_I_OS=Escherichia_coli_(strain_K12)_GN=polA_PE=1_SV=1	4.00E-62
comp28235_c0_seq3.p2		
comp28236_c0_seq1.p1	sp|Q5HME0|Y1688_STAEQ_Probable_DEAD-box_ATP-dependent_RNA_helicase_SERP1688_OS=Staphylococcus_epidermidis_(strain_ATCC_35984_/_RP62A)_GN=SERP1688_PE=3_SV=1	3.00E-18
comp28238_c0_seq2.p1	sp|Q8TB22|SPT20_HUMAN_Spermatogenesis-associated_protein_20_OS=Homo_sapiens_GN=SPATA20_PE=2_SV=3	4.00E-164
comp28238_c0_seq3.p1	sp|Q8TB22|SPT20_HUMAN_Spermatogenesis-associated_protein_20_OS=Homo_sapiens_GN=SPATA20_PE=2_SV=3	3.00E-168
comp28239_c0_seq1.p1	sp|Q9BIB3|PPME1_CAEEL_Probable_protein_phosphatase_methylesterase_1_OS=Caenorhabditis_elegans_GN=B0464.9_PE=3_SV=1	6.00E-30
comp28239_c1_seq3.p1	sp|Q9D0L4|ADCK1_MOUSE_Uncharacterized_aarF_domain-containing_protein_kinase_1_OS=Mus_musculus_GN=Adck1_PE=2_SV=1	5.00E-16
comp2824_c0_seq1.p1		
comp28242_c0_seq1.p1	sp|Q9FJV0|M2K6_ARATH_Mitogen-activated_protein_kinase_kinase_6_OS=Arabidopsis_thaliana_GN=MKK6_PE=1_SV=1	7.00E-45
comp28244_c0_seq1.p1		
comp28244_c0_seq2.p2		
comp28245_c0_seq1.p1		
comp28246_c0_seq1.p1		
comp28247_c0_seq2.p2		
comp28248_c0_seq1.p1		
comp28248_c0_seq2.p1	sp|Q3AYC6|SYT_SYNS9_Threonine--tRNA_ligase_OS=Synechococcus_sp._(strain_CC9902)_GN=thrS_PE=3_SV=1	0
comp28251_c0_seq1.p1	sp|O59667|HIS2_SCHPO_Histidine_biosynthesis_bifunctional_protein_his7_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=his7_PE=2_SV=1	2.00E-55
comp28252_c0_seq1.p1	sp|P0C1J5|FKB2B_RHIOR_FK506-binding_protein_2B_OS=Rhizopus_oryzae_GN=FKBP3_PE=3_SV=1	1.00E-27
comp28254_c0_seq3.p1		
comp28256_c0_seq1.p1		
comp28257_c0_seq1.p1	sp|Q2QKL5|PCS3_LOTJA_Glutathione_gamma-glutamylcysteinyltransferase_3_OS=Lotus_japonicus_GN=PCS3_PE=2_SV=1	2.00E-88
comp28258_c0_seq2.p1	sp|Q87AJ9|MSRB_XYLFT_Peptide_methionine_sulfoxide_reductase_MsrB_OS=Xylella_fastidiosa_(strain_Temecula1_/_ATCC_700964)_GN=msrB_PE=3_SV=1	6.00E-16
comp28258_c0_seq4.p2		
comp28259_c0_seq1.p1		
comp28259_c0_seq1.p2		
comp28259_c0_seq2.p1		
comp28259_c0_seq2.p3		
comp28259_c0_seq3.p1		
comp28259_c0_seq6.p2		
comp28261_c0_seq3.p1		
comp28262_c0_seq1.p1		
comp28263_c0_seq3.p5		
comp28266_c0_seq2.p1		
comp28266_c0_seq3.p1		
comp28268_c0_seq1.p1		
comp28269_c0_seq1.p1		
comp28270_c0_seq1.p3		
comp28270_c0_seq1.p4		
comp28270_c0_seq2.p2		
comp28272_c0_seq3.p1	sp|Q5UR04|YR911_MIMIV_Putative_ankyrin_repeat_protein_R911_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R911_PE=4_SV=1	1.00E-13
comp28273_c0_seq3.p1	sp|C3YDS7|NNRE_BRAFL_NAD(P)H-hydrate_epimerase_OS=Branchiostoma_floridae_GN=BRAFLDRAFT_104103_PE=3_SV=1	4.00E-73
comp28273_c0_seq4.p1		
comp28274_c0_seq1.p1		
comp28275_c0_seq2.p1		
comp28276_c0_seq1.p1	sp|Q8L5Y6|CAND1_ARATH_Cullin-associated_NEDD8-dissociated_protein_1_OS=Arabidopsis_thaliana_GN=CAND1_PE=1_SV=1	0
comp28277_c0_seq1.p1		
comp28277_c0_seq4.p1		
comp28279_c0_seq2.p1	sp|Q9FF61|SM3L1_ARATH_Putative_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A_member_3-like_1_OS=Arabidopsis_thaliana_GN=At5g05130_PE=2_SV=1	1.00E-26
comp28279_c0_seq3.p1	sp|Q9FNI6|SM3L2_ARATH_Putative_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A_member_3-like_2_OS=Arabidopsis_thaliana_GN=At5g22750_PE=2_SV=1	1.00E-99
comp28285_c0_seq1.p1		
comp28287_c0_seq2.p1		
comp28287_c0_seq3.p1		
comp28289_c0_seq1.p1	sp|Q8NB90|SPAT5_HUMAN_Spermatogenesis-associated_protein_5_OS=Homo_sapiens_GN=SPATA5_PE=1_SV=3	6.00E-42
comp28290_c0_seq3.p1	sp|Q9JJN0|POLH_MOUSE_DNA_polymerase_eta_OS=Mus_musculus_GN=Polh_PE=1_SV=1	3.00E-43
comp28290_c0_seq4.p1	sp|Q9Y253|POLH_HUMAN_DNA_polymerase_eta_OS=Homo_sapiens_GN=POLH_PE=1_SV=1	9.00E-34
comp28291_c0_seq1.p1		
comp28291_c0_seq2.p1		
comp28291_c0_seq2.p2		
comp28291_c0_seq5.p1		
comp28291_c0_seq5.p2		
comp28292_c1_seq1.p2		
comp28294_c0_seq1.p1		
comp28295_c0_seq2.p1		
comp28295_c0_seq4.p1		
comp28296_c0_seq1.p2	sp|P62975|UBIQ_RABIT_Ubiquitin_OS=Oryctolagus_cuniculus_PE=1_SV=1	8.00E-37
comp28296_c0_seq3.p1	sp|P22589|UBIQP_PHYIN_Polyubiquitin_OS=Phytophthora_infestans_PE=1_SV=2	8.00E-65
comp28298_c0_seq5.p1		
comp28298_c0_seq5.p3	sp|Q60482|RPC9_CAVPO_DNA-directed_RNA_polymerase_III_subunit_RPC9_OS=Cavia_porcellus_GN=CRCP_PE=2_SV=1	4.00E-13
comp28299_c0_seq3.p1	sp|Q8RNT4|LOX_PSEA1_Oleic_acid_lipoxygenase_OS=Pseudomonas_aeruginosa_GN=lox_PE=1_SV=2	3.00E-26
comp28300_c1_seq2.p1		
comp28300_c2_seq2.p1		
comp28301_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	2.00E-32
comp28301_c0_seq2.p1		
comp28302_c0_seq1.p1		
comp28302_c0_seq2.p1		
comp28302_c0_seq3.p1		
comp28303_c1_seq3.p1	sp|Q0VND7|RLMN_ALCBS_Ribosomal_RNA_large_subunit_methyltransferase_N_OS=Alcanivorax_borkumensis_(strain_SK2_/_ATCC_700651_/_DSM_11573)_GN=rlmN_PE=3_SV=1	1.00E-58
comp28304_c0_seq1.p1	sp|Q15027|ACAP1_HUMAN_Arf-GAP_with_coiled-coil,_ANK_repeat_and_PH_domain-containing_protein_1_OS=Homo_sapiens_GN=ACAP1_PE=1_SV=1	2.00E-42
comp28305_c0_seq1.p1		
comp28307_c0_seq1.p1	sp|Q9LT31|VPS9A_ARATH_Vacuolar_protein_sorting-associated_protein_9A_OS=Arabidopsis_thaliana_GN=VPS9A_PE=1_SV=1	8.00E-23
comp28308_c0_seq1.p1	sp|Q9Z2D7|MBD4_MOUSE_Methyl-CpG-binding_domain_protein_4_OS=Mus_musculus_GN=Mbd4_PE=1_SV=1	3.00E-26
comp28308_c0_seq2.p1	sp|Q9Z2D7|MBD4_MOUSE_Methyl-CpG-binding_domain_protein_4_OS=Mus_musculus_GN=Mbd4_PE=1_SV=1	2.00E-26
comp28309_c0_seq1.p1	sp|Q61493|DPOLZ_MOUSE_DNA_polymerase_zeta_catalytic_subunit_OS=Mus_musculus_GN=Rev3l_PE=2_SV=3	1.00E-96
comp28309_c0_seq3.p3		
comp28310_c0_seq1.p1		
comp28310_c1_seq1.p1		
comp28310_c2_seq1.p1		
comp28310_c3_seq1.p2		
comp28310_c3_seq3.p1		
comp28311_c0_seq1.p1		
comp28312_c0_seq3.p1		
comp28314_c0_seq1.p1		
comp28314_c0_seq1.p2	sp|O74918|RRP45_SCHPO_Exosome_complex_component_rrp45_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rrp45_PE=2_SV=1	6.00E-54
comp28315_c0_seq1.p1	sp|Q8CFJ7|S2545_MOUSE_Solute_carrier_family_25_member_45_OS=Mus_musculus_GN=Slc25a45_PE=2_SV=1	3.00E-36
comp28315_c0_seq2.p3		
comp28316_c0_seq4.p1		
comp28316_c0_seq7.p1		
comp28317_c0_seq1.p1	sp|P14672|GTR4_HUMAN_Solute_carrier_family_2,_facilitated_glucose_transporter_member_4_OS=Homo_sapiens_GN=SLC2A4_PE=1_SV=1	7.00E-71
comp28318_c1_seq1.p2		
comp28318_c1_seq7.p1		
comp28319_c1_seq2.p1		
comp28319_c1_seq3.p1		
comp28320_c0_seq1.p1		
comp28320_c0_seq1.p3	sp|Q6GLK2|THEM4_XENLA_Thioesterase_superfamily_member_4_OS=Xenopus_laevis_GN=them4_PE=2_SV=2	3.00E-12
comp28320_c0_seq3.p1		
comp28320_c0_seq4.p1		
comp28320_c0_seq4.p3	sp|Q6GLK2|THEM4_XENLA_Thioesterase_superfamily_member_4_OS=Xenopus_laevis_GN=them4_PE=2_SV=2	3.00E-12
comp28321_c0_seq1.p1		
comp28321_c0_seq3.p1		
comp28321_c0_seq4.p1		
comp28322_c0_seq2.p1	sp|Q94A68|Y1669_ARATH_Uncharacterized_oxidoreductase_At1g06690,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g06690_PE=1_SV=1	9.00E-68
comp28322_c0_seq3.p1	sp|Q94A68|Y1669_ARATH_Uncharacterized_oxidoreductase_At1g06690,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g06690_PE=1_SV=1	9.00E-68
comp28323_c0_seq1.p1	sp|P55786|PSA_HUMAN_Puromycin-sensitive_aminopeptidase_OS=Homo_sapiens_GN=NPEPPS_PE=1_SV=2	0
comp28323_c0_seq3.p1		
comp28324_c0_seq3.p1	sp|B5F860|MSRB_SALA4_Peptide_methionine_sulfoxide_reductase_MsrB_OS=Salmonella_agona_(strain_SL483)_GN=msrB_PE=3_SV=1	2.00E-14
comp28325_c0_seq4.p1	sp|Q51371|ALGG_PSEAE_Poly(beta-D-mannuronate)_C5_epimerase_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=algG_PE=1_SV=1	4.00E-19
comp28326_c0_seq1.p3		
comp28327_c0_seq2.p1		
comp28328_c0_seq1.p1	sp|Q9UPV0|CE164_HUMAN_Centrosomal_protein_of_164_kDa_OS=Homo_sapiens_GN=CEP164_PE=1_SV=3	6.00E-26
comp28328_c0_seq2.p1	sp|Q9UPV0|CE164_HUMAN_Centrosomal_protein_of_164_kDa_OS=Homo_sapiens_GN=CEP164_PE=1_SV=3	1.00E-24
comp28328_c0_seq3.p1	sp|Q9UPV0|CE164_HUMAN_Centrosomal_protein_of_164_kDa_OS=Homo_sapiens_GN=CEP164_PE=1_SV=3	6.00E-25
comp28328_c0_seq3.p2		
comp28328_c0_seq4.p1	sp|Q9UPV0|CE164_HUMAN_Centrosomal_protein_of_164_kDa_OS=Homo_sapiens_GN=CEP164_PE=1_SV=3	6.00E-25
comp28328_c0_seq4.p2		
comp28329_c0_seq1.p1		
comp28330_c0_seq2.p2		
comp28331_c0_seq2.p1		
comp28333_c0_seq1.p1		
comp28333_c0_seq2.p1		
comp28334_c0_seq1.p2	sp|Q4KM49|SYYC_RAT_Tyrosine--tRNA_ligase,_cytoplasmic_OS=Rattus_norvegicus_GN=Yars_PE=2_SV=3	9.00E-20
comp28334_c0_seq1.p3	sp|Q9ZTS1|SYM_ORYSJ_Probable_methionine--tRNA_ligase_OS=Oryza_sativa_subsp._japonica_GN=Os06g0508700_PE=2_SV=2	7.00E-11
comp28334_c0_seq2.p1	sp|Q9ZTS1|SYM_ORYSJ_Probable_methionine--tRNA_ligase_OS=Oryza_sativa_subsp._japonica_GN=Os06g0508700_PE=2_SV=2	4.00E-36
comp28336_c0_seq6.p2		
comp28342_c0_seq1.p1		
comp28342_c0_seq2.p1		
comp28343_c0_seq2.p1	sp|Q54GX5|PEX1_DICDI_Peroxisome_biogenesis_factor_1_OS=Dictyostelium_discoideum_GN=pex1_PE=3_SV=1	8.00E-84
comp28343_c0_seq2.p2	sp|Q54GX5|PEX1_DICDI_Peroxisome_biogenesis_factor_1_OS=Dictyostelium_discoideum_GN=pex1_PE=3_SV=1	1.00E-14
comp28344_c1_seq3.p1	sp|Q86VS8|HOOK3_HUMAN_Protein_Hook_homolog_3_OS=Homo_sapiens_GN=HOOK3_PE=1_SV=2	5.00E-55
comp28345_c0_seq1.p1		
comp28345_c0_seq2.p1		
comp28351_c0_seq1.p1	sp|Q99733|NP1L4_HUMAN_Nucleosome_assembly_protein_1-like_4_OS=Homo_sapiens_GN=NAP1L4_PE=1_SV=1	8.00E-28
comp28351_c0_seq2.p1	sp|Q99ND9|RWDD1_RAT_RWD_domain-containing_protein_1_OS=Rattus_norvegicus_GN=Rwdd1_PE=2_SV=1	2.00E-13
comp28351_c1_seq1.p1	sp|Q0VGM9|RTEL1_MOUSE_Regulator_of_telomere_elongation_helicase_1_OS=Mus_musculus_GN=Rtel1_PE=2_SV=2	1.00E-155
comp28352_c0_seq4.p1		
comp28355_c0_seq1.p1		
comp28355_c0_seq3.p1		
comp28355_c0_seq6.p1		
comp28355_c0_seq7.p1		
comp28355_c0_seq9.p1		
comp28356_c0_seq1.p2	sp|P23358|RL12_RAT_60S_ribosomal_protein_L12_OS=Rattus_norvegicus_GN=Rpl12_PE=2_SV=1	1.00E-61
comp28357_c0_seq1.p1	sp|Q9ZVH4|CUL3A_ARATH_Cullin-3A_OS=Arabidopsis_thaliana_GN=CUL3A_PE=1_SV=1	0
comp28359_c0_seq1.p1		
comp28362_c0_seq1.p1	sp|A0KJ48|DER_AERHH_GTPase_Der_OS=Aeromonas_hydrophila_subsp._hydrophila_(strain_ATCC_7966_/_NCIB_9240)_GN=der_PE=3_SV=1	5.00E-25
comp28362_c0_seq2.p1	sp|Q2GA15|DER_NOVAD_GTPase_Der_OS=Novosphingobium_aromaticivorans_(strain_DSM_12444)_GN=der_PE=3_SV=1	1.00E-102
comp28364_c0_seq1.p1	sp|B2GUZ1|UBP4_RAT_Ubiquitin_carboxyl-terminal_hydrolase_4_OS=Rattus_norvegicus_GN=Usp4_PE=1_SV=1	2.00E-61
comp28364_c0_seq2.p1	sp|B2GUZ1|UBP4_RAT_Ubiquitin_carboxyl-terminal_hydrolase_4_OS=Rattus_norvegicus_GN=Usp4_PE=1_SV=1	2.00E-61
comp28365_c0_seq1.p1	sp|Q54C67|CLCF_DICDI_Chloride_channel_protein_F_OS=Dictyostelium_discoideum_GN=clcF_PE=3_SV=1	2.00E-46
comp28366_c0_seq1.p1	sp|Q4KLF8|ARPC5_RAT_Actin-related_protein_2/3_complex_subunit_5_OS=Rattus_norvegicus_GN=Arpc5_PE=1_SV=3	9.00E-18
comp28367_c0_seq2.p1		
comp28367_c0_seq2.p2		
comp28367_c0_seq2.p5		
comp28370_c0_seq1.p1		
comp28370_c0_seq4.p1		
comp28372_c0_seq1.p1		
comp28376_c0_seq1.p1	sp|P20449|DBP5_YEAST_ATP-dependent_RNA_helicase_DBP5_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=DBP5_PE=1_SV=2	5.00E-91
comp28376_c0_seq2.p1	sp|P20449|DBP5_YEAST_ATP-dependent_RNA_helicase_DBP5_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=DBP5_PE=1_SV=2	7.00E-97
comp28376_c0_seq3.p1	sp|P20449|DBP5_YEAST_ATP-dependent_RNA_helicase_DBP5_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=DBP5_PE=1_SV=2	6.00E-79
comp28376_c0_seq4.p1	sp|P20449|DBP5_YEAST_ATP-dependent_RNA_helicase_DBP5_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=DBP5_PE=1_SV=2	3.00E-73
comp28377_c0_seq1.p1		
comp28381_c0_seq1.p1		
comp28382_c0_seq2.p1	sp|Q21YM7|F16A1_RHOFD_Fructose-1,6-bisphosphatase_class_1_1_OS=Rhodoferax_ferrireducens_(strain_DSM_15236_/_ATCC_BAA-621_/_T118)_GN=fbp1_PE=3_SV=1	1.00E-24
comp28382_c0_seq4.p1	sp|Q07204|F16P1_BRANA_Fructose-1,6-bisphosphatase,_chloroplastic_OS=Brassica_napus_GN=FBP_PE=2_SV=1	4.00E-35
comp28383_c0_seq1.p1		
comp28383_c0_seq12.p1		
comp28383_c0_seq15.p4		
comp28383_c0_seq17.p2		
comp28383_c0_seq5.p4		
comp28383_c0_seq7.p1		
comp28383_c0_seq9.p4		
comp28385_c0_seq7.p1		
comp28385_c0_seq7.p2	sp|Q9LEV3|CBSX3_ARATH_CBS_domain-containing_protein_CBSX3,_mitochondrial_OS=Arabidopsis_thaliana_GN=CBSX3_PE=1_SV=1	6.00E-18
comp28386_c0_seq2.p2		

comp28388_c0_seq1.p1	sp|Q3SWX9|RAD21_BOVIN_Double-strand-break_repair_protein_rad21_homolog_OS=Bos_taurus_GN=RAD21_PE=2_SV=1	4.00E-35	GO:0000228,GO:0000775,GO:0000775,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0006281,GO:0006357,GO:0006915,GO:0006974,GO:0007049,GO:0007059,GO:0007067,GO:0008278,GO:0016020,GO:0034991,GO:0051301,GO:0071168,GO:0071168	nuclear chromosome,chromosome, centromeric region,chromosome, centromeric region,nucleus,nucleus,nucleus,chromosome,chromosome,DNA repair,regulation of transcription from RNA polymerase II promoter,apoptotic process,cellular response to DNA damage stimulus,cell cycle,chromosome segregation,mitotic nuclear division,cohesin complex,membrane,nuclear meiotic cohesin complex,cell division,protein localization to chromatin,protein localization to chromatin
comp28390_c0_seq1.p1	sp|Q5E9I7|MEP50_BOVIN_Methylosome_protein_50_OS=Bos_taurus_GN=WDR77_PE=2_SV=1	4.00E-26	GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0034709	nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,cytosol,methylosome
comp28390_c0_seq3.p1				
comp28391_c0_seq1.p2	sp|P17804|HSP70_LEIDO_Heat_shock_70_kDa_protein_OS=Leishmania_donovani_GN=HSP70_PE=3_SV=1	2.00E-155	GO:0000166,GO:0005524	nucleotide binding,ATP binding
comp28393_c0_seq2.p1				
comp28394_c0_seq1.p1				
comp28394_c0_seq2.p1				
comp28395_c0_seq1.p1				
comp28396_c0_seq1.p2				
comp28396_c0_seq1.p4				
comp28397_c0_seq1.p1	sp|Q9NR09|BIRC6_HUMAN_Baculoviral_IAP_repeat-containing_protein_6_OS=Homo_sapiens_GN=BIRC6_PE=1_SV=2	4.00E-44	GO:0000922,GO:0000922,GO:0001890,GO:0004842,GO:0004842,GO:0004842,GO:0004869,GO:0004869,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005768,GO:0005768,GO:0005768,GO:0005794,GO:0005794,GO:0005802,GO:0005815,GO:0005815,GO:0005856,GO:0006468,GO:0006915,GO:0006915,GO:0007049,GO:0007067,GO:0008284,GO:0010466,GO:0010951,GO:0010951,GO:0016020,GO:0016020,GO:0016020,GO:0016567,GO:0016874,GO:0016881,GO:0030414,GO:0030496,GO:0030496,GO:0032465,GO:0032465,GO:0042127,GO:0042127,GO:0043066,GO:0043066,GO:0043066,GO:0051301,GO:0060711,GO:0060712,GO:2001237	spindle pole,spindle pole,placenta development,ubiquitin-protein transferase activity,ubiquitin-protein transferase activity,ubiquitin-protein transferase activity,cysteine-type endopeptidase inhibitor activity,cysteine-type endopeptidase inhibitor activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,cytoplasm,endosome,endosome,endosome,Golgi apparatus,Golgi apparatus,trans-Golgi network,microtubule organizing center,microtubule organizing center,cytoskeleton,protein phosphorylation,apoptotic process,apoptotic process,cell cycle,mitotic nuclear division,positive regulation of cell proliferation,negative regulation of peptidase activity,negative regulation of endopeptidase activity,negative regulation of endopeptidase activity,membrane,membrane,membrane,protein ubiquitination,ligase activity,acid-amino acid ligase activity,peptidase inhibitor activity,midbody,midbody,regulation of cytokinesis,regulation of cytokinesis,regulation of cell proliferation,regulation of cell proliferation,negative regulation of apoptotic process,negative regulation of apoptotic process,negative regulation of apoptotic process,cell division,labyrinthine layer development,spongiotrophoblast layer development,negative regulation of extrinsic apoptotic signaling pathway
comp28397_c0_seq1.p2				
comp28398_c0_seq3.p1				
comp28399_c0_seq1.p1				
comp28401_c0_seq3.p1	sp|Q54YD4|SYIC_DICDI_Probable_isoleucine--tRNA_ligase,_cytoplasmic_OS=Dictyostelium_discoideum_GN=ileS_PE=3_SV=1	0	GO:0000166,GO:0000166,GO:0002161,GO:0004812,GO:0004812,GO:0004822,GO:0004822,GO:0004822,GO:0004822,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0006412,GO:0006418,GO:0006428,GO:0006428,GO:0006450,GO:0016874,GO:0044351	nucleotide binding,nucleotide binding,aminoacyl-tRNA editing activity,aminoacyl-tRNA ligase activity,aminoacyl-tRNA ligase activity,isoleucine-tRNA ligase activity,isoleucine-tRNA ligase activity,isoleucine-tRNA ligase activity,isoleucine-tRNA ligase activity,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytosol,cytosol,translation,tRNA aminoacylation for protein translation,isoleucyl-tRNA aminoacylation,isoleucyl-tRNA aminoacylation,regulation of translational fidelity,ligase activity,macropinocytosis
comp28402_c0_seq1.p1				
comp28402_c0_seq2.p1	sp|Q9LZF6|CD48E_ARATH_Cell_division_control_protein_48_homolog_E_OS=Arabidopsis_thaliana_GN=CDC48E_PE=1_SV=2	0	GO:0000166,GO:0005515,GO:0005524,GO:0005524,GO:0005618,GO:0005634,GO:0005634,GO:0005737,GO:0005794,GO:0005829,GO:0005856,GO:0006810,GO:0007049,GO:0008152,GO:0009524,GO:0015031,GO:0016787,GO:0051301	nucleotide binding,protein binding,ATP binding,ATP binding,cell wall,nucleus,nucleus,cytoplasm,Golgi apparatus,cytosol,cytoskeleton,transport,cell cycle,metabolic process,phragmoplast,protein transport,hydrolase activity,cell division
comp28402_c1_seq2.p1	sp|Q8K3A0|HSC20_MOUSE_Iron-sulfur_cluster_co-chaperone_protein_HscB,_mitochondrial_OS=Mus_musculus_GN=Hscb_PE=2_SV=2	7.00E-23	GO:0003674,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0005739,GO:0005739,GO:0005813,GO:0005886,GO:0006457,GO:0016226,GO:0046872,GO:0051087,GO:0051259	molecular_function,cytoplasm,cytoplasm,cytoplasm,mitochondrion,mitochondrion,mitochondrion,centrosome,plasma membrane,protein folding,iron-sulfur cluster assembly,metal ion binding,chaperone binding,protein oligomerization
comp28402_c1_seq2.p2				
comp28402_c2_seq2.p1				
comp28403_c0_seq1.p1				
comp28403_c1_seq1.p1				
comp28403_c1_seq2.p1				
comp28403_c1_seq3.p1				
comp28406_c0_seq2.p1				
comp28407_c0_seq1.p1				
comp28408_c0_seq2.p1				
comp28408_c0_seq3.p1	sp|P49695|PKWA_THECU_Probable_serine/threonine-protein_kinase_pkwA_OS=Thermomonospora_curvata_GN=pkwA_PE=3_SV=1	6.00E-14	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp28408_c0_seq4.p1				
comp28408_c0_seq6.p1	sp|O15736|TIPD_DICDI_Protein_tipD_OS=Dictyostelium_discoideum_GN=tipD_PE=3_SV=1	6.00E-39	GO:0000045,GO:0000421,GO:0016236,GO:0019776,GO:0030587,GO:0031154,GO:0034274	autophagic vacuole assembly,autophagic vacuole membrane,macroautophagy,Atg8 ligase activity,sorocarp development,culmination involved in sorocarp development,Atg12-Atg5-Atg16 complex
comp28409_c0_seq1.p1	sp|Q90W04|NGB_TETNG_Neuroglobin_OS=Tetraodon_nigroviridis_GN=ngb_PE=2_SV=1	5.00E-12	GO:0001666,GO:0005344,GO:0005506,GO:0005737,GO:0005737,GO:0006810,GO:0015671,GO:0015671,GO:0019825,GO:0020037,GO:0043204,GO:0046872	response to hypoxia,oxygen transporter activity,iron ion binding,cytoplasm,cytoplasm,transport,oxygen transport,oxygen transport,oxygen binding,heme binding,perikaryon,metal ion binding
comp28410_c0_seq1.p1	sp|Q68EI0|WDR18_DANRE_WD_repeat-containing_protein_18_OS=Danio_rerio_GN=wdr18_PE=2_SV=1	1.00E-34	GO:0007275,GO:0007368,GO:0007368,GO:0007368,GO:0007368,GO:0070121,GO:0070121,GO:0070121	multicellular organismal development,determination of left/right symmetry,determination of left/right symmetry,determination of left/right symmetry,determination of left/right symmetry,Kupffer's vesicle development,Kupffer's vesicle development,Kupffer's vesicle development
comp28411_c0_seq1.p1				
comp28411_c0_seq2.p1				
comp28411_c0_seq4.p1				
comp28411_c0_seq5.p2				
comp28417_c0_seq1.p1	sp|P28998|DHE4_CHLSO_NADP-specific_glutamate_dehydrogenase_(Fragment)_OS=Chlorella_sorokiniana_PE=2_SV=1	9.00E-119	GO:0004354,GO:0006520,GO:0009507,GO:0009507,GO:0009536,GO:0016491,GO:0016491,GO:0016639,GO:0055114,GO:0055114	glutamate dehydrogenase (NADP+) activity,cellular amino acid metabolic process,chloroplast,chloroplast,plastid,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,oxidation-reduction process,oxidation-reduction process
comp28418_c0_seq1.p1				
comp28420_c0_seq2.p1				
comp28420_c0_seq5.p1				
comp28420_c0_seq5.p4				
comp28420_c0_seq6.p1				
comp28421_c0_seq1.p1				

comp28636_c0_seq8.p1	sp|P0AEB5|YNAI_ECOLI_MscS_family_inner_membrane_protein_YnaI_OS=Escherichia_coli_(strain_K12)_GN=ynaI_PE=1_SV=1	1.00E-27	[illegible]	[illegible]
comp28636_c0_seq8.p2	sp|Q8PHB6|Y3343_XANAC_Macro_domain-containing_protein_XAC3343_OS=Xanthomonas_axonopodis_pv._citri_(strain_306)_GN=XAC3343_PE=4_SV=2	1.00E-44		
comp28637_c0_seq2.p1				
comp28638_c0_seq1.p3				
comp28638_c0_seq2.p1				
comp28642_c0_seq2.p2				
comp28642_c0_seq3.p1				
comp28643_c0_seq2.p1				
comp28644_c0_seq1.p1	sp|O67716|DHAS_AQUAE_Aspartate-semialdehyde_dehydrogenase_OS=Aquifex_aeolicus_(strain_VF5)_GN=asd_PE=3_SV=1	7.00E-93	[illegible]	[illegible]
comp28644_c0_seq1.p2				
comp28644_c0_seq2.p1	sp|O67716|DHAS_AQUAE_Aspartate-semialdehyde_dehydrogenase_OS=Aquifex_aeolicus_(strain_VF5)_GN=asd_PE=3_SV=1	7.00E-93	[illegible]	[illegible]
comp28644_c0_seq2.p2				
comp28646_c0_seq1.p1	sp|Q99638|RAD9A_HUMAN_Cell_cycle_checkpoint_control_protein_RAD9A_OS=Homo_sapiens_GN=RAD9A_PE=1_SV=1	3.00E-24	[illegible]	[illegible]
comp28647_c0_seq1.p1				
comp28647_c0_seq1.p4				
comp28647_c0_seq5.p1	sp|Q8BRC6|AAT1_MOUSE_AMY-1-associating_protein_expressed_in_testis_1_homolog_OS=Mus_musculus_GN=Aat1_PE=2_SV=2	5.00E-14	[illegible]	[illegible]
comp28651_c0_seq1.p1				
comp28653_c0_seq2.p1				
comp28653_c0_seq2.p3				
comp28654_c0_seq2.p1				
comp28655_c0_seq1.p1				
comp28659_c0_seq1.p1	sp|P42593|FADH_ECOLI_2,4-dienoyl-CoA_reductase_[NADPH]_OS=Escherichia_coli_(strain_K12)_GN=fadH_PE=1_SV=3	0	[illegible]	[illegible]
comp28659_c0_seq2.p1	sp|P42593|FADH_ECOLI_2,4-dienoyl-CoA_reductase_[NADPH]_OS=Escherichia_coli_(strain_K12)_GN=fadH_PE=1_SV=3	2.00E-25	[illegible]	[illegible]
comp28661_c0_seq1.p1	sp|Q9M0V3|DDB1A_ARATH_DNA_damage-binding_protein_1a_OS=Arabidopsis_thaliana_GN=DDB1A_PE=1_SV=1	0	[illegible]	[illegible]
comp28661_c0_seq1.p2				
comp28662_c0_seq2.p1				
comp28663_c0_seq1.p1				
comp28664_c0_seq1.p1				
comp28664_c0_seq2.p1	sp|P41150|CAYP1_RABIT_Calcyphosin_OS=Oryctolagus_cuniculus_GN=CAPS_PE=1_SV=1	7.00E-25	GO:0005509,GO:0005737,GO:0005737,GO:0046872	[illegible]
comp28665_c0_seq4.p1				
comp28665_c0_seq5.p1				
comp28666_c0_seq1.p1				
comp28667_c0_seq1.p1	sp|Q5R7X2|SR140_PONAB_U2_snRNP-associated_SURP_motif-containing_protein_OS=Pongo_abelii_GN=U2SURP_PE=2_SV=1	5.00E-45	GO:0000166,GO:0003676,GO:0003723,GO:0003723,GO:0005634,GO:0005634,GO:0006396	[illegible]
comp28667_c0_seq2.p1				
comp28669_c0_seq1.p1				
comp28669_c1_seq1.p1				
comp28669_c1_seq2.p1				
comp28670_c0_seq3.p1				
comp28671_c0_seq2.p1	sp|Q9JHW4|SELB_MOUSE_Selenocysteine-specific_elongation_factor_OS=Mus_musculus_GN=Eefsec_PE=2_SV=2	2.00E-52	[illegible]	[illegible]
comp28671_c0_seq2.p2	sp|Q9DAN9|CQ105_MOUSE_Uncharacterized_protein_C17orf105_homolog_OS=Mus_musculus_PE=2_SV=1	6.00E-12	GO:0003674,GO:0005575,GO:0008150	[illegible]
comp28672_c0_seq3.p1				
comp28673_c0_seq1.p1	sp|Q39027|MPK7_ARATH_Mitogen-activated_protein_kinase_7_OS=Arabidopsis_thaliana_GN=MPK7_PE=2_SV=2	5.00E-97	[illegible]	[illegible]
comp28673_c0_seq2.p1	sp|Q84UI5|MPK1_ORYSJ_Mitogen-activated_protein_kinase_1_OS=Oryza_sativa_subsp._japonica_GN=MPK1_PE=1_SV=1	1.00E-62	[illegible]	[illegible]
comp28673_c0_seq3.p1	sp|P78575|ERG24_ASCIM_Delta(14)-sterol_reductase_OS=Ascobolus_immersus_GN=ERG3_PE=3_SV=1	1.00E-109	[illegible]	[illegible]
comp28673_c0_seq3.p2	sp|Q40531|NTF6_TOBAC_Mitogen-activated_protein_kinase_homolog_NTF6_OS=Nicotiana_tabacum_GN=NTF6_PE=2_SV=1	3.00E-112	[illegible]	[illegible]
comp28674_c0_seq1.p1				
comp28675_c0_seq1.p1	sp|Q12874|SF3A3_HUMAN_Splicing_factor_3A_subunit_3_OS=Homo_sapiens_GN=SF3A3_PE=1_SV=1	1.00E-117	[illegible]	[illegible]
comp28675_c0_seq1.p2				
comp28676_c0_seq3.p1				
comp28677_c0_seq1.p1	sp|Q3UF64|RNFT2_MOUSE_RING_finger_and_transmembrane_domain-containing_protein_2_OS=Mus_musculus_GN=Rnft2_PE=2_SV=2	4.00E-15	[illegible]	[illegible]
comp28677_c0_seq2.p1				
comp28678_c0_seq2.p1	sp|Q9VTF9|UFD1_DROME_Ubiquitin_fusion_degradation_protein_1_homolog_OS=Drosophila_melanogaster_GN=Ufd1-like_PE=2_SV=1	1.00E-17	GO:0000502,GO:0006508,GO:0006511,GO:0006511,GO:0032436,GO:0098586	[illegible]
comp28678_c0_seq3.p1	sp|Q8K2U2|ALKB6_MOUSE_Probable_alpha-ketoglutarate-dependent_dioxygenase_ABH6_OS=Mus_musculus_GN=Alkbh6_PE=2_SV=2	3.00E-15	[illegible]	[illegible]
comp28678_c0_seq4.p1	sp|Q9VTF9|UFD1_DROME_Ubiquitin_fusion_degradation_protein_1_homolog_OS=Drosophila_melanogaster_GN=Ufd1-like_PE=2_SV=1	2.00E-13	GO:0000502,GO:0006508,GO:0006511,GO:0006511,GO:0032436,GO:0098586	[illegible]
comp28679_c0_seq1.p1	sp|Q5JTH9|RRP12_HUMAN_RRP12-like_protein_OS=Homo_sapiens_GN=RRP12_PE=1_SV=2	3.00E-48	[illegible]	[illegible]
comp28680_c0_seq1.p1	sp|Q58CW5|SERC2_BOVIN_Serine_incorporator_2_OS=Bos_taurus_GN=SERINC2_PE=2_SV=1	2.00E-12	[illegible]	[illegible]
comp28680_c0_seq2.p1	sp|Q58CW5|SERC2_BOVIN_Serine_incorporator_2_OS=Bos_taurus_GN=SERINC2_PE=2_SV=1	3.00E-12	[illegible]	[illegible]
comp28681_c0_seq1.p1	sp|Q54VF1|DDX56_DICDI_Probable_ATP-dependent_RNA_helicase_ddx56_OS=Dictyostelium_discoideum_GN=ddx56_PE=3_SV=1	3.00E-95	[illegible]	[illegible]
comp28681_c0_seq3.p1	sp|Q54VF1|DDX56_DICDI_Probable_ATP-dependent_RNA_helicase_ddx56_OS=Dictyostelium_discoideum_GN=ddx56_PE=3_SV=1	3.00E-92	[illegible]	[illegible]
comp28683_c0_seq3.p2				
comp28683_c0_seq4.p2				
comp28683_c0_seq4.p3	sp|Q8DHM0|SSRP_THEEB_SsrA-binding_protein_OS=Thermosynechococcus_elongatus_(strain_BP-1)_GN=smpB_PE=3_SV=1	1.00E-30	GO:0003723,GO:0003723,GO:0003723,GO:0005737,GO:0005737,GO:0005737	[illegible]
comp28683_c0_seq5.p1				
comp28683_c0_seq5.p2	sp|Q8DHM0|SSRP_THEEB_SsrA-binding_protein_OS=Thermosynechococcus_elongatus_(strain_BP-1)_GN=smpB_PE=3_SV=1	1.00E-30	GO:0003723,GO:0003723,GO:0003723,GO:0005737,GO:0005737,GO:0005737	[illegible]
comp28683_c0_seq5.p3				
comp28684_c0_seq1.p1				
comp28684_c0_seq2.p1				
comp28685_c0_seq4.p1				
comp28686_c0_seq1.p1	sp|Q99JN2|KLH22_MOUSE_Kelch-like_protein_22_OS=Mus_musculus_GN=Klhl22_PE=1_SV=1	3.00E-12	[illegible]	[illegible]
comp28689_c0_seq2.p1	sp|Q5PQL2|RCD1_RAT_Cell_differentiation_protein_RCD1_homolog_OS=Rattus_norvegicus_GN=Rqcd1_PE=1_SV=1	6.00E-130	[illegible]	[illegible]
comp28690_c0_seq2.p1				
comp28690_c0_seq2.p2				
comp28691_c0_seq1.p1				
comp28692_c0_seq2.p1	sp|B1XIF6|DCUP_SYNP2_Uroporphyrinogen_decarboxylase_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=hemE_PE=3_SV=1	6.00E-143	[illegible]	[illegible]
comp28693_c0_seq1.p1				
comp28693_c0_seq2.p1				
comp28694_c0_seq1.p1	sp|P47959|HPRT_MERUN_Hypoxanthine-guanine_phosphoribosyltransferase_OS=Meriones_unguiculatus_GN=HPRT1_PE=2_SV=2	1.00E-64	[illegible]	[illegible]
comp28694_c0_seq2.p1	sp|P27605|HPRT_RAT_Hypoxanthine-guanine_phosphoribosyltransferase_OS=Rattus_norvegicus_GN=Hprt1_PE=1_SV=1	6.00E-53	[illegible]	[illegible]
comp28695_c0_seq2.p1				
comp28695_c0_seq3.p1				
comp28695_c0_seq4.p1				
comp28696_c0_seq1.p1				
comp28696_c0_seq2.p1				
comp28696_c0_seq3.p1				
comp28696_c0_seq4.p1				
comp28698_c0_seq2.p1				
comp28700_c0_seq2.p1	sp|O34355|YTCJ_BACSU_Putative_amidohydrolase_ytcJ_OS=Bacillus_subtilis_GN=ytcJ_PE=4_SV=1	8.00E-53	GO:0008152,GO:0008152,GO:0016787,GO:0016810	[illegible]
comp28701_c0_seq1.p2				
comp28702_c0_seq1.p1				
comp28702_c0_seq2.p1				
comp28702_c0_seq5.p1				
comp28702_c0_seq6.p1				
comp28702_c0_seq7.p1				
comp28703_c0_seq2.p1				
comp28703_c0_seq3.p1				
comp28703_c0_seq4.p1				
comp28704_c0_seq2.p1	sp|P63159|HMGB1_RAT_High_mobility_group_protein_B1_OS=Rattus_norvegicus_GN=Hmgb1_PE=1_SV=2	6.00E-29	[illegible]	[illegible]
comp28705_c0_seq6.p1				
comp28707_c0_seq3.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-32	[illegible]	[illegible]
comp28707_c0_seq5.p1	sp|Q9SKX0|AB13C_ARATH_ABC_transporter_C_family_member_13_OS=Arabidopsis_thaliana_GN=ABCC13_PE=2_SV=3	2.00E-124	[illegible]	[illegible]
comp28707_c0_seq7.p1	sp|Q9SKX0|AB13C_ARATH_ABC_transporter_C_family_member_13_OS=Arabidopsis_thaliana_GN=ABCC13_PE=2_SV=3	2.00E-124	[illegible]	[illegible]
comp28707_c1_seq1.p2				
comp28708_c1_seq1.p1				
comp28711_c0_seq2.p1	sp|Q55158|RIBD_SYNY3_Riboflavin_biosynthesis_protein_RibD_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=ribD_PE=3_SV=1	2.00E-37	[illegible]	[illegible]
comp28711_c0_seq2.p3				
comp28712_c0_seq1.p1	sp|O76460|RAD54_DROME_DNA_repair_and_recombination_protein_RAD54-like_OS=Drosophila_melanogaster_GN=okr_PE=1_SV=1	2.00E-43	[illegible]	[illegible]
comp28712_c0_seq2.p1	sp|P41410|RAD54_SCHPO_DNA_repair_protein_rhp54_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rhp54_PE=1_SV=2	1.00E-52	[illegible]	[illegible]
comp28713_c0_seq3.p1	sp|Q54BW6|TTC27_DICDI_Tetratricopeptide_repeat_protein_27_homolog_OS=Dictyostelium_discoideum_GN=ttc27_PE=3_SV=1	5.00E-78		
comp28713_c0_seq5.p1	sp|Q54BW6|TTC27_DICDI_Tetratricopeptide_repeat_protein_27_homolog_OS=Dictyostelium_discoideum_GN=ttc27_PE=3_SV=1	3.00E-70		
comp28716_c0_seq1.p1	sp|Q56X52|AOX4_ARATH_Alternative_oxidase_4,_chloroplastic/chromoplastic_OS=Arabidopsis_thaliana_GN=AOX4_PE=1_SV=2	5.00E-66	[illegible]	[illegible]
comp28716_c0_seq1.p3	sp|Q9NRN9|METL5_HUMAN_Methyltransferase-like_protein_5_OS=Homo_sapiens_GN=METTL5_PE=1_SV=1	2.00E-45	GO:0003676,GO:0008168,GO:0008168,GO:0016740,GO:0032259,GO:0032259	[illegible]
comp28717_c0_seq1.p1				
comp28718_c0_seq1.p1	sp|Q6GL69|MK67I_XENTR_MKI67_FHA_domain-interacting_nucleolar_phosphoprotein-like_OS=Xenopus_tropicalis_GN=mki67ipl_PE=2_SV=1	3.00E-36	GO:0000166,GO:0003676,GO:0003723,GO:0005634,GO:0005730,GO:0010923	[illegible]
comp28718_c0_seq1.p2	sp|Q8VY21|TLP3_ARATH_Tubby-like_F-box_protein_3_OS=Arabidopsis_thaliana_GN=TULP3_PE=2_SV=1	1.00E-15	[illegible]	[illegible]
comp28720_c0_seq1.p1				
comp28720_c0_seq3.p1				
comp28720_c0_seq4.p1				
comp28721_c0_seq1.p1				
comp28722_c0_seq11.p1				
comp28722_c0_seq13.p1				
comp28722_c0_seq2.p1				
comp28722_c0_seq5.p1				
comp28722_c0_seq5.p2				
comp28722_c0_seq6.p1				
comp28722_c0_seq7.p1				
comp28722_c0_seq7.p2				
comp28723_c0_seq1.p1	sp|Q6AXU4|RN181_RAT_E3_ubiquitin-protein_ligase_RNF181_OS=Rattus_norvegicus_GN=Rnf181_PE=1_SV=1	4.00E-12	GO:0004842,GO:0008270,GO:0016567,GO:0016874,GO:0046872,GO:0051865	[illegible]
comp28725_c0_seq1.p1	sp|Q55CT5|SEC31_DICDI_Protein_transport_protein_SEC31_OS=Dictyostelium_discoideum_GN=sec31_PE=3_SV=1	5.00E-107	[illegible]	[illegible]
comp28728_c1_seq1.p4				
comp28729_c0_seq2.p1				
comp28730_c0_seq1.p1				
comp28731_c0_seq2.p1				
comp28732_c0_seq1.p1	sp|P45181|PQQL_HAEIN_Probable_zinc_protease_pqqL_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=pqqL_PE=3_SV=1	3.00E-37	[illegible]	[illegible]
comp28733_c0_seq2.p1				
comp28734_c0_seq2.p1				
comp28734_c0_seq3.p1				
comp28735_c0_seq5.p1				
comp28735_c1_seq1.p1				
comp28736_c0_seq2.p1				
comp28737_c0_seq1.p1				
comp28737_c1_seq1.p1	sp|Q02357|ANK1_MOUSE_Ankyrin-1_OS=Mus_musculus_GN=Ank1_PE=1_SV=2	1.00E-20	[illegible]	[illegible]
comp28737_c1_seq2.p1				
comp28739_c0_seq3.p1				
comp28739_c0_seq4.p1				
comp28740_c0_seq2.p1				
comp28740_c0_seq4.p1				
comp28741_c0_seq1.p1	sp|Q2QV94|EXOC5_ORYSJ_Exocyst_complex_component_5_OS=Oryza_sativa_subsp._japonica_GN=SEC10_PE=2_SV=1	5.00E-18	[illegible]	[illegible]
comp28741_c0_seq3.p1	sp|Q2QV94|EXOC5_ORYSJ_Exocyst_complex_component_5_OS=Oryza_sativa_subsp._japonica_GN=SEC10_PE=2_SV=1	7.00E-18	[illegible]	[illegible]
comp28741_c0_seq4.p1				
comp28742_c1_seq1.p1	sp|Q86GL4|NOXB_DICDI_Superoxide-generating_NADPH_oxidase_heavy_chain_subunit_B_OS=Dictyostelium_discoideum_GN=noxB_PE=2_SV=1	1.00E-24	[illegible]	[illegible]
comp28744_c0_seq3.p1				
comp28745_c0_seq1.p1	sp|Q6DEH3|KC2D1_DANRE_Calcium/calmodulin-dependent_protein_kinase_type_II_delta_1_chain_OS=Danio_rerio_GN=camk2d1_PE=2_SV=2	1.00E-44	[illegible]	[illegible]
comp28745_c1_seq1.p1	sp|Q55GU0|Y9955_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0267514_OS=Dictyostelium_discoideum_GN=DDB_G0267514_PE=3_SV=1	2.00E-28	[illegible]	[illegible]
comp28745_c1_seq3.p1	sp|Q8BW96|KCC1D_MOUSE_Calcium/calmodulin-dependent_protein_kinase_type_1D_OS=Mus_musculus_GN=Camk1d_PE=1_SV=2	7.00E-39	[illegible]	[illegible]
comp28746_c0_seq3.p1	sp|B2UQ30|OBG_AKKM8_GTPase_obg_OS=Akkermansia_muciniphila_(strain_ATCC_BAA-835)_GN=obg_PE=3_SV=2	1.00E-63	[illegible]	[illegible]
comp28747_c0_seq1.p1				
comp28747_c0_seq1.p2				
comp28747_c0_seq1.p4				
comp28747_c0_seq3.p1				
comp28747_c0_seq3.p2				
comp28747_c0_seq4.p1				
comp28747_c1_seq1.p1				
comp28747_c1_seq1.p4				
comp28747_c1_seq2.p1				
comp28747_c1_seq2.p6				
comp28747_c1_seq3.p1				
comp28748_c0_seq1.p1				
comp28748_c0_seq3.p2				
comp28749_c0_seq1.p1	sp|P42663|CTAQ_THEAQ_Thermostable_carboxypeptidase_1_OS=Thermus_aquaticus_PE=1_SV=2	7.00E-77	[illegible]	[illegible]
comp28749_c0_seq1.p2				
comp28750_c0_seq2.p1				
comp28751_c0_seq1.p1				
comp28751_c0_seq2.p1				
comp28752_c0_seq1.p1	sp|Q6Z382|COPG2_ORYSJ_Coatomer_subunit_gamma-2_OS=Oryza_sativa_subsp._japonica_GN=Os07g0201100_PE=2_SV=1	4.00E-145	[illegible]	[illegible]
comp28752_c0_seq1.p3	sp|Q0WW26|COPG_ARATH_Coatomer_subunit_gamma_OS=Arabidopsis_thaliana_GN=At4g34450_PE=1_SV=2	1.00E-83	[illegible]	[illegible]
comp28753_c0_seq1.p1				
comp28754_c0_seq2.p1	sp|Q9Y4D2|DGLA_HUMAN_Sn1-specific_diacylglycerol_lipase_alpha_OS=Homo_sapiens_GN=DAGLA_PE=1_SV=3	9.00E-21	[illegible]	[illegible]
comp28754_c0_seq2.p2	sp|A4FV42|MT21A_BOVIN_Methyltransferase-like_protein_21A_OS=Bos_taurus_GN=METTL21A_PE=2_SV=1	2.00E-12	[illegible]	[illegible]
comp28754_c0_seq3.p1				
comp28755_c0_seq2.p1	sp|Q9S7J8|HMA7_ARATH_Copper-transporting_ATPase_RAN1_OS=Arabidopsis_thaliana_GN=RAN1_PE=1_SV=1	1.00E-136	[illegible]	[illegible]
comp28757_c0_seq1.p1				
comp28757_c0_seq1.p2	sp|Q4FZU3|NSRP1_RAT_Nuclear_speckle_splicing_regulatory_protein_1_OS=Rattus_norvegicus_GN=Nsrp1_PE=2_SV=1	4.00E-22	[illegible]	[illegible]
comp28757_c0_seq1.p6				
comp28758_c0_seq3.p1	sp|P34046|GPA8_DICDI_Guanine_nucleotide-binding_protein_alpha-8_subunit_OS=Dictyostelium_discoideum_GN=gpaH_PE=2_SV=2	3.00E-90	[illegible]	[illegible]
comp28759_c0_seq2.p1				
comp28760_c0_seq2.p2				
comp28760_c0_seq3.p1				
comp28760_c0_seq4.p1	sp|P27862|YIGZ_ECOLI_IMPACT_family_member_yigZ_OS=Escherichia_coli_(strain_K12)_GN=yigZ_PE=1_SV=2	1.00E-25		
comp28760_c0_seq4.p2	sp|Q86SZ2|TPC6B_HUMAN_Trafficking_protein_particle_complex_subunit_6B_OS=Homo_sapiens_GN=TRAPPC6B_PE=1_SV=1	2.00E-22	GO:0005515,GO:0005783,GO:0005783,GO:0005794,GO:0005794,GO:0006810,GO:0016192	[illegible]
comp28760_c0_seq6.p1				
comp28760_c0_seq6.p2				
comp28760_c0_seq7.p1	sp|P27862|YIGZ_ECOLI_IMPACT_family_member_yigZ_OS=Escherichia_coli_(strain_K12)_GN=yigZ_PE=1_SV=2	4.00E-23		
comp28760_c0_seq7.p2	sp|Q86SZ2|TPC6B_HUMAN_Trafficking_protein_particle_complex_subunit_6B_OS=Homo_sapiens_GN=TRAPPC6B_PE=1_SV=1	2.00E-22	GO:0005515,GO:0005783,GO:0005783,GO:0005794,GO:0005794,GO:0006810,GO:0016192	[illegible]
comp28760_c0_seq9.p2				
comp28761_c0_seq1.p1	sp|Q93TL6|PEBA_NOSP7_15,16-dihydrobiliverdin:ferredoxin_oxidoreductase_OS=Nostoc_punctiforme_(strain_ATCC_29133_/_PCC_73102)_GN=pebA_PE=3_SV=1	4.00E-49	[illegible]	[illegible]
comp28761_c1_seq2.p1	sp|Q8CIK8|RFWD3_MOUSE_E3_ubiquitin-protein_ligase_RFWD3_OS=Mus_musculus_GN=Rfwd3_PE=2_SV=1	1.00E-18	[illegible]	[illegible]
comp28762_c0_seq1.p1				
comp28762_c0_seq3.p1				
comp28762_c0_seq5.p1				
comp28763_c0_seq1.p1	sp|Q502K3|ANR52_DANRE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_C_OS=Danio_rerio_GN=ankrd52_PE=2_SV=1	2.00E-28	GO:0003674,GO:0005575,GO:0008150	[illegible]
comp28764_c0_seq1.p1	sp|P59015|VPS18_DANRE_Vacuolar_protein_sorting-associated_protein_18_homolog_OS=Danio_rerio_GN=vps18_PE=2_SV=2	1.00E-111	[illegible]	[illegible]
comp28765_c0_seq1.p1	sp|P94026|RBCMT_TOBAC_Ribulose-1,5_bisphosphate_carboxylase/oxygenase_large_subunit_N-methyltransferase,_chloroplastic_OS=Nicotiana_tabacum_GN=RBCMT_PE=2_SV=1	1.00E-33	[illegible]	[illegible]
comp28768_c0_seq1.p1				
comp28769_c0_seq1.p1	sp|P07756|CPSM_RAT_Carbamoyl-phosphate_synthase_[ammonia],_mitochondrial_OS=Rattus_norvegicus_GN=Cps1_PE=1_SV=1	0	[illegible]	[illegible]
comp28769_c1_seq1.p1	sp|Q8K3P7|HINT3_RAT_Histidine_triad_nucleotide-binding_protein_3_OS=Rattus_norvegicus_GN=Hint3_PE=2_SV=2	1.00E-14	[illegible]	[illegible]
comp28770_c0_seq1.p1				
comp28771_c0_seq1.p1	sp|Q93890|SRF3_CAEEL_UDP-galactose/UDP-N-acetylglucosamine_transporter_srf-3_OS=Caenorhabditis_elegans_GN=srf-3_PE=1_SV=5	4.00E-28	[illegible]	[illegible]
comp28772_c0_seq1.p1	sp|Q9GTN7|TAGA_DICDI_Serine_protease/ABC_transporter_B_family_protein_tagA_OS=Dictyostelium_discoideum_GN=tagA_PE=1_SV=2	2.00E-23	[illegible]	[illegible]
comp28774_c0_seq4.p1				
comp28775_c0_seq1.p1	sp|Q8T1E3|DCAM_DICDI_S-adenosylmethionine_decarboxylase_proenzyme_OS=Dictyostelium_discoideum_GN=amd1_PE=3_SV=3	2.00E-77	[illegible]	[illegible]
comp28776_c0_seq2.p1				
comp28777_c0_seq4.p1	sp|Q9WWW2|ALKJ_PSEPU_Alcohol_dehydrogenase_[acceptor]_OS=Pseudomonas_putida_GN=alkJ_PE=3_SV=1	2.00E-109	[illegible]	[illegible]
comp28777_c0_seq5.p2				
comp28777_c0_seq8.p1	sp|Q9WWW2|ALKJ_PSEPU_Alcohol_dehydrogenase_[acceptor]_OS=Pseudomonas_putida_GN=alkJ_PE=3_SV=1	8.00E-69	[illegible]	[illegible]
comp28778_c0_seq1.p1				
comp28779_c0_seq1.p1				
comp28779_c0_seq1.p2	sp|Q5Z859|MPK4_ORYSJ_Mitogen-activated_protein_kinase_4_OS=Oryza_sativa_subsp._japonica_GN=MPK4_PE=2_SV=1	1.00E-73	[illegible]	[illegible]
comp28779_c0_seq2.p1	sp|Q39022|MPK2_ARATH_Mitogen-activated_protein_kinase_2_OS=Arabidopsis_thaliana_GN=MPK2_PE=1_SV=2	3.00E-81	[illegible]	[illegible]
comp28779_c0_seq3.p1				
comp28780_c0_seq1.p1				
comp28780_c0_seq3.p1				
comp28781_c0_seq1.p1				
comp28781_c0_seq1.p2				
comp28782_c0_seq2.p1				
comp28783_c0_seq1.p2				
comp28784_c1_seq4.p2				
comp28784_c1_seq7.p1	sp|Q54DW2|ERGI3_DICDI_Probable_endoplasmic_reticulum-Golgi_intermediate_compartment_protein_3_OS=Dictyostelium_discoideum_GN=ergic3_PE=3_SV=1	4.00E-71	[illegible]	[illegible]
comp28785_c0_seq2.p1				
comp28786_c0_seq1.p1	sp|Q7ZU29|NUP93_DANRE_Nuclear_pore_complex_protein_Nup93_OS=Danio_rerio_GN=dye_PE=2_SV=1	2.00E-21	[illegible]	[illegible]
comp28786_c0_seq3.p1				
comp28787_c0_seq1.p2	sp|Q4UMH6|Y381_RICFE_Putative_ankyrin_repeat_protein_RF_0381_OS=Rickettsia_felis_(strain_ATCC_VR-1525_/_URRWXCal2)_GN=RF_0381_PE=4_SV=1	2.00E-15	GO:0015969	[illegible]
comp28787_c0_seq2.p1	sp|Q54HW1|PSD10_DICDI_26S_proteasome_non-ATPase_regulatory_subunit_10_OS=Dictyostelium_discoideum_GN=psmD10_PE=2_SV=1	1.00E-24	GO:0003674,GO:0008150	[illegible]
comp28787_c0_seq3.p1	sp|Q4UMH6|Y381_RICFE_Putative_ankyrin_repeat_protein_RF_0381_OS=Rickettsia_felis_(strain_ATCC_VR-1525_/_URRWXCal2)_GN=RF_0381_PE=4_SV=1	6.00E-20	GO:0015969	[illegible]
comp28787_c0_seq4.p1	sp|Q4UMH6|Y381_RICFE_Putative_ankyrin_repeat_protein_RF_0381_OS=Rickettsia_felis_(strain_ATCC_VR-1525_/_URRWXCal2)_GN=RF_0381_PE=4_SV=1	9.00E-20	GO:0015969	[illegible]
comp28788_c0_seq2.p1	sp|B0DZL3|AMPP1_LACBS_Probable_Xaa-Pro_aminopeptidase_P_OS=Laccaria_bicolor_(strain_S238N-H82_/_ATCC_MYA-4686)_GN=AMPP_PE=3_SV=1	5.00E-171	GO:0004177,GO:0006508,GO:0008233,GO:0008237,GO:0016787,GO:0016787,GO:0046872	[illegible]
comp28789_c0_seq1.p1				
comp28789_c0_seq1.p5				
comp28789_c0_seq4.p1				
comp28789_c0_seq6.p1				
comp28790_c0_seq1.p1	sp|Q92562|FIG4_HUMAN_Polyphosphoinositide_phosphatase_OS=Homo_sapiens_GN=FIG4_PE=1_SV=1	9.00E-23	[illegible]	[illegible]
comp28790_c0_seq2.p1	sp|Q91WF7|FIG4_MOUSE_Polyphosphoinositide_phosphatase_OS=Mus_musculus_GN=Fig4_PE=1_SV=1	2.00E-78	[illegible]	[illegible]
comp28791_c0_seq3.p1				
comp28791_c0_seq4.p1				
comp28793_c0_seq1.p1				
comp28793_c0_seq3.p2				
comp28793_c0_seq4.p1				
comp28794_c0_seq2.p1				
comp28794_c0_seq2.p2	sp|Q5R4M2|ULK4_PONAB_Serine/threonine-protein_kinase_ULK4_OS=Pongo_abelii_GN=ULK4_PE=2_SV=1	3.00E-53	[illegible]	[illegible]
comp28795_c0_seq2.p1				
comp28795_c0_seq3.p1				
comp28796_c0_seq1.p1				
comp28796_c0_seq3.p1				
comp28798_c0_seq1.p1	sp|Q9YHY9|OTC_CHICK_Ornithine_carbamoyltransferase,_mitochondrial_OS=Gallus_gallus_GN=OTC_PE=1_SV=1	3.00E-115	[illegible]	[illegible]
comp28799_c0_seq2.p1				
comp28799_c0_seq3.p2				
comp28799_c0_seq4.p1				
comp28800_c0_seq1.p1				
comp28800_c0_seq2.p1				
comp28802_c0_seq3.p1	sp|O04379|AGO1_ARATH_Protein_argonaute_1_OS=Arabidopsis_thaliana_GN=AGO1_PE=1_SV=1	0	[illegible]	[illegible]
comp28803_c0_seq1.p2	sp|Q9ZBD8|HELY_MYCLE_Probable_helicase_helY_OS=Mycobacterium_leprae_GN=helY_PE=3_SV=1	3.00E-14	[illegible]	[illegible]
comp28803_c0_seq3.p1	sp|B9DFG3|ISE2_ARATH_DEAD-box_ATP-dependent_RNA_helicase_ISE2,_chloroplastic_OS=Arabidopsis_thaliana_GN=ISE2_PE=1_SV=2	1.00E-17	[illegible]	[illegible]
comp28803_c0_seq4.p1	sp|B9DFG3|ISE2_ARATH_DEAD-box_ATP-dependent_RNA_helicase_ISE2,_chloroplastic_OS=Arabidopsis_thaliana_GN=ISE2_PE=1_SV=2	1.00E-43	[illegible]	[illegible]
comp28804_c0_seq1.p1	sp|P74893|PRIM_SYNE7_DNA_primase_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=dnaG_PE=1_SV=3	2.00E-34	[illegible]	[illegible]
comp28805_c0_seq1.p1	sp|Q767L0|ABCF1_PIG_ATP-binding_cassette_sub-family_F_member_1_OS=Sus_scrofa_GN=ABCF1_PE=3_SV=1	0	[illegible]	[illegible]
comp28806_c0_seq1.p1				
comp28807_c0_seq1.p1				
comp28807_c0_seq1.p2				
comp28807_c0_seq3.p1				
comp28808_c0_seq1.p1	sp|P72780|HHOA_SYNY3_Putative_serine_protease_HhoA_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=hhoA_PE=1_SV=1	4.00E-53	[illegible]	[illegible]
comp28808_c0_seq1.p2				
comp28808_c0_seq3.p1	sp|P72780|HHOA_SYNY3_Putative_serine_protease_HhoA_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=hhoA_PE=1_SV=1	9.00E-91	[illegible]	[illegible]
comp28809_c0_seq1.p1	sp|Q1L8U8|STB1A_DANRE_Histone-lysine_N-methyltransferase_SETDB1-A_OS=Danio_rerio_GN=setdb1a_PE=2_SV=1	3.00E-25	[illegible]	[illegible]
comp28809_c0_seq1.p8				
comp28810_c0_seq1.p1				
comp28813_c0_seq3.p2				
comp28813_c0_seq4.p1				
comp28813_c0_seq7.p1				
comp28813_c0_seq7.p3				
comp28813_c0_seq7.p6				
comp28814_c0_seq1.p1				
comp28816_c0_seq2.p3				
comp28816_c0_seq3.p3				
comp28817_c0_seq2.p1	sp|Q08DI8|PUS7_BOVIN_Pseudouridylate_synthase_7_homolog_OS=Bos_taurus_GN=PUS7_PE=2_SV=1	2.00E-22	GO:0001522,GO:0003723,GO:0008033,GO:0009451,GO:0009982,GO:0016853	[illegible]
comp28817_c0_seq2.p2				
comp28818_c0_seq1.p1	sp|Q9R9S0|YADS_AERPU_UPF0126_membrane_protein_OS=Aeromonas_punctata_GN=yadS_PE=3_SV=1	3.00E-28	GO:0005886,GO:0005886,GO:0016020,GO:0016021	[illegible]
comp28818_c0_seq2.p1	sp|Q9R9S0|YADS_AERPU_UPF0126_membrane_protein_OS=Aeromonas_punctata_GN=yadS_PE=3_SV=1	5.00E-23	GO:0005886,GO:0005886,GO:0016020,GO:0016021	[illegible]
comp28820_c0_seq1.p1				
comp28821_c0_seq1.p1				
comp28821_c0_seq1.p2				
comp28822_c0_seq1.p1				
comp28822_c0_seq3.p1				
comp28822_c0_seq4.p1				
comp28824_c0_seq3.p1	sp|O81242|RHL1_ARATH_DNA-binding_protein_RHL1_OS=Arabidopsis_thaliana_GN=RHL1_PE=1_SV=1	3.00E-11	[illegible]	[illegible]
comp28824_c0_seq3.p2	sp|Q38936|FK152_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP15-2_OS=Arabidopsis_thaliana_GN=FKBP15-2_PE=2_SV=1	6.00E-16	[illegible]	[illegible]
comp28824_c0_seq3.p3	sp|Q160X4|RL1_ROSDO_50S_ribosomal_protein_L1_OS=Roseobacter_denitrificans_(strain_ATCC_33942_/_OCh_114)_GN=rplA_PE=3_SV=1	4.00E-69	[illegible]	[illegible]
comp28825_c0_seq1.p1				
comp28825_c0_seq2.p1				
comp28825_c0_seq2.p2	sp|Q9Y7J3|YOI7_SCHPO_UPF0586_protein_C1778.07_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC1778.07_PE=2_SV=1	8.00E-66	[illegible]	[illegible]
comp28826_c0_seq1.p1	sp|A6QLH6|NTKL_BOVIN_N-terminal_kinase-like_protein_OS=Bos_taurus_GN=SCYL1_PE=2_SV=1	3.00E-66	[illegible]	[illegible]
comp28827_c0_seq1.p1	sp|Q6NS19|ERGI1_XENLA_Endoplasmic_reticulum-Golgi_intermediate_compartment_protein_1_OS=Xenopus_laevis_GN=ergic1_PE=2_SV=1	3.00E-25	[illegible]	[illegible]
comp28827_c0_seq1.p2	sp|Q55CM7|DDRGK_DICDI_DDRGK_domain-containing_protein_1_OS=Dictyostelium_discoideum_GN=DDB_G0269994_PE=3_SV=1	4.00E-11	GO:0005783	[illegible]
comp28828_c0_seq1.p1				
comp28829_c0_seq1.p1	sp|P54680|FIMB_DICDI_Fimbrin_OS=Dictyostelium_discoideum_GN=fimA_PE=2_SV=2	1.00E-48	[illegible]	[illegible]
comp28830_c0_seq2.p1	sp|Q7Z6E9|RBBP6_HUMAN_E3_ubiquitin-protein_ligase_RBBP6_OS=Homo_sapiens_GN=RBBP6_PE=1_SV=1	5.00E-28	[illegible]	[illegible]
comp28830_c1_seq1.p1				
comp28831_c0_seq3.p1	sp|Q5ZIP4|XRN2_CHICK_5'-3'_exoribonuclease_2_OS=Gallus_gallus_GN=XRN2_PE=2_SV=1	3.00E-94	[illegible]	[illegible]
comp28832_c0_seq5.p1				
comp28832_c0_seq5.p2	sp|P62912|RL32_RAT_60S_ribosomal_protein_L32_OS=Rattus_norvegicus_GN=Rpl32_PE=1_SV=2	4.00E-60	[illegible]	[illegible]
comp28832_c0_seq6.p1				
comp28834_c0_seq1.p1	sp|Q96SK2|TM209_HUMAN_Transmembrane_protein_209_OS=Homo_sapiens_GN=TMEM209_PE=1_SV=2	4.00E-18	GO:0016020,GO:0016020,GO:0016021	[illegible]
comp28834_c0_seq2.p1				
comp28835_c0_seq2.p1	sp|P28998|DHE4_CHLSO_NADP-specific_glutamate_dehydrogenase_(Fragment)_OS=Chlorella_sorokiniana_PE=2_SV=1	6.00E-95	[illegible]	[illegible]
comp28835_c1_seq1.p1	sp|P69834|ISPD_ARATH_2-C-methyl-D-erythritol_4-phosphate_cytidylyltransferase,_chloroplastic_OS=Arabidopsis_thaliana_GN=ISPD_PE=1_SV=1	2.00E-67	[illegible]	[illegible]
comp28835_c1_seq3.p1	sp|P69834|ISPD_ARATH_2-C-methyl-D-erythritol_4-phosphate_cytidylyltransferase,_chloroplastic_OS=Arabidopsis_thaliana_GN=ISPD_PE=1_SV=1	9.00E-43	[illegible]	[illegible]
comp28837_c0_seq2.p1	sp|Q8BMS1|ECHA_MOUSE_Trifunctional_enzyme_subunit_alpha,_mitochondrial_OS=Mus_musculus_GN=Hadha_PE=1_SV=1	0	[illegible]	[illegible]
comp28838_c0_seq2.p1	sp|Q875Q8|MYO2_LACKL_Myosin-2_OS=Lachancea_kluyveri_GN=MYO2_PE=3_SV=1	7.00E-14	[illegible]	[illegible]
comp28838_c0_seq3.p1				
comp28839_c0_seq1.p1				
comp28839_c1_seq1.p1				
comp28839_c1_seq2.p1	sp|Q4U2R1|HERC2_MOUSE_E3_ubiquitin-protein_ligase_HERC2_OS=Mus_musculus_GN=Herc2_PE=1_SV=3	1.00E-26	[illegible]	[illegible]
comp28840_c0_seq2.p1	sp|Q09475|YP93_CAEEL_Uncharacterized_helicase_C28H8.3_OS=Caenorhabditis_elegans_GN=C28H8.3_PE=2_SV=2	1.00E-40	[illegible]	[illegible]
comp28840_c0_seq3.p1				
comp28841_c0_seq1.p1	sp|P28737|MSP1_YEAST_Protein_MSP1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=MSP1_PE=1_SV=2	2.00E-59	[illegible]	[illegible]
comp28842_c0_seq1.p1				
comp28842_c0_seq2.p1				

comp28842_c0_seq3.p2		
comp28843_c0_seq2.p1		
comp28843_c0_seq4.p1		
comp28843_c0_seq5.p1		
comp28843_c1_seq1.p1	sp|Q54JS5|WDR24_DICDI_WD_repeat-containing_protein_24_homolog_OS=Dictyostelium_discoideum_GN=wdr24_PE=3_SV=1	1.00E-28
comp28844_c0_seq1.p1	sp|Q6PGY5|DJC21_DANRE_DnaJ_homolog_subfamily_C_member_21_OS=Danio_rerio_GN=dnajc21_PE=2_SV=1	5.00E-43
comp28845_c0_seq1.p1		
comp28845_c0_seq2.p2		
comp28845_c0_seq3.p1		
comp28846_c0_seq3.p1	sp|Q9FIX3|PP407_ARATH_Pentatricopeptide_repeat-containing_protein_At5g39710_OS=Arabidopsis_thaliana_GN=EMB2745_PE=2_SV=1	2.00E-11
comp28846_c1_seq1.p1	sp|Q66GI4|PP179_ARATH_Pentatricopeptide_repeat-containing_protein_At2g32230,_mitochondrial_OS=Arabidopsis_thaliana_GN=At2g32230_PE=2_SV=1	1.00E-13
comp28847_c0_seq2.p1	sp|Q5R9K4|VMP1_PONAB_Vacuole_membrane_protein_1_OS=Pongo_abelii_GN=VMP1_PE=2_SV=1	1.00E-37
comp28848_c0_seq2.p1	sp|Q9LKW9|NHX7_ARATH_Sodium/hydrogen_exchanger_7_OS=Arabidopsis_thaliana_GN=NHX7_PE=1_SV=1	3.00E-64
comp28852_c0_seq1.p1	sp|P37383|RAD51_CHICK_DNA_repair_protein_RAD51_homolog_1_OS=Gallus_gallus_GN=RAD51A_PE=2_SV=1	2.00E-147
comp28852_c0_seq2.p1	sp|Q9MA98|ERCC1_ARATH_DNA_excision_repair_protein_ERCC-1_OS=Arabidopsis_thaliana_GN=ERCC1_PE=2_SV=1	4.00E-30
comp28852_c0_seq6.p1	sp|P37383|RAD51_CHICK_DNA_repair_protein_RAD51_homolog_1_OS=Gallus_gallus_GN=RAD51A_PE=2_SV=1	2.00E-147
comp28853_c0_seq1.p1		
comp28856_c0_seq1.p1		
comp28856_c0_seq2.p1	sp|Q3T042|NOB1_BOVIN_RNA-binding_protein_NOB1_OS=Bos_taurus_GN=NOB1_PE=2_SV=1	5.00E-34
comp28856_c1_seq1.p1		
comp28856_c1_seq2.p1		
comp28857_c0_seq2.p1	sp|A8MR93|ALG12_ARATH_Dol-P-Man:Man(7)GlcNAc(2)-PP-Dol_alpha-1,6-mannosyltransferase_OS=Arabidopsis_thaliana_GN=ALG12_PE=1_SV=1	2.00E-58
comp28858_c0_seq10.p1		
comp28858_c0_seq12.p1		
comp28858_c0_seq12.p2		
comp28858_c0_seq6.p1		
comp28858_c0_seq9.p1		
comp28858_c0_seq9.p2		
comp28859_c0_seq2.p1		
comp28860_c0_seq4.p1	sp|Q9VR91|HERC2_DROME_Probable_E3_ubiquitin-protein_ligase_HERC2_OS=Drosophila_melanogaster_GN=HERC2_PE=1_SV=3	3.00E-37
comp28861_c0_seq1.p1		
comp28862_c0_seq1.p1	sp|P48457|PP2B_EMENI_Serine/threonine-protein_phosphatase_2B_catalytic_subunit_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=cnaA_PE=3_SV=3	2.00E-75
comp28862_c0_seq1.p2		
comp28863_c0_seq1.p1		
comp28863_c0_seq2.p1		
comp28863_c0_seq2.p2		
comp28863_c0_seq3.p2		
comp28864_c0_seq1.p1	sp|Q5REP9|KLHL3_PONAB_Kelch-like_protein_3_OS=Pongo_abelii_GN=KLHL3_PE=2_SV=1	6.00E-27
comp28865_c0_seq1.p1		
comp28865_c1_seq2.p1	sp|P0AGJ4|TRMH_SHIFL_tRNA_(guanosine(18)-2'-O)-methyltransferase_OS=Shigella_flexneri_GN=trmH_PE=3_SV=1	3.00E-26
comp28865_c1_seq2.p2	sp|O13870|NOT3_SCHPO_General_negative_regulator_of_transcription_subunit_3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=not3_PE=1_SV=2	6.00E-42
comp28865_c1_seq4.p1	sp|P0AGJ4|TRMH_SHIFL_tRNA_(guanosine(18)-2'-O)-methyltransferase_OS=Shigella_flexneri_GN=trmH_PE=3_SV=1	7.00E-27
comp28865_c1_seq4.p2	sp|O13870|NOT3_SCHPO_General_negative_regulator_of_transcription_subunit_3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=not3_PE=1_SV=2	6.00E-42
comp28866_c0_seq3.p1	sp|Q8K2Z4|CND1_MOUSE_Condensin_complex_subunit_1_OS=Mus_musculus_GN=Ncapd2_PE=1_SV=2	8.00E-84
comp28869_c0_seq2.p2	sp|Q9ZMU4|BCP_HELPJ_Putative_peroxiredoxin_bcp_OS=Helicobacter_pylori_(strain_J99)_GN=bcp_PE=3_SV=1	8.00E-23
comp28869_c0_seq3.p1		
comp28869_c0_seq4.p1	sp|Q9ZMU4|BCP_HELPJ_Putative_peroxiredoxin_bcp_OS=Helicobacter_pylori_(strain_J99)_GN=bcp_PE=3_SV=1	3.00E-27
comp28870_c0_seq2.p1	sp|Q08CL8|CNOTA_DANRE_CCR4-NOT_transcription_complex_subunit_10_OS=Danio_rerio_GN=cnot10_PE=2_SV=1	2.00E-21
comp28871_c0_seq1.p1		
comp28872_c1_seq1.p1		
comp28872_c1_seq1.p2		
comp28873_c0_seq6.p1		
comp28876_c0_seq1.p1		
comp28876_c1_seq2.p1		
comp28876_c1_seq2.p2		
comp28876_c1_seq4.p1	sp|Q7PR68|MED7_ANOGA_Mediator_of_RNA_polymerase_II_transcription_subunit_7_OS=Anopheles_gambiae_GN=MED7_PE=3_SV=2	4.00E-12
comp28877_c0_seq2.p1		
comp28877_c0_seq3.p1		
comp28877_c0_seq4.p1		
comp28877_c0_seq5.p1		
comp28878_c0_seq2.p1	sp|Q924C1|XPO5_MOUSE_Exportin-5_OS=Mus_musculus_GN=Xpo5_PE=2_SV=1	2.00E-16
comp28879_c0_seq1.p1	sp|O75800|ZMY10_HUMAN_Zinc_finger_MYND_domain-containing_protein_10_OS=Homo_sapiens_GN=ZMYND10_PE=1_SV=2	1.00E-56
comp28880_c0_seq2.p2		
comp28881_c0_seq1.p1	sp|Q55C16|UBA1_DICDI_Ubiquitin-like_modifier-activating_enzyme_1_OS=Dictyostelium_discoideum_GN=uba1_PE=3_SV=1	6.00E-26
comp28881_c0_seq2.p1	sp|P92974|UBE12_ARATH_Ubiquitin-activating_enzyme_E1_2_OS=Arabidopsis_thaliana_GN=UBA2_PE=2_SV=1	3.00E-173
comp28882_c0_seq1.p1	sp|Q9QXG2|RAE1_MOUSE_Rab_proteins_geranylgeranyltransferase_component_A_1_OS=Mus_musculus_GN=Chm_PE=2_SV=1	4.00E-29
comp28882_c0_seq1.p2		
comp28882_c0_seq3.p1		
comp28884_c0_seq1.p1		
comp28884_c0_seq1.p3	sp|Q55AR8|SNR40_DICDI_U5_small_nuclear_ribonucleoprotein_40_kDa_protein_OS=Dictyostelium_discoideum_GN=snrnp40_PE=3_SV=1	1.00E-15
comp28884_c0_seq3.p1		
comp28884_c0_seq3.p3	sp|Q55AR8|SNR40_DICDI_U5_small_nuclear_ribonucleoprotein_40_kDa_protein_OS=Dictyostelium_discoideum_GN=snrnp40_PE=3_SV=1	9.00E-15
comp28885_c0_seq10.p1		
comp28886_c0_seq1.p1		
comp28887_c0_seq1.p1		
comp28887_c0_seq1.p2		
comp28887_c0_seq2.p1		
comp28887_c0_seq2.p2		
comp2889_c1_seq1.p1	sp|P07001|PNTA_ECOLI_NAD(P)_transhydrogenase_subunit_alpha_OS=Escherichia_coli_(strain_K12)_GN=pntA_PE=1_SV=2	5.00E-105
comp28890_c1_seq1.p1	sp|P22147|XRN1_YEAST_5'-3'_exoribonuclease_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=KEM1_PE=1_SV=1	7.00E-15
comp28891_c0_seq1.p1	sp|Q55G83|ABKC_DICDI_Probable_serine/threonine-protein_kinase_abkC_OS=Dictyostelium_discoideum_GN=abkC_PE=3_SV=1	1.00E-51
comp28891_c0_seq2.p1	sp|Q55G83|ABKC_DICDI_Probable_serine/threonine-protein_kinase_abkC_OS=Dictyostelium_discoideum_GN=abkC_PE=3_SV=1	3.00E-34
comp28892_c0_seq1.p1		
comp28892_c0_seq6.p1		
comp28892_c0_seq7.p1		
comp28893_c1_seq1.p1	sp|Q8CAA7|PGM2L_MOUSE_Glucose_1,6-bisphosphate_synthase_OS=Mus_musculus_GN=Pgm2l1_PE=1_SV=1	6.00E-42
comp28893_c1_seq1.p2	sp|Q96G03|PGM2_HUMAN_Phosphoglucomutase-2_OS=Homo_sapiens_GN=PGM2_PE=1_SV=4	9.00E-79
comp28893_c1_seq3.p3		
comp28893_c2_seq1.p1		
comp28896_c0_seq1.p1		
comp28896_c0_seq1.p8		
comp28897_c0_seq1.p1		
comp28897_c0_seq1.p2		
comp28897_c0_seq1.p5		
comp28899_c0_seq2.p1		
comp28899_c0_seq2.p2		
comp28900_c0_seq2.p1	sp|Q9C671|P4K2B_ARATH_Probable_phosphatidylinositol_4-kinase_type_2-beta_At1g26270_OS=Arabidopsis_thaliana_GN=At1g26270_PE=1_SV=1	7.00E-24
comp28901_c0_seq3.p1	sp|Q7ZYV9|SYMPK_XENLA_Symplekin_OS=Xenopus_laevis_GN=sympk_PE=1_SV=1	9.00E-23
comp28902_c0_seq1.p1	sp|Q9ZS34|CHLP_TOBAC_Geranylgeranyl_diphosphate_reductase,_chloroplastic_OS=Nicotiana_tabacum_GN=CHLP_PE=2_SV=1	5.00E-167
comp28903_c0_seq1.p1	sp|Q726S7|PTA_DESVH_Phosphate_acetyltransferase_OS=Desulfovibrio_vulgaris_(strain_Hildenborough_/_ATCC_29579_/_NCIMB_8303)_GN=pta_PE=3_SV=1	7.00E-13
comp28903_c0_seq4.p1		
comp28904_c0_seq2.p1		
comp28905_c0_seq1.p1		
comp28905_c0_seq2.p1	sp|Q5ZJ85|PRPF3_CHICK_U4/U6_small_nuclear_ribonucleoprotein_Prp3_OS=Gallus_gallus_GN=PRPF3_PE=2_SV=1	1.00E-48
comp28905_c0_seq2.p3		
comp28905_c0_seq2.p4		
comp28905_c0_seq4.p1	sp|P96554|Y319_MYXXA_Uncharacterized_membrane_protein_STKORF319_OS=Myxococcus_xanthus_PE=3_SV=1	2.00E-61
comp28906_c0_seq1.p1	sp|Q08BT9|P20D1_XENTR_Probable_carboxypeptidase_PM20D1_OS=Xenopus_tropicalis_GN=pm20d1_PE=2_SV=1	1.00E-17
comp28907_c0_seq1.p1	sp|Q54KR1|SYCC_DICDI_Cysteine--tRNA_ligase,_cytoplasmic_OS=Dictyostelium_discoideum_GN=cysS_PE=3_SV=1	6.00E-111
comp28909_c0_seq1.p1	sp|Q9SLA1|P2C22_ARATH_Probable_protein_phosphatase_2C_22_OS=Arabidopsis_thaliana_GN=At2g25620_PE=1_SV=1	2.00E-26
comp28910_c0_seq1.p1		
comp28911_c0_seq2.p1	sp|Q9UIF7|MUTYH_HUMAN_A/G-specific_adenine_DNA_glycosylase_OS=Homo_sapiens_GN=MUTYH_PE=1_SV=1	4.00E-62
comp28911_c0_seq3.p1	sp|Q9UIF7|MUTYH_HUMAN_A/G-specific_adenine_DNA_glycosylase_OS=Homo_sapiens_GN=MUTYH_PE=1_SV=1	6.00E-77
comp28912_c0_seq1.p1	sp|P37574|YACP_BACSU_Uncharacterized_protein_yacP_OS=Bacillus_subtilis_GN=yacP_PE=4_SV=1	9.00E-12
comp28913_c0_seq1.p1	sp|Q9M5P3|CCDA_ARATH_Cytochrome_c-type_biogenesis_ccda-like_chloroplastic_protein_OS=Arabidopsis_thaliana_GN=CCDA_PE=1_SV=1	7.00E-45
comp28913_c0_seq1.p2	sp|Q96WV0|UREG_SCHPO_Uncharacterized_urease_accessory_protein_ureG-like_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCPB16A4.05c_PE=2_SV=1	8.00E-101
comp28913_c0_seq3.p1	sp|Q96WV0|UREG_SCHPO_Uncharacterized_urease_accessory_protein_ureG-like_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCPB16A4.05c_PE=2_SV=1	8.00E-101
comp28913_c0_seq3.p2	sp|Q9M5P3|CCDA_ARATH_Cytochrome_c-type_biogenesis_ccda-like_chloroplastic_protein_OS=Arabidopsis_thaliana_GN=CCDA_PE=1_SV=1	2.00E-15
comp28914_c0_seq1.p1	sp|Q9SHJ8|HIBC8_ARATH_3-hydroxyisobutyryl-CoA_hydrolase-like_protein_5_OS=Arabidopsis_thaliana_GN=At1g06550_PE=2_SV=2	8.00E-29
comp28916_c0_seq1.p1	sp|Q9UAG7|FHBA_DICDI_Flavohemoprotein_A_OS=Dictyostelium_discoideum_GN=fhbA_PE=2_SV=1	2.00E-51
comp28917_c0_seq3.p1		
comp28917_c0_seq4.p1		
comp28918_c0_seq1.p1	sp|Q9PKX5|TLC1_CHLMU_ADP,ATP_carrier_protein_1_OS=Chlamydia_muridarum_(strain_MoPn_/_Nigg)_GN=tlcA_PE=3_SV=1	1.00E-106
comp28918_c0_seq1.p2	sp|Q54FR4|PX24D_DICDI_PXMP2/4_family_protein_4_OS=Dictyostelium_discoideum_GN=DDB_G0290631_PE=3_SV=1	6.00E-12
comp28919_c0_seq2.p1		
comp28919_c0_seq2.p2	sp|Q01890|YPT1_PHYIN_Ras-like_GTP-binding_protein_YPT1_OS=Phytophthora_infestans_GN=YPT1_PE=3_SV=1	3.00E-117
comp28919_c0_seq3.p1		
comp28919_c0_seq3.p2	sp|Q01890|YPT1_PHYIN_Ras-like_GTP-binding_protein_YPT1_OS=Phytophthora_infestans_GN=YPT1_PE=3_SV=1	3.00E-117
comp28920_c0_seq3.p1	sp|Q9QXN3|TRIP4_MOUSE_Activating_signal_cointegrator_1_OS=Mus_musculus_GN=Trip4_PE=1_SV=2	8.00E-20
comp28920_c0_seq3.p2		
comp28922_c0_seq1.p1	sp|Q9FZ36|M3K2_ARATH_Mitogen-activated_protein_kinase_kinase_kinase_2_OS=Arabidopsis_thaliana_GN=ANP2_PE=2_SV=1	5.00E-69
comp28923_c0_seq6.p1	sp|Q16932|STX_APLCA_Syntaxin_OS=Aplysia_californica_PE=2_SV=1	3.00E-29
comp28923_c0_seq6.p2	sp|Q9QYJ0|DNJA2_MOUSE_DnaJ_homolog_subfamily_A_member_2_OS=Mus_musculus_GN=Dnaja2_PE=1_SV=1	5.00E-44
comp28923_c0_seq6.p5		
comp28923_c0_seq8.p1	sp|O60884|DNJA2_HUMAN_DnaJ_homolog_subfamily_A_member_2_OS=Homo_sapiens_GN=DNAJA2_PE=1_SV=1	8.00E-56
comp28923_c0_seq8.p2	sp|Q16932|STX_APLCA_Syntaxin_OS=Aplysia_californica_PE=2_SV=1	3.00E-29
comp28923_c0_seq8.p5		
comp28924_c0_seq3.p1	sp|A4IFP3|FADS3_BOVIN_Fatty_acid_desaturase_3_OS=Bos_taurus_GN=FADS3_PE=2_SV=1	1.00E-40
comp28925_c0_seq3.p1	sp|Q9H0L4|CSTFT_HUMAN_Cleavage_stimulation_factor_subunit_2_tau_variant_OS=Homo_sapiens_GN=CSTF2T_PE=1_SV=1	3.00E-24
comp28925_c0_seq7.p1	sp|Q8HXM1|CSTF2_BOVIN_Cleavage_stimulation_factor_subunit_2_OS=Bos_taurus_GN=CSTF2_PE=2_SV=1	1.00E-30
comp28925_c0_seq8.p1	sp|Q8K339|KIN17_MOUSE_DNA/RNA-binding_protein_KIN17_OS=Mus_musculus_GN=Kin_PE=2_SV=1	5.00E-37
comp28926_c0_seq2.p1	sp|Q54YD9|FOL1_DICDI_Folic_acid_synthesis_protein_FOL1_OS=Dictyostelium_discoideum_GN=fol1_PE=3_SV=1	4.00E-47
comp28926_c0_seq6.p1	sp|P29251|FOL1_PNECA_Folic_acid_synthesis_protein_fol1_OS=Pneumocystis_carinii_GN=fol1_PE=1_SV=1	7.00E-91
comp28927_c0_seq2.p1	sp|Q54XC1|5NTC_DICDI_Cytosolic_purine_5'-nucleotidase_OS=Dictyostelium_discoideum_GN=nt5c2_PE=3_SV=1	1.00E-68
comp28928_c0_seq3.p1	sp|Q9P7X8|RPA2_SCHPO_Probable_DNA-directed_RNA_polymerase_I_subunit_RPA2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpa2_PE=2_SV=2	0
comp28928_c0_seq3.p2	sp|Q9SVS0|PUS6_ARATH_RNA_pseudouridine_synthase_6,_chloroplastic_OS=Arabidopsis_thaliana_GN=At4g21770_PE=2_SV=1	3.00E-12
comp28929_c0_seq1.p1	sp|Q55BF2|NMD3_DICDI_60S_ribosomal_export_protein_NMD3_OS=Dictyostelium_discoideum_GN=nmd3_PE=3_SV=1	2.00E-132
comp28930_c0_seq2.p1	sp|P42925|PXMP2_MOUSE_Peroxisomal_membrane_protein_2_OS=Mus_musculus_GN=Pxmp2_PE=2_SV=2	4.00E-14
comp28930_c0_seq3.p1	sp|P42925|PXMP2_MOUSE_Peroxisomal_membrane_protein_2_OS=Mus_musculus_GN=Pxmp2_PE=2_SV=2	7.00E-26
comp28931_c0_seq3.p1		
comp28931_c0_seq5.p1		
comp28931_c0_seq6.p1		
comp28932_c0_seq1.p1	sp|Q9UR24|RHP26_SCHPO_DNA_repair_protein_rhp26_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rhp26_PE=2_SV=1	1.00E-176
comp28932_c0_seq1.p5		
comp28932_c0_seq5.p1	sp|Q9UR24|RHP26_SCHPO_DNA_repair_protein_rhp26_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rhp26_PE=2_SV=1	2.00E-180
comp28932_c0_seq5.p2		
comp28932_c0_seq5.p4		
comp28933_c0_seq1.p2		
comp28933_c0_seq2.p1	sp|Q51330|OXLT_OXAFO_Oxalate:formate_antiporter_OS=Oxalobacter_formigenes_GN=oxlT_PE=1_SV=3	6.00E-12
comp28934_c0_seq1.p1		
comp28934_c0_seq2.p1		
comp28935_c0_seq1.p1	sp|O09748|YB68_SCHPO_Dynamin-like_protein_C12C2.08_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC12C2.08_PE=2_SV=1	2.00E-25
comp28936_c0_seq2.p1	sp|P39623|SPSC_BACSU_Spore_coat_polysaccharide_biosynthesis_protein_spsC_OS=Bacillus_subtilis_GN=spsC_PE=3_SV=1	5.00E-32
comp28937_c0_seq3.p1		
comp28937_c0_seq4.p1		
comp28938_c0_seq3.p1		
comp28939_c0_seq2.p1		
comp28940_c0_seq2.p1		
comp28940_c0_seq2.p3		
comp28941_c0_seq3.p1	sp|Q8R151|ZNFX1_MOUSE_NFX1-type_zinc_finger-containing_protein_1_OS=Mus_musculus_GN=Znfx1_PE=2_SV=3	8.00E-33
comp28942_c0_seq1.p1	sp|Q5ZIY5|2ABD_CHICK_Serine/threonine-protein_phosphatase_2A_55_kDa_regulatory_subunit_B_delta_isoform_OS=Gallus_gallus_GN=PPP2R2D_PE=2_SV=1	4.00E-142
comp28942_c0_seq1.p2	sp|Q8LDQ4|TAP46_ARATH_PP2A_regulatory_subunit_TAP46_OS=Arabidopsis_thaliana_GN=TAP46_PE=1_SV=2	5.00E-12
comp28942_c0_seq2.p1	sp|P53031|2ABA_CANTR_Protein_phosphatase_PP2A_regulatory_subunit_B_OS=Candida_tropicalis_GN=CDC55_PE=3_SV=1	1.00E-132
comp28942_c0_seq3.p1	sp|Q5ZIY5|2ABD_CHICK_Serine/threonine-protein_phosphatase_2A_55_kDa_regulatory_subunit_B_delta_isoform_OS=Gallus_gallus_GN=PPP2R2D_PE=2_SV=1	4.00E-142
comp28942_c0_seq3.p2		
comp28943_c0_seq4.p1	sp|Q9H4G4|GAPR1_HUMAN_Golgi-associated_plant_pathogenesis-related_protein_1_OS=Homo_sapiens_GN=GLIPR2_PE=1_SV=3	2.00E-12
comp28943_c0_seq4.p2	sp|Q80ZK9|WDTC1_MOUSE_WD_and_tetratricopeptide_repeats_protein_1_OS=Mus_musculus_GN=Wdtc1_PE=1_SV=1	6.00E-18
comp28943_c0_seq5.p1	sp|Q80ZK9|WDTC1_MOUSE_WD_and_tetratricopeptide_repeats_protein_1_OS=Mus_musculus_GN=Wdtc1_PE=1_SV=1	6.00E-27
comp28944_c0_seq1.p1		
comp28944_c0_seq2.p1		
comp28945_c0_seq1.p1	sp|Q02357|ANK1_MOUSE_Ankyrin-1_OS=Mus_musculus_GN=Ank1_PE=1_SV=2	2.00E-20
comp28946_c0_seq1.p1		
comp28947_c0_seq1.p1		
comp28947_c0_seq2.p1		
comp28948_c0_seq1.p1	sp|Q01968|OCRL_HUMAN_Inositol_polyphosphate_5-phosphatase_OCRL-1_OS=Homo_sapiens_GN=OCRL_PE=1_SV=3	1.00E-60
comp28948_c0_seq3.p1	sp|Q01968|OCRL_HUMAN_Inositol_polyphosphate_5-phosphatase_OCRL-1_OS=Homo_sapiens_GN=OCRL_PE=1_SV=3	5.00E-57
comp28948_c0_seq3.p2		
comp28949_c0_seq1.p1		
comp28949_c0_seq2.p1		
comp28950_c0_seq2.p1		
comp28951_c0_seq4.p1	sp|Q8N5T2|TBC19_HUMAN_TBC1_domain_family_member_19_OS=Homo_sapiens_GN=TBC1D19_PE=1_SV=2	1.00E-58
comp28951_c0_seq4.p2		
comp28951_c0_seq5.p1	sp|Q8N5T2|TBC19_HUMAN_TBC1_domain_family_member_19_OS=Homo_sapiens_GN=TBC1D19_PE=1_SV=2	1.00E-58
comp28951_c0_seq5.p2		
comp28952_c0_seq1.p1		
comp28952_c0_seq2.p1		
comp28953_c0_seq2.p1	sp|Q8ETH0|HMP_OCEIH_Flavohemoprotein_OS=Oceanobacillus_iheyensis_(strain_DSM_14371_/_JCM_11309_/_KCTC_3954_/_HTE831)_GN=hmp_PE=3_SV=1	9.00E-14
comp28954_c0_seq1.p1		
comp28954_c0_seq3.p1		
comp28955_c0_seq2.p1		
comp28956_c1_seq3.p1		
comp28956_c1_seq4.p1	sp|Q7SC45|BTN1_NEUCR_Protein_btn-1_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=btn-1_PE=3_SV=2	3.00E-36
comp28956_c1_seq5.p1	sp|Q7SC45|BTN1_NEUCR_Protein_btn-1_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=btn-1_PE=3_SV=2	1.00E-18
comp28957_c0_seq2.p1	sp|P01104|MYB_AVIMB_Transforming_protein_Myb_OS=Avian_myeloblastosis_virus_GN=V-MYB_PE=1_SV=2	5.00E-34
comp28957_c0_seq2.p3	sp|Q39565|DYHB_CHLRE_Dynein_beta_chain,_flagellar_outer_arm_OS=Chlamydomonas_reinhardtii_GN=ODA4_PE=3_SV=1	1.00E-24
comp28958_c1_seq1.p1	sp|Q54QG9|UBA3_DICDI_NEDD8-activating_enzyme_E1_catalytic_subunit_OS=Dictyostelium_discoideum_GN=uba3_PE=1_SV=1	2.00E-65
comp28958_c1_seq3.p1	sp|Q54QG9|UBA3_DICDI_NEDD8-activating_enzyme_E1_catalytic_subunit_OS=Dictyostelium_discoideum_GN=uba3_PE=1_SV=1	2.00E-118
comp28959_c0_seq1.p1	sp|Q9BRQ3|NUD22_HUMAN_Nucleoside_diphosphate-linked_moiety_X_motif_22_OS=Homo_sapiens_GN=NUDT22_PE=2_SV=3	2.00E-35
comp28961_c0_seq1.p1		
comp28961_c0_seq2.p1		
comp28961_c0_seq3.p1		
comp28962_c0_seq1.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	1.00E-33
comp28963_c0_seq1.p1	sp|Q9FG87|KCS19_ARATH_3-ketoacyl-CoA_synthase_19_OS=Arabidopsis_thaliana_GN=KCS19_PE=2_SV=1	5.00E-86
comp28963_c0_seq4.p1	sp|Q9FG87|KCS19_ARATH_3-ketoacyl-CoA_synthase_19_OS=Arabidopsis_thaliana_GN=KCS19_PE=2_SV=1	2.00E-130
comp28964_c0_seq1.p1	sp|Q7TNH6|NPHP3_MOUSE_Nephrocystin-3_OS=Mus_musculus_GN=Nphp3_PE=1_SV=2	2.00E-52
comp28967_c0_seq1.p1	sp|Q9SIC9|PP178_ARATH_Pentatricopeptide_repeat-containing_protein_At2g31400,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g31400_PE=2_SV=1	2.00E-28
comp28967_c0_seq3.p1		
comp28968_c0_seq1.p1		
comp28970_c0_seq2.p1	sp|A6SXQ2|ACP_JANMA_Acyl_carrier_protein_OS=Janthinobacterium_sp._(strain_Marseille)_GN=acpP_PE=3_SV=1	9.00E-14
comp28971_c0_seq2.p1	sp|Q9M8D3|PUR4_ARATH_Probable_phosphoribosylformylglycinamidine_synthase,_chloroplastic/mitochondrial_OS=Arabidopsis_thaliana_GN=At1g74260_PE=1_SV=2	0
comp28971_c1_seq1.p1	sp|Q5R5A1|ADT2_PONAB_ADP/ATP_translocase_2_OS=Pongo_abelii_GN=SLC25A5_PE=2_SV=3	2.00E-82
comp28971_c1_seq2.p1		
comp28972_c0_seq1.p1		
comp28975_c0_seq1.p1		
comp28975_c0_seq1.p2	sp|Q54QY3|YIPF5_DICDI_Protein_YIPF5_homolog_OS=Dictyostelium_discoideum_GN=yipf5_PE=3_SV=1	7.00E-54
comp28976_c0_seq2.p1		
comp28976_c0_seq4.p1		
comp28977_c0_seq1.p1		
comp28977_c0_seq2.p1		
comp28977_c0_seq3.p1		
comp28978_c0_seq1.p1		
comp28978_c0_seq3.p1		
comp28979_c0_seq2.p1		
comp28980_c1_seq3.p1	sp|Q2RQW1|RL4_RHORT_50S_ribosomal_protein_L4_OS=Rhodospirillum_rubrum_(strain_ATCC_11170_/_NCIB_8255)_GN=rplD_PE=3_SV=1	1.00E-49
comp28981_c0_seq2.p1		
comp28981_c1_seq1.p1		
comp28981_c2_seq2.p1		
comp28983_c0_seq2.p1	sp|Q52KI8|SRRM1_MOUSE_Serine/arginine_repetitive_matrix_protein_1_OS=Mus_musculus_GN=Srrm1_PE=1_SV=2	6.00E-13
comp28984_c0_seq2.p1		
comp28985_c0_seq1.p1	sp|P62255|UB2G1_RAT_Ubiquitin-conjugating_enzyme_E2_G1_OS=Rattus_norvegicus_GN=Ube2g1_PE=2_SV=3	1.00E-67
comp28987_c0_seq1.p1	sp|Q54T82|Y1931_DICDI_Putative_leucine-rich_repeat-containing_protein_DDB_G0281931_OS=Dictyostelium_discoideum_GN=DDB_G0281931_PE=4_SV=1	2.00E-14
comp28987_c0_seq2.p1		
comp28988_c0_seq1.p1		
comp28988_c0_seq1.p2	sp|Q5R6Q2|STX6_PONAB_Syntaxin-6_OS=Pongo_abelii_GN=STX6_PE=2_SV=1	2.00E-17
comp28989_c0_seq1.p1	sp|Q8VXZ0|NUD20_ARATH_Nudix_hydrolase_20,_chloroplastic_OS=Arabidopsis_thaliana_GN=NUDT20_PE=2_SV=1	4.00E-50
comp28990_c0_seq1.p1	sp|Q695U0|RHBL1_TOXGO_Rhomboid-like_protease_1_OS=Toxoplasma_gondii_GN=ROM1_PE=2_SV=1	5.00E-22
comp28990_c0_seq2.p1	sp|Q695T9|RHBL2_TOXGO_Rhomboid-like_protease_2_OS=Toxoplasma_gondii_GN=ROM2_PE=2_SV=1	8.00E-15
comp28991_c0_seq2.p1	sp|Q9CWL8|CTBL1_MOUSE_Beta-catenin-like_protein_1_OS=Mus_musculus_GN=Ctnnbl1_PE=1_SV=1	7.00E-99
comp28992_c0_seq1.p1		
comp28992_c0_seq4.p1		
comp28992_c0_seq4.p2	sp|Q9CWY3|SETD6_MOUSE_N-lysine_methyltransferase_SETD6_OS=Mus_musculus_GN=Setd6_PE=2_SV=1	5.00E-18
comp28993_c0_seq1.p1	sp|Q54QU8|Y3629_DICDI_Probable_zinc_transporter_protein_DDB_G0283629_OS=Dictyostelium_discoideum_GN=DDB_G0283629_PE=3_SV=1	2.00E-30
comp28994_c0_seq2.p1	sp|Q1GIE5|POTA_SILST_Spermidine/putrescine_import_ATP-binding_protein_PotA_OS=Silicibacter_sp._(strain_TM1040)_GN=potA_PE=3_SV=1	2.00E-20
comp28997_c0_seq1.p1		
comp28997_c0_seq2.p1		
comp28998_c0_seq2.p1	sp|Q55BF4|UCPA_DICDI_Mitochondrial_substrate_carrier_family_protein_ucpA_OS=Dictyostelium_discoideum_GN=ucpA_PE=3_SV=1	1.00E-75
comp28999_c0_seq1.p1	sp|Q9BZE2|PUS3_HUMAN_tRNA_pseudouridine(38/39)_synthase_OS=Homo_sapiens_GN=PUS3_PE=1_SV=3	4.00E-55
comp28999_c0_seq2.p1	sp|Q9BZE2|PUS3_HUMAN_tRNA_pseudouridine(38/39)_synthase_OS=Homo_sapiens_GN=PUS3_PE=1_SV=3	2.00E-58
comp28999_c0_seq3.p1	sp|Q9BZE2|PUS3_HUMAN_tRNA_pseudouridine(38/39)_synthase_OS=Homo_sapiens_GN=PUS3_PE=1_SV=3	2.00E-17
comp29000_c0_seq1.p1		
comp29001_c0_seq1.p1		
comp29002_c0_seq1.p1	sp|P55786|PSA_HUMAN_Puromycin-sensitive_aminopeptidase_OS=Homo_sapiens_GN=NPEPPS_PE=1_SV=2	9.00E-135
comp29003_c0_seq1.p1	sp|P22813|HSF_DROME_Heat_shock_factor_protein_OS=Drosophila_melanogaster_GN=Hsf_PE=1_SV=1	2.00E-13
comp29004_c0_seq1.p1	sp|P49193|RALB_TODPA_Retinal-binding_protein_OS=Todarodes_pacificus_PE=1_SV=2	2.00E-11
comp29005_c0_seq2.p1	sp|Q9JI39|ABCBA_MOUSE_ATP-binding_cassette_sub-family_B_member_10,_mitochondrial_OS=Mus_musculus_GN=Abcb10_PE=2_SV=1	4.00E-31
comp29005_c0_seq4.p1	sp|Q9JI39|ABCBA_MOUSE_ATP-binding_cassette_sub-family_B_member_10,_mitochondrial_OS=Mus_musculus_GN=Abcb10_PE=2_SV=1	3.00E-31
comp29005_c0_seq4.p2	sp|Q9NRK6|ABCBA_HUMAN_ATP-binding_cassette_sub-family_B_member_10,_mitochondrial_OS=Homo_sapiens_GN=ABCB10_PE=1_SV=2	7.00E-88
comp29005_c0_seq5.p1	sp|Q9NRK6|ABCBA_HUMAN_ATP-binding_cassette_sub-family_B_member_10,_mitochondrial_OS=Homo_sapiens_GN=ABCB10_PE=1_SV=2	7.00E-88
comp29005_c0_seq5.p2		
comp29005_c0_seq5.p4	sp|Q9JI39|ABCBA_MOUSE_ATP-binding_cassette_sub-family_B_member_10,_mitochondrial_OS=Mus_musculus_GN=Abcb10_PE=2_SV=1	4.00E-12
comp29005_c0_seq8.p1	sp|Q9JI39|ABCBA_MOUSE_ATP-binding_cassette_sub-family_B_member_10,_mitochondrial_OS=Mus_musculus_GN=Abcb10_PE=2_SV=1	5.00E-132
comp29005_c0_seq9.p1		
comp29005_c0_seq9.p3	sp|Q9JI39|ABCBA_MOUSE_ATP-binding_cassette_sub-family_B_member_10,_mitochondrial_OS=Mus_musculus_GN=Abcb10_PE=2_SV=1	7.00E-12
comp29006_c0_seq3.p1	sp|P38530|HSF2_CHICK_Heat_shock_factor_protein_2_OS=Gallus_gallus_GN=HSF2_PE=2_SV=1	8.00E-18
comp29006_c0_seq3.p2	sp|Q6XI71|NDKA_DROYA_Nucleoside_diphosphate_kinase_(Fragment)_OS=Drosophila_yakuba_GN=awd_PE=2_SV=1	2.00E-63
comp29009_c0_seq1.p1	sp|Q8T1C6|GNT1_DICDI_[Skp1-protein]-hydroxyproline_N-acetylglucosaminyltransferase_OS=Dictyostelium_discoideum_GN=gnt1_PE=1_SV=2	1.00E-26
comp29009_c0_seq2.p1	sp|Q8T1C6|GNT1_DICDI_[Skp1-protein]-hydroxyproline_N-acetylglucosaminyltransferase_OS=Dictyostelium_discoideum_GN=gnt1_PE=1_SV=2	8.00E-27
comp29010_c0_seq3.p1	sp|Q6NTW6|ULA1_XENLA_NEDD8-activating_enzyme_E1_regulatory_subunit_OS=Xenopus_laevis_GN=nae1_PE=2_SV=1	8.00E-141
comp29011_c0_seq1.p1		
comp29011_c0_seq1.p5		
comp29011_c0_seq2.p1		
comp29011_c0_seq2.p5		
comp29012_c0_seq2.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	5.00E-36
comp29013_c0_seq1.p1	sp|Q2TBN3|CETN2_BOVIN_Centrin-2_OS=Bos_taurus_GN=CETN2_PE=2_SV=1	1.00E-32
comp29013_c0_seq6.p1	sp|Q24956|CATR_GIAIN_Caltractin_OS=Giardia_intestinalis_GN=CAL_PE=3_SV=1	2.00E-16
comp29014_c0_seq1.p2		
comp29015_c0_seq2.p1		
comp29016_c0_seq1.p1	sp|Q8W471|AAE15_ARATH_Long-chain-fatty-acid--[acyl-carrier-protein]_ligase_AEE15,_chloroplastic_OS=Arabidopsis_thaliana_GN=AAE15_PE=1_SV=1	2.00E-109
comp29018_c0_seq1.p1		
comp29018_c0_seq2.p1		
comp29019_c0_seq1.p1		
comp29020_c0_seq1.p1		
comp29021_c0_seq1.p1		
comp29021_c0_seq2.p1		
comp29021_c0_seq3.p1		
comp29022_c0_seq1.p1	sp|P45816|SEC14_YARLI_SEC14_cytosolic_factor_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=SEC14_PE=3_SV=2	8.00E-16
comp29022_c0_seq2.p1		
comp29023_c0_seq2.p1	sp|Q9ZMJ9|HCPE_HELPJ_Putative_beta-lactamase_hcpE_OS=Helicobacter_pylori_(strain_J99)_GN=hcpE_PE=3_SV=1	2.00E-15
comp29024_c0_seq2.p1	sp|Q93VV0|ZDHC6_ARATH_Probable_S-acyltransferase_At3g09320_OS=Arabidopsis_thaliana_GN=At3g09320_PE=2_SV=1	1.00E-33
comp29025_c1_seq1.p1		
comp29025_c1_seq1.p4		
comp29026_c0_seq2.p1		
comp29026_c0_seq3.p1		
comp29026_c1_seq1.p1		
comp29027_c0_seq3.p1		
comp29027_c0_seq4.p1		
comp29028_c0_seq1.p1	sp|Q6PFX9|TNKS1_MOUSE_Tankyrase-1_OS=Mus_musculus_GN=Tnks_PE=1_SV=1	1.00E-16
comp29028_c0_seq2.p1	sp|Q6PFX9|TNKS1_MOUSE_Tankyrase-1_OS=Mus_musculus_GN=Tnks_PE=1_SV=1	1.00E-16

comp29028_c0_seq3.p1	sp|Q6PFX9|TNKS1_MOUSE_Tankyrase-1_OS=Mus_musculus_GN=Tnks_PE=1_SV=1	1.00E-16
comp29028_c0_seq5.p1	sp|Q6PFX9|TNKS1_MOUSE_Tankyrase-1_OS=Mus_musculus_GN=Tnks_PE=1_SV=1	1.00E-16
comp29029_c0_seq1.p1	sp|Q703I2|ALF_THECA_Fructose-bisphosphate_aldolase_OS=Thermus_caldophilus_GN=fba_PE=1_SV=1	1.00E-38
comp29030_c0_seq1.p1		
comp29030_c0_seq2.p1		
comp29031_c0_seq1.p1	sp|Q14974|IMB1_HUMAN_Importin_subunit_beta-1_OS=Homo_sapiens_GN=KPNB1_PE=1_SV=2	0
comp29031_c0_seq2.p1	sp|Q14974|IMB1_HUMAN_Importin_subunit_beta-1_OS=Homo_sapiens_GN=KPNB1_PE=1_SV=2	0
comp29031_c1_seq1.p3		
comp29032_c0_seq3.p1	sp|Q06190|P2R3A_HUMAN_Serine/threonine-protein_phosphatase_2A_regulatory_subunit_B''_subunit_alpha_OS=Homo_sapiens_GN=PPP2R3A_PE=1_SV=1	7.00E-79
comp29032_c0_seq3.p4	sp|Q54FM3|EI2BD_DICDI_Translation_initiation_factor_eIF-2B_subunit_delta_OS=Dictyostelium_discoideum_GN=eif2b4_PE=3_SV=1	7.00E-11
comp29032_c0_seq4.p1	sp|Q61749|EI2BD_MOUSE_Translation_initiation_factor_eIF-2B_subunit_delta_OS=Mus_musculus_GN=Eif2b4_PE=2_SV=2	5.00E-82
comp29033_c0_seq2.p1	sp|Q9SRH6|HIR3_ARATH_Hypersensitive-induced_response_protein_3_OS=Arabidopsis_thaliana_GN=HIR3_PE=1_SV=1	2.00E-16
comp29034_c0_seq2.p1		
comp29034_c0_seq3.p1		
comp29035_c0_seq1.p1		
comp29035_c0_seq3.p1		
comp29035_c0_seq4.p2		
comp29035_c0_seq8.p1		
comp29036_c1_seq3.p1	sp|Q2R2Z4|GDT12_ORYSJ_GDT1-like_protein_2,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=Os11g0544500_PE=2_SV=1	3.00E-37
comp29037_c1_seq2.p1		
comp29041_c0_seq2.p1	sp|Q8L7M4|SDN5_ARATH_Small_RNA_degrading_nuclease_5_OS=Arabidopsis_thaliana_GN=SDN5_PE=2_SV=2	2.00E-45
comp29041_c0_seq2.p3		
comp29043_c0_seq1.p1	sp|Q9M9Y8|CRTSO_ARATH_Prolycopene_isomerase,_chloroplastic_OS=Arabidopsis_thaliana_GN=CRTISO_PE=2_SV=2	4.00E-57
comp29043_c0_seq2.p1	sp|Q9M9Y8|CRTSO_ARATH_Prolycopene_isomerase,_chloroplastic_OS=Arabidopsis_thaliana_GN=CRTISO_PE=2_SV=2	2.00E-49
comp29043_c0_seq2.p3	sp|Q6NUM9|RETST_HUMAN_All-trans-retinol_13,14-reductase_OS=Homo_sapiens_GN=RETSAT_PE=2_SV=2	2.00E-11
comp29044_c0_seq1.p1		
comp29045_c0_seq2.p1		
comp29045_c0_seq7.p1		
comp29045_c0_seq8.p1		
comp29045_c0_seq9.p1		
comp29046_c0_seq1.p1	sp|Q0P5L5|SUMF1_BOVIN_Sulfatase-modifying_factor_1_OS=Bos_taurus_GN=SUMF1_PE=2_SV=1	3.00E-62
comp29047_c0_seq2.p1		
comp29048_c0_seq1.p2		
comp29049_c0_seq2.p1	sp|Q1D4R3|NADD_MYXXD_Probable_nicotinate-nucleotide_adenylyltransferase_OS=Myxococcus_xanthus_(strain_DK_1622)_GN=nadD_PE=3_SV=1	9.00E-12
comp29049_c0_seq3.p1		
comp29050_c0_seq1.p2	sp|Q9QYF1|RDH11_MOUSE_Retinol_dehydrogenase_11_OS=Mus_musculus_GN=Rdh11_PE=2_SV=2	9.00E-14
comp29051_c1_seq1.p1	sp|Q8BFY9|TNPO1_MOUSE_Transportin-1_OS=Mus_musculus_GN=Tnpo1_PE=1_SV=2	3.00E-59
comp29051_c1_seq3.p1	sp|Q8BFY9|TNPO1_MOUSE_Transportin-1_OS=Mus_musculus_GN=Tnpo1_PE=1_SV=2	4.00E-115
comp29053_c0_seq1.p1	sp|Q9XHL5|HMDH3_ORYSJ_3-hydroxy-3-methylglutaryl-coenzyme_A_reductase_3_OS=Oryza_sativa_subsp._japonica_GN=HMG3_PE=2_SV=2	2.00E-156
comp29056_c0_seq1.p1		
comp29057_c0_seq2.p1	sp|Q5SXJ3|FANCJ_MOUSE_Fanconi_anemia_group_J_protein_homolog_OS=Mus_musculus_GN=Brip1_PE=2_SV=1	9.00E-118
comp29058_c0_seq2.p1		
comp29059_c0_seq2.p1		
comp29059_c0_seq3.p1		
comp29059_c0_seq6.p1		
comp29059_c0_seq6.p2	sp|P87149|MRS2_SCHPO_Mitochondrial_inner_membrane_magnesium_transporter_mrs2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=mrs2_PE=2_SV=1	3.00E-30
comp29060_c0_seq2.p1		
comp29060_c0_seq3.p1	sp|P23641|MPCP_YEAST_Mitochondrial_phosphate_carrier_protein_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=MIR1_PE=1_SV=1	8.00E-17
comp29060_c0_seq3.p2		
comp29061_c0_seq2.p2	sp|Q9SAC0|ZCIS_ARATH_15-cis-zeta-carotene_isomerase,_chloroplastic_OS=Arabidopsis_thaliana_GN=Z-ISO_PE=1_SV=1	1.00E-77
comp29061_c1_seq1.p1		
comp29061_c1_seq2.p1		
comp29061_c1_seq3.p1		
comp29063_c0_seq10.p1		
comp29063_c0_seq10.p2	sp|Q8W593|LGUC_ARATH_Probable_lactoylglutathione_lyase,_chloroplast_OS=Arabidopsis_thaliana_GN=At1g67280_PE=2_SV=1	2.00E-14
comp29063_c0_seq13.p1	sp|Q54E04|VATM_DICDI_Vacuolar_proton_translocating_ATPase_100_kDa_subunit_OS=Dictyostelium_discoideum_GN=vatM_PE=1_SV=2	2.00E-173
comp29063_c0_seq5.p1		
comp29063_c0_seq5.p2	sp|Q8W593|LGUC_ARATH_Probable_lactoylglutathione_lyase,_chloroplast_OS=Arabidopsis_thaliana_GN=At1g67280_PE=2_SV=1	2.00E-14
comp29063_c0_seq8.p1		
comp29063_c0_seq8.p2	sp|Q8W593|LGUC_ARATH_Probable_lactoylglutathione_lyase,_chloroplast_OS=Arabidopsis_thaliana_GN=At1g67280_PE=2_SV=1	2.00E-14
comp29064_c0_seq2.p1		
comp29065_c0_seq1.p1		
comp29065_c2_seq1.p2		
comp29065_c2_seq3.p1		
comp29066_c0_seq2.p1	sp|P96554|Y319_MYXXA_Uncharacterized_membrane_protein_STKORF319_OS=Myxococcus_xanthus_PE=3_SV=1	6.00E-21
comp29066_c0_seq3.p1	sp|Q622Z7|GRK1_CAEBR_G_protein-coupled_receptor_kinase_1_OS=Caenorhabditis_briggsae_GN=grk-1_PE=3_SV=1	8.00E-59
comp29066_c0_seq3.p2	sp|P96554|Y319_MYXXA_Uncharacterized_membrane_protein_STKORF319_OS=Myxococcus_xanthus_PE=3_SV=1	7.00E-55
comp29066_c0_seq3.p4		
comp29066_c0_seq6.p1	sp|P32865|GPRK1_DROME_G_protein-coupled_receptor_kinase_1_OS=Drosophila_melanogaster_GN=Gprk1_PE=2_SV=2	9.00E-74
comp29066_c0_seq6.p2	sp|P96554|Y319_MYXXA_Uncharacterized_membrane_protein_STKORF319_OS=Myxococcus_xanthus_PE=3_SV=1	7.00E-55
comp29066_c0_seq7.p1	sp|Q622Z7|GRK1_CAEBR_G_protein-coupled_receptor_kinase_1_OS=Caenorhabditis_briggsae_GN=grk-1_PE=3_SV=1	5.00E-61
comp29066_c0_seq7.p3		
comp29066_c0_seq8.p1	sp|P32865|GPRK1_DROME_G_protein-coupled_receptor_kinase_1_OS=Drosophila_melanogaster_GN=Gprk1_PE=2_SV=2	7.00E-76
comp29067_c0_seq1.p1		
comp29067_c0_seq1.p2		
comp29067_c0_seq1.p3	sp|A5UY83|RUVX_ROSS1_Putative_Holliday_junction_resolvase_OS=Roseiflexus_sp._(strain_RS-1)_GN=RoseRS_3225_PE=3_SV=1	9.00E-16
comp29068_c0_seq1.p1	sp|A6VV03|RLMN_MARMS_Ribosomal_RNA_large_subunit_methyltransferase_N_OS=Marinomonas_sp._(strain_MWYL1)_GN=rlmN_PE=3_SV=1	4.00E-53
comp29068_c0_seq2.p1	sp|Q2Y6F3|RLMN_NITMU_Ribosomal_RNA_large_subunit_methyltransferase_N_OS=Nitrosospira_multiformis_(strain_ATCC_25196_/_NCIMB_11849)_GN=rlmN_PE=3_SV=1	2.00E-36
comp29068_c0_seq2.p2		
comp29070_c0_seq1.p1	sp|Q8WUK0|PTPM1_HUMAN_Protein-tyrosine_phosphatase_mitochondrial_1_OS=Homo_sapiens_GN=PTPMT1_PE=1_SV=1	1.00E-17
comp29070_c0_seq1.p2	sp|P36101|YKC7_YEAST_Uncharacterized_protein_YKL027W_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YKL027W_PE=1_SV=1	4.00E-34
comp29070_c0_seq1.p3	sp|O13861|YEXA_SCHPO_Uncharacterized_protein_C1A6.10_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC1A6.10_PE=2_SV=1	1.00E-14
comp29070_c0_seq3.p1	sp|P36101|YKC7_YEAST_Uncharacterized_protein_YKL027W_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YKL027W_PE=1_SV=1	4.00E-34
comp29070_c0_seq3.p3	sp|O13861|YEXA_SCHPO_Uncharacterized_protein_C1A6.10_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC1A6.10_PE=2_SV=1	1.00E-14
comp29070_c0_seq4.p1	sp|O13861|YEXA_SCHPO_Uncharacterized_protein_C1A6.10_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC1A6.10_PE=2_SV=1	8.00E-53
comp29070_c0_seq4.p2	sp|Q8WUK0|PTPM1_HUMAN_Protein-tyrosine_phosphatase_mitochondrial_1_OS=Homo_sapiens_GN=PTPMT1_PE=1_SV=1	1.00E-17
comp29070_c0_seq5.p1	sp|O13861|YEXA_SCHPO_Uncharacterized_protein_C1A6.10_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC1A6.10_PE=2_SV=1	8.00E-53
comp29073_c0_seq1.p1		
comp29074_c1_seq1.p1		
comp29076_c0_seq3.p1	sp|P49760|CLK2_HUMAN_Dual_specificity_protein_kinase_CLK2_OS=Homo_sapiens_GN=CLK2_PE=1_SV=1	1.00E-12
comp29077_c0_seq1.p1		
comp29078_c0_seq1.p1	sp|B1XIF6|DCUP_SYNP2_Uroporphyrinogen_decarboxylase_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=hemE_PE=3_SV=1	1.00E-111
comp29078_c0_seq2.p1	sp|B1XIF6|DCUP_SYNP2_Uroporphyrinogen_decarboxylase_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=hemE_PE=3_SV=1	2.00E-112
comp29078_c0_seq3.p1	sp|B1XIF6|DCUP_SYNP2_Uroporphyrinogen_decarboxylase_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=hemE_PE=3_SV=1	2.00E-111
comp29078_c0_seq4.p1	sp|B1XIF6|DCUP_SYNP2_Uroporphyrinogen_decarboxylase_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=hemE_PE=3_SV=1	2.00E-112
comp29079_c0_seq1.p1		
comp29080_c0_seq2.p1	sp|Q6B9X6|VWKA_DICDI_Alpha-protein_kinase_vwkA_OS=Dictyostelium_discoideum_GN=vwkA_PE=1_SV=1	3.00E-17
comp29082_c0_seq1.p1	sp|Q54JC0|CMBB_DICDI_Calmodulin-binding_protein_CmbB_OS=Dictyostelium_discoideum_GN=cmbB_PE=1_SV=1	4.00E-23
comp29082_c0_seq4.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	7.00E-34
comp29083_c1_seq1.p1	sp|Q5RCE2|STT3A_PONAB_Dolichyl-diphosphooligosaccharide--protein_glycosyltransferase_subunit_STT3A_OS=Pongo_abelii_GN=STT3A_PE=2_SV=1	0
comp29084_c0_seq1.p1		
comp29086_c0_seq1.p1	sp|Q96ST2|IWS1_HUMAN_Protein_IWS1_homolog_OS=Homo_sapiens_GN=IWS1_PE=1_SV=2	4.00E-30
comp29086_c1_seq1.p1	sp|Q5F259|AN13B_MOUSE_Ankyrin_repeat_domain-containing_protein_13B_OS=Mus_musculus_GN=Ankrd13b_PE=2_SV=1	2.00E-26
comp29086_c1_seq2.p1		
comp29087_c0_seq11.p1	sp|Q43415|LCYB_CAPAN_Lycopene_beta_cyclase,_chloroplastic/chromoplastic_OS=Capsicum_annuum_GN=LCY1_PE=2_SV=1	1.00E-71
comp29087_c0_seq13.p1	sp|Q945S8|ASHH3_ARATH_Histone-lysine_N-methyltransferase_ASHH3_OS=Arabidopsis_thaliana_GN=ASHH3_PE=2_SV=2	9.00E-37
comp29087_c0_seq2.p1		
comp29087_c0_seq6.p1	sp|Q38933|LCYB_ARATH_Lycopene_beta_cyclase,_chloroplastic_OS=Arabidopsis_thaliana_GN=LCY1_PE=2_SV=1	2.00E-33
comp29087_c0_seq7.p1	sp|Q43415|LCYB_CAPAN_Lycopene_beta_cyclase,_chloroplastic/chromoplastic_OS=Capsicum_annuum_GN=LCY1_PE=2_SV=1	6.00E-72
comp29087_c0_seq8.p1		
comp29088_c0_seq2.p1	sp|P06876|MYB_MOUSE_Transcriptional_activator_Myb_OS=Mus_musculus_GN=Myb_PE=1_SV=2	1.00E-42
comp29090_c0_seq2.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	7.00E-57
comp29091_c0_seq3.p1	sp|Q5UR04|YR911_MIMIV_Putative_ankyrin_repeat_protein_R911_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R911_PE=4_SV=1	1.00E-24
comp29093_c0_seq1.p1		
comp29093_c0_seq1.p3		
comp29095_c0_seq1.p1		
comp29096_c0_seq1.p1	sp|P32486|KRE6_YEAST_Beta-glucan_synthesis-associated_protein_KRE6_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=KRE6_PE=1_SV=2	8.00E-46
comp29097_c0_seq2.p1	sp|Q3KRC5|DUS3L_RAT_tRNA-dihydrouridine(47)_synthase_[NAD(P)(+)]-like_OS=Rattus_norvegicus_GN=Dus3l_PE=2_SV=1	1.00E-135
comp29098_c0_seq1.p1	sp|Q9FGW9|GTE10_ARATH_Transcription_factor_GTE10_OS=Arabidopsis_thaliana_GN=GTE10_PE=1_SV=2	3.00E-15
comp29098_c0_seq1.p2		
comp29098_c0_seq2.p1	sp|Q9FGW9|GTE10_ARATH_Transcription_factor_GTE10_OS=Arabidopsis_thaliana_GN=GTE10_PE=1_SV=2	6.00E-15
comp29098_c0_seq2.p3		
comp29100_c0_seq1.p1		
comp29100_c0_seq1.p2	sp|Q72GN6|DNAJ_THET2_Chaperone_protein_DnaJ_OS=Thermus_thermophilus_(strain_HB27_/_ATCC_BAA-163_/_DSM_7039)_GN=dnaJ_PE=3_SV=1	2.00E-16
comp29101_c0_seq4.p1		
comp29102_c0_seq1.p1	sp|Q9BXT6|M10L1_HUMAN_Putative_helicase_Mov10l1_OS=Homo_sapiens_GN=MOV10L1_PE=1_SV=1	2.00E-86
comp29103_c0_seq2.p1	sp|P83941|ELOC_RAT_Transcription_elongation_factor_B_polypeptide_1_OS=Rattus_norvegicus_GN=Tceb1_PE=1_SV=1	2.00E-21
comp29104_c0_seq3.p1		
comp29105_c0_seq2.p1		
comp29105_c0_seq2.p2	sp|P55189|YBAR_BACSU_Putative_sulfate_transporter_ybaR_OS=Bacillus_subtilis_GN=ybaR_PE=3_SV=2	4.00E-48
comp29105_c0_seq2.p5		
comp29105_c0_seq2.p8	sp|Q8W4P1|CDKC2_ARATH_Cyclin-dependent_kinase_C-2_OS=Arabidopsis_thaliana_GN=CDKC-2_PE=1_SV=2	2.00E-14
comp29105_c1_seq2.p1	sp|Q2LAE1|ASHH2_ARATH_Histone-lysine_N-methyltransferase_ASHH2_OS=Arabidopsis_thaliana_GN=ASHH2_PE=1_SV=1	4.00E-35
comp29106_c0_seq1.p1		
comp29106_c0_seq2.p1	sp|Q5UPD5|YL059_MIMIV_Putative_ankyrin_repeat_protein_L59_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L59_PE=4_SV=1	2.00E-15
comp29108_c0_seq1.p1	sp|Q9MA55|ACBP4_ARATH_Acyl-CoA-binding_domain-containing_protein_4_OS=Arabidopsis_thaliana_GN=ACBP4_PE=1_SV=1	1.00E-14
comp29109_c0_seq1.p1	sp|Q8H0V6|AB3F_ARATH_ABC_transporter_F_family_member_3_OS=Arabidopsis_thaliana_GN=ABCF3_PE=2_SV=1	1.00E-179
comp29111_c0_seq1.p1		
comp29111_c0_seq2.p1		
comp29111_c0_seq4.p1		
comp29112_c0_seq1.p1	sp|Q9GPF1|AP3M_DICDI_AP-3_complex_subunit_mu_OS=Dictyostelium_discoideum_GN=apm3_PE=2_SV=1	3.00E-128
comp29112_c0_seq1.p2	sp|Q54XM0|CAPTB_DICDI_Uncharacterized_CDP-alcohol_phosphatidyltransferase_class-I_family_protein_2_OS=Dictyostelium_discoideum_GN=captB_PE=3_SV=1	9.00E-46
comp29113_c0_seq1.p1		
comp29115_c0_seq1.p1		
comp29115_c0_seq1.p2		
comp29115_c0_seq4.p1		
comp29116_c1_seq1.p1	sp|Q0WL80|UGGG_ARATH_UDP-glucose:glycoprotein_glucosyltransferase_OS=Arabidopsis_thaliana_GN=UGGT_PE=1_SV=1	2.00E-31
comp29116_c1_seq2.p2		
comp29116_c2_seq1.p1		
comp29118_c0_seq3.p1		
comp29118_c0_seq3.p2		
comp29118_c0_seq4.p1	sp|Q9Y6D6|BIG1_HUMAN_Brefeldin_A-inhibited_guanine_nucleotide-exchange_protein_1_OS=Homo_sapiens_GN=ARFGEF1_PE=1_SV=2	3.00E-153
comp29119_c0_seq2.p1		
comp29120_c0_seq1.p1	sp|Q08DJ7|CT004_BOVIN_Uncharacterized_protein_C20orf4_homolog_OS=Bos_taurus_PE=2_SV=1	1.00E-33
comp29120_c0_seq3.p1		
comp29120_c0_seq3.p2	sp|Q08DJ7|CT004_BOVIN_Uncharacterized_protein_C20orf4_homolog_OS=Bos_taurus_PE=2_SV=1	6.00E-19
comp29121_c0_seq2.p1		
comp29122_c0_seq2.p1	sp|C0LGF5|Y1341_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At1g34110_OS=Arabidopsis_thaliana_GN=At1g34110_PE=2_SV=2	1.00E-93
comp29122_c0_seq3.p1	sp|Q9LP24|Y1571_ARATH_Probable_leucine-rich_repeat_receptor-like_protein_kinase_At1g35710_OS=Arabidopsis_thaliana_GN=At1g35710_PE=2_SV=1	9.00E-42
comp29123_c0_seq1.p1		
comp29123_c0_seq3.p1		
comp29124_c0_seq3.p2		
comp29125_c0_seq10.p1	sp|P28606|Y1628_SYNP2_Uncharacterized_protein_SYNPCC7002_A1628_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=SYNPCC7002_A1628_PE=3_SV=2	2.00E-62
comp29125_c0_seq10.p3	sp|Q54FE6|MCFS_DICDI_Mitochondrial_substrate_carrier_family_protein_S_OS=Dictyostelium_discoideum_GN=mcfS_PE=3_SV=1	3.00E-34
comp29125_c0_seq12.p1	sp|P28606|Y1628_SYNP2_Uncharacterized_protein_SYNPCC7002_A1628_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=SYNPCC7002_A1628_PE=3_SV=2	2.00E-62
comp29125_c0_seq12.p3	sp|Q54FE6|MCFS_DICDI_Mitochondrial_substrate_carrier_family_protein_S_OS=Dictyostelium_discoideum_GN=mcfS_PE=3_SV=1	3.00E-34
comp29125_c0_seq2.p1	sp|Q54FE6|MCFS_DICDI_Mitochondrial_substrate_carrier_family_protein_S_OS=Dictyostelium_discoideum_GN=mcfS_PE=3_SV=1	8.00E-26
comp29127_c0_seq2.p1	sp|Q9Z0H3|SNF5_MOUSE_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_B_member_1_OS=Mus_musculus_GN=Smarcb1_PE=1_SV=1	2.00E-20
comp29128_c0_seq2.p2		
comp29128_c0_seq2.p3		
comp29130_c0_seq1.p1	sp|Q9V6G5|TAZ_DROME_Tafazzin_homolog_OS=Drosophila_melanogaster_GN=Taz_PE=2_SV=2	2.00E-29
comp29130_c0_seq3.p1		
comp29130_c0_seq3.p2		
comp29132_c0_seq3.p1		
comp29133_c0_seq2.p2		
comp29133_c0_seq3.p2		
comp29134_c0_seq1.p1	sp|A6H909|TBPL2_RAT_TATA_box-binding_protein-like_protein_2_OS=Rattus_norvegicus_GN=Tbpl2_PE=2_SV=1	2.00E-40
comp29134_c0_seq2.p1	sp|P46272|TBP_ACECL_TATA-box-binding_protein_OS=Acetabularia_cliftonii_PE=2_SV=1	1.00E-37
comp29134_c0_seq4.p1	sp|P26356|TBP1_WHEAT_TATA-box-binding_protein_1_OS=Triticum_aestivum_GN=TBP1_PE=2_SV=1	1.00E-16
comp29135_c0_seq2.p1		
comp29135_c0_seq2.p3		
comp29137_c0_seq1.p1	sp|Q84VQ3|CIPKQ_ARATH_CBL-interacting_serine/threonine-protein_kinase_26_OS=Arabidopsis_thaliana_GN=CIPK26_PE=2_SV=2	1.00E-55
comp29137_c0_seq2.p1		
comp29137_c0_seq2.p2	sp|Q84VQ3|CIPKQ_ARATH_CBL-interacting_serine/threonine-protein_kinase_26_OS=Arabidopsis_thaliana_GN=CIPK26_PE=2_SV=2	1.00E-55
comp29138_c0_seq1.p1	sp|A3AVH5|RH13_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_13_OS=Oryza_sativa_subsp._japonica_GN=Os04g0510400_PE=2_SV=2	8.00E-40
comp29138_c0_seq1.p2		
comp29138_c0_seq2.p1	sp|A3AVH5|RH13_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_13_OS=Oryza_sativa_subsp._japonica_GN=Os04g0510400_PE=2_SV=2	4.00E-40
comp29138_c0_seq2.p3		
comp29139_c0_seq1.p1	sp|Q4V837|DTLA_XENLA_Denticleless_protein_homolog_A_OS=Xenopus_laevis_GN=dtl-a_PE=2_SV=1	3.00E-21
comp29139_c0_seq1.p2	sp|P53490|ARP3_ACACA_Actin-related_protein_3_OS=Acanthamoeba_castellanii_GN=ARP3_PE=2_SV=1	0
comp29139_c1_seq1.p1	sp|Q76MY7|CYH2_CHLAE_Cytohesin-2_OS=Chlorocebus_aethiops_GN=CYTH2_PE=2_SV=1	2.00E-58
comp29139_c1_seq2.p1		
comp29141_c1_seq1.p1		
comp29141_c1_seq2.p1		
comp29141_c1_seq2.p2	sp|D0N761|GATB_PHYIT_Glutamyl-tRNA(Gln)_amidotransferase_subunit_B,_mitochondrial_OS=Phytophthora_infestans_(strain_T30-4)_GN=PITG_07062_PE=3_SV=1	8.00E-127
comp29141_c1_seq4.p1		
comp29141_c1_seq4.p2	sp|D0N761|GATB_PHYIT_Glutamyl-tRNA(Gln)_amidotransferase_subunit_B,_mitochondrial_OS=Phytophthora_infestans_(strain_T30-4)_GN=PITG_07062_PE=3_SV=1	4.00E-119
comp29142_c0_seq1.p1	sp|P49595|PP2C1_CAEEL_Probable_protein_phosphatase_2C_F42G9.1_OS=Caenorhabditis_elegans_GN=F42G9.1_PE=2_SV=2	5.00E-54
comp29143_c0_seq1.p1		
comp29143_c0_seq1.p3	sp|Q9Z0V7|TI17B_MOUSE_Mitochondrial_import_inner_membrane_translocase_subunit_Tim17-B_OS=Mus_musculus_GN=Timm17b_PE=2_SV=1	8.00E-37
comp29143_c0_seq1.p5		
comp29145_c0_seq1.p1		
comp29145_c0_seq2.p1	sp|Q8BPM0|DAAM1_MOUSE_Disheveled-associated_activator_of_morphogenesis_1_OS=Mus_musculus_GN=Daam1_PE=2_SV=4	9.00E-31
comp29146_c0_seq1.p1	sp|Q9SYM1|MSL6_ARATH_Mechanosensitive_ion_channel_protein_6_OS=Arabidopsis_thaliana_GN=MSL6_PE=1_SV=1	3.00E-19
comp29147_c0_seq1.p1	sp|P54644|KRAC_DICDI_RAC_family_serine/threonine-protein_kinase_homolog_OS=Dictyostelium_discoideum_GN=pkbA_PE=1_SV=1	2.00E-43
comp29148_c0_seq3.p1		
comp29148_c0_seq4.p1		
comp29149_c0_seq2.p1		
comp29150_c0_seq2.p1		
comp29150_c0_seq4.p1		
comp29151_c0_seq1.p1		
comp29152_c0_seq3.p2		
comp29152_c0_seq4.p1	sp|Q9M1K2|PI5K4_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_4_OS=Arabidopsis_thaliana_GN=PIP5K4_PE=1_SV=1	3.00E-19
comp29154_c0_seq1.p1	sp|Q6WWW4|UPL3_ARATH_E3_ubiquitin-protein_ligase_UPL3_OS=Arabidopsis_thaliana_GN=UPL3_PE=1_SV=1	3.00E-51
comp29156_c0_seq1.p1		
comp29157_c0_seq1.p2		
comp29157_c0_seq2.p1		
comp29158_c0_seq2.p1		
comp29159_c0_seq1.p1		
comp29159_c0_seq3.p1		
comp29161_c0_seq1.p1	sp|O43670|ZN207_HUMAN_Zinc_finger_protein_207_OS=Homo_sapiens_GN=ZNF207_PE=1_SV=1	2.00E-29
comp29161_c0_seq1.p2		
comp29161_c0_seq3.p1	sp|O43670|ZN207_HUMAN_Zinc_finger_protein_207_OS=Homo_sapiens_GN=ZNF207_PE=1_SV=1	2.00E-29
comp29161_c0_seq5.p1	sp|O43670|ZN207_HUMAN_Zinc_finger_protein_207_OS=Homo_sapiens_GN=ZNF207_PE=1_SV=1	1.00E-29
comp29161_c0_seq5.p2		
comp29161_c0_seq6.p1	sp|O43670|ZN207_HUMAN_Zinc_finger_protein_207_OS=Homo_sapiens_GN=ZNF207_PE=1_SV=1	2.00E-29
comp29161_c0_seq8.p1	sp|O43670|ZN207_HUMAN_Zinc_finger_protein_207_OS=Homo_sapiens_GN=ZNF207_PE=1_SV=1	1.00E-29
comp29162_c0_seq2.p1		
comp29162_c0_seq6.p1		
comp29162_c0_seq8.p2		
comp29162_c0_seq9.p1		
comp29163_c0_seq1.p1	sp|Q9P2D7|DYH1_HUMAN_Dynein_heavy_chain_1,_axonemal_OS=Homo_sapiens_GN=DNAH1_PE=1_SV=4	0
comp29163_c0_seq2.p1	sp|Q63164|DYH1_RAT_Dynein_heavy_chain_1,_axonemal_OS=Rattus_norvegicus_GN=Dnah1_PE=2_SV=2	9.00E-125
comp29163_c0_seq3.p1	sp|Q9P2D7|DYH1_HUMAN_Dynein_heavy_chain_1,_axonemal_OS=Homo_sapiens_GN=DNAH1_PE=1_SV=4	2.00E-121
comp29163_c0_seq4.p1	sp|Q9P2D7|DYH1_HUMAN_Dynein_heavy_chain_1,_axonemal_OS=Homo_sapiens_GN=DNAH1_PE=1_SV=4	6.00E-122
comp29163_c0_seq5.p1	sp|Q63164|DYH1_RAT_Dynein_heavy_chain_1,_axonemal_OS=Rattus_norvegicus_GN=Dnah1_PE=2_SV=2	0
comp29163_c0_seq6.p1	sp|Q63164|DYH1_RAT_Dynein_heavy_chain_1,_axonemal_OS=Rattus_norvegicus_GN=Dnah1_PE=2_SV=2	0
comp29163_c0_seq7.p1	sp|Q63164|DYH1_RAT_Dynein_heavy_chain_1,_axonemal_OS=Rattus_norvegicus_GN=Dnah1_PE=2_SV=2	2.00E-136
comp29163_c0_seq8.p1	sp|Q9P2D7|DYH1_HUMAN_Dynein_heavy_chain_1,_axonemal_OS=Homo_sapiens_GN=DNAH1_PE=1_SV=4	0
comp29164_c0_seq1.p1	sp|Q0V9F1|VTC2_XENTR_GDP-D-glucose_phosphorylase_C15orf58_homolog_OS=Xenopus_tropicalis_PE=2_SV=1	7.00E-14
comp29164_c0_seq2.p1	sp|Q8RWE8|GGAP1_ARATH_GDP-L-galactose_phosphorylase_1_OS=Arabidopsis_thaliana_GN=VTC2_PE=1_SV=1	3.00E-13
comp29164_c0_seq4.p1		
comp29165_c0_seq2.p1		
comp29165_c0_seq3.p1		
comp29165_c0_seq5.p1		
comp29166_c0_seq1.p1		
comp29167_c0_seq1.p1	sp|O00462|MANBA_HUMAN_Beta-mannosidase_OS=Homo_sapiens_GN=MANBA_PE=1_SV=3	4.00E-44
comp29167_c0_seq1.p2		
comp29167_c0_seq10.p2		
comp29167_c0_seq3.p1	sp|Q5BCI8|MANBA_EMENI_Probable_beta-mannosidase_A_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=mndA_PE=3_SV=1	1.00E-13
comp29167_c0_seq7.p1	sp|Q5BCI8|MANBA_EMENI_Probable_beta-mannosidase_A_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=mndA_PE=3_SV=1	4.00E-12
comp29167_c0_seq9.p1	sp|O00462|MANBA_HUMAN_Beta-mannosidase_OS=Homo_sapiens_GN=MANBA_PE=1_SV=3	3.00E-42
comp29168_c0_seq2.p1		
comp29169_c0_seq1.p2		
comp29170_c0_seq2.p1		
comp29170_c0_seq3.p1		
comp29171_c0_seq1.p1	sp|Q54BF6|MCFN_DICDI_Mitochondrial_substrate_carrier_family_protein_N_OS=Dictyostelium_discoideum_GN=mcfN_PE=1_SV=2	3.00E-31
comp29172_c0_seq1.p3		
comp29173_c0_seq1.p1		
comp29174_c0_seq1.p1		
comp29174_c0_seq2.p1		
comp29176_c0_seq3.p1	sp|Q6GJZ6|LIP2_STAAR_Lipase_2_OS=Staphylococcus_aureus_(strain_MRSA252)_GN=lip2_PE=3_SV=1	8.00E-17
comp29177_c0_seq1.p1	sp|Q5R495|OXSR1_PONAB_Serine/threonine-protein_kinase_OSR1_OS=Pongo_abelii_GN=OXSR1_PE=2_SV=1	1.00E-91
comp29177_c1_seq2.p1	sp|P23231|TOM70_NEUCR_Mitochondrial_import_receptor_subunit_tom-70_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=tom-70_PE=2_SV=2	2.00E-19
comp29178_c0_seq1.p1	sp|O64530|STR1_ARATH_Thiosulfate/3-mercaptopyruvate_sulfurtransferase_1,_mitochondrial_OS=Arabidopsis_thaliana_GN=STR1_PE=1_SV=1	2.00E-67
comp29179_c0_seq1.p1		
comp29179_c0_seq2.p1		
comp29181_c0_seq2.p1	sp|Q9UJK0|TSR3_HUMAN_Probable_ribosome_biogenesis_protein_C16orf42_OS=Homo_sapiens_GN=C16orf42_PE=1_SV=1	3.00E-34
comp29181_c0_seq2.p3		
comp29181_c0_seq4.p2	sp|Q9UJK0|TSR3_HUMAN_Probable_ribosome_biogenesis_protein_C16orf42_OS=Homo_sapiens_GN=C16orf42_PE=1_SV=1	2.00E-57
comp29181_c0_seq4.p4	sp|Q2N2K3|PHYK_WHEAT_Probable_phytol_kinase,_chloroplastic_OS=Triticum_aestivum_PE=2_SV=1	1.00E-15
comp29181_c0_seq6.p1	sp|Q9UJK0|TSR3_HUMAN_Probable_ribosome_biogenesis_protein_C16orf42_OS=Homo_sapiens_GN=C16orf42_PE=1_SV=1	2.00E-57
comp29181_c0_seq7.p1	sp|Q2N2K3|PHYK_WHEAT_Probable_phytol_kinase,_chloroplastic_OS=Triticum_aestivum_PE=2_SV=1	1.00E-38
comp29181_c0_seq7.p2	sp|Q9UJK0|TSR3_HUMAN_Probable_ribosome_biogenesis_protein_C16orf42_OS=Homo_sapiens_GN=C16orf42_PE=1_SV=1	2.00E-57
comp29183_c0_seq1.p1		
comp29184_c0_seq1.p1		
comp29184_c0_seq3.p1		
comp29184_c0_seq4.p1		
comp29184_c0_seq5.p1		
comp29185_c0_seq1.p1	sp|Q8CIM1|LRC45_MOUSE_Leucine-rich_repeat-containing_protein_45_OS=Mus_musculus_GN=Lrrc45_PE=2_SV=2	2.00E-31
comp29186_c0_seq1.p1	sp|O15976|GNAO_MIZYE_Guanine_nucleotide-binding_protein_G(o)_subunit_alpha_OS=Mizuhopecten_yessoensis_GN=SCGOA_PE=2_SV=3	8.00E-91
comp29186_c0_seq2.p1	sp|P34046|GPA8_DICDI_Guanine_nucleotide-binding_protein_alpha-8_subunit_OS=Dictyostelium_discoideum_GN=gpaH_PE=2_SV=2	9.00E-99
comp29187_c0_seq1.p1	sp|P86491|6HN3M_PSEFL_6-hydroxynicotinate_3-monooxygenase_OS=Pseudomonas_fluorescens_PE=1_SV=1	2.00E-13

comp29188_c0_seq1.p1	sp|Q1XDD1|PSBC_PORYE_Photosystem_II_CP43_chlorophyll_apoprotein_OS=Porphyra_yezoensis_GN=psbC_PE=3_SV=1	0	[illegible]	[illegible]
comp29188_c0_seq1.p2	sp|B2XTH7|PSBD_HETA4_Photosystem_II_D2_protein_OS=Heterosigma_akashiwo_(strain_CCMP452)_GN=psbD1_PE=3_SV=1	0	[illegible]	[illegible]
comp29189_c0_seq1.p1	sp|P15651|ACADS_RAT_Short-chain_specific_acyl-CoA_dehydrogenase,_mitochondrial_OS=Rattus_norvegicus_GN=Acads_PE=1_SV=2	5.00E-173	[illegible]	[illegible]
comp29190_c0_seq4.p1				
comp29190_c0_seq5.p1	sp|Q6M9M7|Y1998_PARUW_Uncharacterized_RNA_methyltransferase_pc1998_OS=Protochlamydia_amoebophila_(strain_UWE25)_GN=pc1998_PE=3_SV=1	1.00E-19	GO:0001510,GO:0006396,GO:0008168,GO:0008173,GO:0016740,GO:0032259,GO:0046872,GO:0051536,GO:0051539	[illegible]
comp29190_c0_seq6.p1	sp|Q6M9M7|Y1998_PARUW_Uncharacterized_RNA_methyltransferase_pc1998_OS=Protochlamydia_amoebophila_(strain_UWE25)_GN=pc1998_PE=3_SV=1	3.00E-65	GO:0001510,GO:0006396,GO:0008168,GO:0008173,GO:0016740,GO:0032259,GO:0046872,GO:0051536,GO:0051539	[illegible]
comp29191_c0_seq2.p1	sp|Q8BKE9|IFT74_MOUSE_Intraflagellar_transport_protein_74_homolog_OS=Mus_musculus_GN=Ift74_PE=1_SV=2	7.00E-68	[illegible]	[illegible]
comp29191_c0_seq3.p1	sp|Q8BKE9|IFT74_MOUSE_Intraflagellar_transport_protein_74_homolog_OS=Mus_musculus_GN=Ift74_PE=1_SV=2	9.00E-30	[illegible]	[illegible]
comp29192_c0_seq3.p1				
comp29192_c0_seq5.p1	sp|Q757J8|IPYR_ASHGO_Inorganic_pyrophosphatase_OS=Ashbya_gossypii_(strain_ATCC_10895_/_CBS_109.51_/_FGSC_9923_/_NRRL_Y-1056)_GN=IPP1_PE=3_SV=1	2.00E-74	GO:0000287,GO:0004427,GO:0004427,GO:0005737,GO:0005737,GO:0005737,GO:0006796,GO:0016787,GO:0046872	[illegible]
comp29193_c0_seq1.p1				
comp29193_c0_seq2.p2				
comp29193_c0_seq4.p1				
comp29194_c0_seq1.p1				
comp29195_c0_seq1.p1	sp|P54689|ILVE_HAEIN_Branched-chain-amino-acid_aminotransferase_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=ilvE_PE=3_SV=1	6.00E-98	[illegible]	[illegible]
comp29195_c0_seq3.p1	sp|P54689|ILVE_HAEIN_Branched-chain-amino-acid_aminotransferase_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=ilvE_PE=3_SV=1	5.00E-90	[illegible]	[illegible]
comp29196_c0_seq1.p1	sp|O14686|MLL2_HUMAN_Histone-lysine_N-methyltransferase_MLL2_OS=Homo_sapiens_GN=MLL2_PE=1_SV=2	3.00E-18	[illegible]	[illegible]
comp29197_c0_seq1.p1				
comp29197_c0_seq3.p1				
comp29198_c0_seq1.p1				
comp29199_c0_seq6.p1				
comp29200_c0_seq1.p1				
comp29200_c0_seq1.p2				
comp29200_c0_seq11.p1				
comp29200_c0_seq11.p2				
comp29200_c0_seq12.p1				
comp29200_c0_seq12.p2				
comp29200_c0_seq2.p1				
comp29200_c0_seq3.p1				
comp29200_c0_seq3.p2				
comp29200_c0_seq4.p1				
comp29200_c0_seq4.p2				
comp29200_c0_seq5.p1				
comp29200_c0_seq5.p2				
comp29200_c0_seq5.p3				
comp29200_c0_seq6.p1				
comp29200_c0_seq7.p1				
comp29200_c0_seq7.p2				
comp29200_c0_seq8.p1				
comp29200_c0_seq8.p2				
comp29200_c0_seq8.p3				
comp29200_c0_seq9.p1				
comp29200_c0_seq9.p2				
comp29201_c0_seq3.p1				
comp29201_c0_seq5.p1	sp|Q12980|NPRL3_HUMAN_Nitrogen_permease_regulator_3-like_protein_OS=Homo_sapiens_GN=NPRL3_PE=1_SV=1	7.00E-20	GO:0003674,GO:0005096,GO:0005575,GO:0008150,GO:0043547	[illegible]
comp29202_c0_seq2.p1	sp|P16171|MERA_BACCE_Mercuric_reductase_OS=Bacillus_cereus_GN=merA_PE=1_SV=1	2.00E-73	[illegible]	[illegible]
comp29202_c0_seq2.p2				
comp29202_c0_seq4.p1				
comp29203_c0_seq4.p1	sp|Q9XGZ9|P2C72_ARATH_Probable_protein_phosphatase_2C_72_OS=Arabidopsis_thaliana_GN=At5g26010_PE=2_SV=1	1.00E-35	[illegible]	[illegible]
comp29203_c1_seq2.p1				
comp29203_c1_seq3.p1				
comp29204_c1_seq1.p1	sp|P28178|PK2_DICDI_Protein_kinase_2_OS=Dictyostelium_discoideum_GN=pkgB_PE=1_SV=1	3.00E-37	[illegible]	[illegible]
comp29205_c0_seq2.p3				
comp29205_c0_seq3.p3				
comp29206_c0_seq1.p1	sp|Q3U3W5|ANM10_MOUSE_Putative_protein_arginine_N-methyltransferase_10_OS=Mus_musculus_GN=Prmt10_PE=2_SV=2	1.00E-17	GO:0003674,GO:0005575,GO:0005737,GO:0006479,GO:0008150,GO:0008168,GO:0008168,GO:0008276,GO:0016740,GO:0032259	[illegible]
comp29206_c0_seq1.p2				
comp29206_c0_seq2.p1	sp|Q3U3W5|ANM10_MOUSE_Putative_protein_arginine_N-methyltransferase_10_OS=Mus_musculus_GN=Prmt10_PE=2_SV=2	3.00E-43	GO:0003674,GO:0005575,GO:0005737,GO:0006479,GO:0008150,GO:0008168,GO:0008168,GO:0008276,GO:0016740,GO:0032259	[illegible]
comp29206_c0_seq2.p2				
comp29207_c0_seq2.p1				
comp29208_c0_seq1.p1	sp|Q9DBV3|DHX34_MOUSE_Probable_ATP-dependent_RNA_helicase_DHX34_OS=Mus_musculus_GN=Dhx34_PE=2_SV=2	0	[illegible]	[illegible]
comp29208_c0_seq1.p2				
comp29210_c0_seq2.p1				
comp29210_c0_seq3.p1				
comp29210_c0_seq5.p1				
comp29211_c0_seq1.p1				
comp29212_c0_seq2.p1	sp|Q01RY8|PSUG_SOLUE_Pseudouridine-5'-phosphate_glycosidase_OS=Solibacter_usitatus_(strain_Ellin6076)_GN=psuG_PE=3_SV=1	2.00E-97	GO:0001522,GO:0001522,GO:0004730,GO:0004730,GO:0008152,GO:0016787,GO:0016798,GO:0016798,GO:0016829,GO:0046113,GO:0046872	[illegible]
comp29212_c0_seq4.p1	sp|Q01RY8|PSUG_SOLUE_Pseudouridine-5'-phosphate_glycosidase_OS=Solibacter_usitatus_(strain_Ellin6076)_GN=psuG_PE=3_SV=1	2.00E-99	GO:0001522,GO:0001522,GO:0004730,GO:0004730,GO:0008152,GO:0016787,GO:0016798,GO:0016798,GO:0016829,GO:0046113,GO:0046872	[illegible]
comp29212_c0_seq4.p3				
comp29213_c0_seq4.p2	sp|Q9S7Q2|PP124_ARATH_Pentatricopeptide_repeat-containing_protein_At1g74850,_chloroplastic_OS=Arabidopsis_thaliana_GN=PTAC2_PE=2_SV=1	9.00E-34	[illegible]	[illegible]
comp29213_c0_seq4.p3				
comp29214_c0_seq1.p1				
comp29215_c0_seq1.p2	sp|P49030|MGN_ORYSJ_Protein_mago_nashi_homolog_OS=Oryza_sativa_subsp._japonica_GN=Os12g0287200_PE=2_SV=1	2.00E-81	GO:0005634,GO:0005634,GO:0005634	[illegible]
comp29215_c0_seq1.p3	sp|Q9LJ98|PFD2_ARATH_Probable_prefoldin_subunit_2_OS=Arabidopsis_thaliana_GN=At3g22480_PE=2_SV=1	4.00E-24	GO:0006457,GO:0016272,GO:0051082	[illegible]
comp29216_c0_seq5.p1				
comp29216_c0_seq5.p2	sp|Q9UNH5|CC14A_HUMAN_Dual_specificity_protein_phosphatase_CDC14A_OS=Homo_sapiens_GN=CDC14A_PE=1_SV=1	1.00E-41	[illegible]	[illegible]
comp29217_c0_seq1.p1				
comp29217_c1_seq1.p1				
comp29217_c1_seq2.p1				
comp29217_c1_seq2.p2				
comp29217_c1_seq3.p1				
comp29217_c1_seq7.p1				
comp29217_c1_seq7.p2				
comp29217_c1_seq9.p1				
comp29219_c0_seq1.p1				
comp29219_c0_seq3.p1				
comp29221_c0_seq1.p1				
comp29221_c0_seq5.p1	sp|P51281|YCF45_PORPU_Uncharacterized_protein_ycf45_OS=Porphyra_purpurea_GN=ycf45_PE=3_SV=1	3.00E-56	GO:0000166,GO:0003676,GO:0005524,GO:0005524,GO:0009507,GO:0009507,GO:0009536	[illegible]
comp29222_c0_seq1.p1				
comp29223_c0_seq1.p1	sp|Q86Y56|HEAT2_HUMAN_HEAT_repeat-containing_protein_2_OS=Homo_sapiens_GN=HEATR2_PE=1_SV=4	7.00E-21	GO:0003341,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0036158,GO:0036158,GO:0036159,GO:0045505,GO:0031514,GO:0031514	[illegible]
comp29225_c0_seq2.p1				
comp29226_c0_seq1.p1				
comp29226_c0_seq2.p1				
comp29227_c0_seq6.p1				
comp29227_c0_seq7.p1				
comp29228_c0_seq1.p1				
comp29228_c0_seq10.p1				
comp29228_c0_seq6.p1				
comp29228_c0_seq9.p1				
comp29229_c0_seq2.p1	sp|Q8P3X4|DUSA_XANCP_tRNA-dihydrouridine_synthase_A_OS=Xanthomonas_campestris_pv._campestris_GN=dusA_PE=3_SV=1	9.00E-23	GO:0002943,GO:0003824,GO:0008033,GO:0008033,GO:0016491,GO:0016491,GO:0017150,GO:0050660,GO:0055114,GO:0055114	[illegible]
comp29229_c0_seq4.p1	sp|Q88KX0|DUSA_PSEPK_tRNA-dihydrouridine_synthase_A_OS=Pseudomonas_putida_(strain_KT2440)_GN=dusA_PE=3_SV=1	2.00E-47	GO:0002943,GO:0003824,GO:0008033,GO:0008033,GO:0016491,GO:0016491,GO:0017150,GO:0050660,GO:0055114,GO:0055114	[illegible]
comp29229_c1_seq2.p1				
comp29230_c0_seq2.p1				
comp29231_c0_seq1.p1	sp|Q62383|SPT6H_MOUSE_Transcription_elongation_factor_SPT6_OS=Mus_musculus_GN=Supt6h_PE=1_SV=2	3.00E-89	[illegible]	[illegible]
comp29233_c0_seq1.p2				
comp29233_c0_seq3.p1				
comp29234_c0_seq1.p1				
comp29238_c0_seq1.p1	sp|Q93VG8|U326_ARATH_UPF0326_protein_At4g17486_OS=Arabidopsis_thaliana_GN=At4g17486_PE=2_SV=1	2.00E-22	GO:0006508,GO:0008150,GO:0008233,GO:0016787	[illegible]
comp29238_c0_seq2.p1				
comp29240_c0_seq2.p1				
comp29240_c0_seq2.p3				
comp29240_c0_seq4.p1				
comp29241_c0_seq1.p1	sp|Q8LDP4|CP19D_ARATH_Peptidyl-prolyl_cis-trans_isomerase_CYP19-4_OS=Arabidopsis_thaliana_GN=CYP19-4_PE=1_SV=2	9.00E-54	[illegible]	[illegible]
comp29241_c0_seq2.p1	sp|Q8LDP4|CP19D_ARATH_Peptidyl-prolyl_cis-trans_isomerase_CYP19-4_OS=Arabidopsis_thaliana_GN=CYP19-4_PE=1_SV=2	8.00E-54	[illegible]	[illegible]
comp29242_c0_seq3.p1				
comp29243_c0_seq1.p1				
comp29244_c0_seq1.p1	sp|P35815|PPM1B_RAT_Protein_phosphatase_1B_OS=Rattus_norvegicus_GN=Ppm1b_PE=2_SV=1	4.00E-38	[illegible]	[illegible]
comp29244_c0_seq2.p1				
comp29244_c0_seq3.p1				
comp29245_c0_seq1.p1				
comp29245_c0_seq6.p1	sp|Q75DK1|SEC14_ASHGO_SEC14_cytosolic_factor_OS=Ashbya_gossypii_(strain_ATCC_10895_/_CBS_109.51_/_FGSC_9923_/_NRRL_Y-1056)_GN=SEC14_PE=3_SV=1	9.00E-18	GO:0000139,GO:0005215,GO:0005622,GO:0005634,GO:0005794,GO:0006810,GO:0006810,GO:0015031,GO:0016020	[illegible]
comp29246_c0_seq2.p1				
comp29246_c0_seq2.p5				
comp29246_c0_seq3.p1	sp|Q9LIE5|FHY3_ARATH_Protein_FAR-RED_ELONGATED_HYPOCOTYL_3_OS=Arabidopsis_thaliana_GN=FHY3_PE=1_SV=1	9.00E-18	[illegible]	[illegible]
comp29246_c0_seq4.p1				
comp29247_c0_seq2.p1				
comp29247_c0_seq3.p1				
comp29247_c0_seq3.p2	sp|Q54NF1|VPS28_DICDI_Vacuolar_protein_sorting-associated_protein_28_OS=Dictyostelium_discoideum_GN=vps28_PE=3_SV=1	6.00E-49	[illegible]	[illegible]
comp29247_c0_seq3.p3				
comp29248_c0_seq12.p1				
comp29248_c0_seq12.p2	sp|Q8AYC9|CHK1_CHICK_Serine/threonine-protein_kinase_Chk1_OS=Gallus_gallus_GN=CHEK1_PE=1_SV=1	1.00E-12	[illegible]	[illegible]
comp29248_c0_seq17.p1	sp|Q8AYC9|CHK1_CHICK_Serine/threonine-protein_kinase_Chk1_OS=Gallus_gallus_GN=CHEK1_PE=1_SV=1	8.00E-12	[illegible]	[illegible]
comp29248_c0_seq19.p1				
comp29248_c0_seq22.p1				
comp29248_c0_seq22.p2	sp|Q8AYC9|CHK1_CHICK_Serine/threonine-protein_kinase_Chk1_OS=Gallus_gallus_GN=CHEK1_PE=1_SV=1	2.00E-12	[illegible]	[illegible]
comp29248_c0_seq4.p1				
comp29248_c0_seq4.p2	sp|Q6CF41|FKBP_YARLI_FK506-binding_protein_1_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=FPR1_PE=3_SV=1	2.00E-17	GO:0000413,GO:0000413,GO:0003755,GO:0003755,GO:0005737,GO:0005737,GO:0006457,GO:0016853	[illegible]
comp29248_c0_seq6.p1				
comp29248_c0_seq8.p1	sp|Q8AYC9|CHK1_CHICK_Serine/threonine-protein_kinase_Chk1_OS=Gallus_gallus_GN=CHEK1_PE=1_SV=1	7.00E-12	[illegible]	[illegible]
comp29249_c0_seq10.p1	sp|A0JM56|LRRC9_XENTR_Leucine-rich_repeat-containing_protein_9_OS=Xenopus_tropicalis_GN=lrrc9_PE=2_SV=2	4.00E-17		
comp29249_c0_seq2.p1	sp|A0JM56|LRRC9_XENTR_Leucine-rich_repeat-containing_protein_9_OS=Xenopus_tropicalis_GN=lrrc9_PE=2_SV=2	3.00E-17		
comp29249_c0_seq2.p3				
comp29249_c0_seq3.p1	sp|A0JM56|LRRC9_XENTR_Leucine-rich_repeat-containing_protein_9_OS=Xenopus_tropicalis_GN=lrrc9_PE=2_SV=2	3.00E-17		
comp29249_c0_seq4.p1	sp|A0JM56|LRRC9_XENTR_Leucine-rich_repeat-containing_protein_9_OS=Xenopus_tropicalis_GN=lrrc9_PE=2_SV=2	2.00E-18		
comp29249_c0_seq8.p1	sp|A0JM56|LRRC9_XENTR_Leucine-rich_repeat-containing_protein_9_OS=Xenopus_tropicalis_GN=lrrc9_PE=2_SV=2	2.00E-17		
comp29249_c0_seq8.p3				
comp29252_c0_seq2.p1	sp|Q9P7R4|UBC8_SCHPO_Ubiquitin-conjugating_enzyme_E2_8_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ubc8_PE=2_SV=1	3.00E-67	[illegible]	[illegible]
comp29253_c0_seq3.p1	sp|Q4PE39|SEC23_USTMA_Protein_transport_protein_SEC23_OS=Ustilago_maydis_(strain_521_/_FGSC_9021)_GN=SEC23_PE=3_SV=1	0	[illegible]	[illegible]
comp29255_c0_seq2.p1				
comp29256_c0_seq1.p1				
comp29257_c0_seq1.p1				
comp29258_c0_seq3.p2				
comp29258_c0_seq4.p2				
comp29258_c0_seq5.p1				
comp29259_c0_seq1.p1	sp|P27774|KPPR_MESCR_Phosphoribulokinase,_chloroplastic_OS=Mesembryanthemum_crystallinum_PE=2_SV=1	2.00E-169	[illegible]	[illegible]
comp29260_c0_seq2.p1	sp|Q9V3G7|PSMD6_DROME_26S_proteasome_non-ATPase_regulatory_subunit_6_OS=Drosophila_melanogaster_GN=Rpn7_PE=2_SV=1	4.00E-106	GO:0000502,GO:0005838,GO:0005838,GO:0006508,GO:0006508,GO:0008541,GO:0009987,GO:0022008,GO:0043161,GO:0043161,GO:0004175	[illegible]
comp29260_c0_seq3.p1				
comp29260_c0_seq4.p1	sp|Q9V3G7|PSMD6_DROME_26S_proteasome_non-ATPase_regulatory_subunit_6_OS=Drosophila_melanogaster_GN=Rpn7_PE=2_SV=1	3.00E-84	GO:0000502,GO:0005838,GO:0005838,GO:0006508,GO:0006508,GO:0008541,GO:0009987,GO:0022008,GO:0043161,GO:0043161,GO:0004175	[illegible]
comp29260_c2_seq1.p1	sp|A8ZWU1|APT_DESOH_Adenine_phosphoribosyltransferase_OS=Desulfococcus_oleovorans_(strain_DSM_6200_/_Hxd3)_GN=apt_PE=3_SV=1	1.00E-38	[illegible]	[illegible]
comp29260_c2_seq2.p1	sp|A8ZWU1|APT_DESOH_Adenine_phosphoribosyltransferase_OS=Desulfococcus_oleovorans_(strain_DSM_6200_/_Hxd3)_GN=apt_PE=3_SV=1	1.00E-38	[illegible]	[illegible]
comp29262_c0_seq1.p1				
comp29263_c0_seq1.p1				
comp29263_c0_seq2.p1				
comp29263_c0_seq3.p1				
comp29263_c0_seq4.p1				
comp29264_c0_seq3.p1				
comp29264_c0_seq5.p1				
comp29265_c0_seq1.p1	sp|P54144|AMT11_ARATH_Ammonium_transporter_1_member_1_OS=Arabidopsis_thaliana_GN=AMT1-1_PE=1_SV=1	7.00E-88	[illegible]	[illegible]
comp29266_c0_seq1.p1				
comp29266_c0_seq2.p1	sp|P61819|CBIX_METMP_Sirohydrochlorin_cobaltochelatase_OS=Methanococcus_maripaludis_(strain_S2_/_LL)_GN=cbiX_PE=3_SV=1	7.00E-14	GO:0009236,GO:0009236,GO:0009236,GO:0016829,GO:0016852,GO:0016852,GO:0016852,GO:0019251,GO:0046872,GO:0050897,GO:0050897	[illegible]
comp29270_c0_seq1.p1	sp|Q3B724|CALS5_ARATH_Callose_synthase_5_OS=Arabidopsis_thaliana_GN=CALS5_PE=1_SV=1	1.00E-180	[illegible]	[illegible]
comp29270_c0_seq1.p7				
comp29271_c1_seq1.p2				
comp29272_c0_seq1.p1	sp|Q99JB3|FUT9_RAT_Alpha-(1,3)-fucosyltransferase_OS=Rattus_norvegicus_GN=Fut9_PE=2_SV=1	1.00E-28	[illegible]	[illegible]
comp29273_c0_seq1.p1	sp|Q9ZAE9|ACBC_ACTS5_2-epi-5-epi-valiolone_synthase_OS=Actinoplanes_sp._(strain_ATCC_31044_/_CBS_674.73_/_SE50/110)_GN=acbC_PE=3_SV=3	2.00E-82	GO:0008152,GO:0016829	[illegible]
comp29273_c0_seq1.p2	sp|Q39239|TRXH4_ARATH_Thioredoxin_H4_OS=Arabidopsis_thaliana_GN=TRX4_PE=2_SV=2	6.00E-15	GO:0005737,GO:0005737,GO:0005829,GO:0006662,GO:0015035,GO:0016671,GO:0045454,GO:0055114	[illegible]
comp29274_c0_seq2.p1	sp|Q54RV9|SGPL_DICDI_Sphingosine-1-phosphate_lyase_OS=Dictyostelium_discoideum_GN=sglA_PE=2_SV=1	1.00E-140	[illegible]	[illegible]
comp29274_c0_seq5.p1				
comp29277_c0_seq1.p1				
comp29277_c0_seq1.p3				
comp29277_c1_seq1.p1	sp|Q7ZYD9|A13CB_XENLA_Ankyrin_repeat_domain-containing_protein_13C-B_OS=Xenopus_laevis_GN=ankrd13c-b_PE=2_SV=1	4.00E-27	GO:0005783,GO:0005789,GO:0016020	[illegible]
comp29279_c0_seq2.p1				
comp29279_c0_seq3.p1	sp|Q8BIY3|ZC12D_MOUSE_Probable_ribonuclease_ZC3H12D_OS=Mus_musculus_GN=Zc3h12d_PE=2_SV=2	5.00E-14	[illegible]	[illegible]
comp29280_c0_seq2.p1	sp|Q43362|VATL_PLECA_V-type_proton_ATPase_16_kDa_proteolipid_subunit_OS=Pleurochrysis_carterae_GN=VAP_PE=2_SV=1	1.00E-72	GO:0005773,GO:0005774,GO:0006810,GO:0006811,GO:0015078,GO:0015991,GO:0015992,GO:0016020,GO:0016021,GO:0033177,GO:0033179	[illegible]
comp29281_c0_seq4.p1				
comp29281_c0_seq6.p1				
comp29281_c0_seq7.p1				
comp29281_c0_seq9.p1				
comp29282_c0_seq2.p1				
comp29284_c0_seq1.p1	sp|P17070|PCNA_ORYSJ_Proliferating_cell_nuclear_antigen_OS=Oryza_sativa_subsp._japonica_GN=Os02g0805200_PE=2_SV=2	6.00E-37	GO:0003677,GO:0003677,GO:0005634,GO:0005634,GO:0006260,GO:0006275,GO:0030337	[illegible]
comp29284_c0_seq3.p1	sp|P17070|PCNA_ORYSJ_Proliferating_cell_nuclear_antigen_OS=Oryza_sativa_subsp._japonica_GN=Os02g0805200_PE=2_SV=2	4.00E-40	GO:0003677,GO:0003677,GO:0005634,GO:0005634,GO:0006260,GO:0006275,GO:0030337	[illegible]
comp29284_c0_seq4.p1				
comp29284_c0_seq4.p2	sp|Q9ZW35|PCNA2_ARATH_Proliferating_cell_nuclear_antigen_2_OS=Arabidopsis_thaliana_GN=At2g29570_PE=1_SV=1	1.00E-93	[illegible]	[illegible]
comp29284_c0_seq4.p4				
comp29284_c0_seq5.p1	sp|Q9ZW35|PCNA2_ARATH_Proliferating_cell_nuclear_antigen_2_OS=Arabidopsis_thaliana_GN=At2g29570_PE=1_SV=1	2.00E-120	[illegible]	[illegible]
comp29285_c0_seq2.p1	sp|Q9ZV15|CDPKK_ARATH_Calcium-dependent_protein_kinase_20_OS=Arabidopsis_thaliana_GN=CPK20_PE=2_SV=1	4.00E-20	[illegible]	[illegible]
comp29285_c0_seq2.p2				
comp29287_c0_seq1.p1				
comp29292_c0_seq2.p1				
comp29292_c0_seq3.p1				
comp29292_c0_seq4.p1	sp|Q14690|RRP5_HUMAN_Protein_RRP5_homolog_OS=Homo_sapiens_GN=PDCD11_PE=1_SV=3	5.00E-64	[illegible]	[illegible]
comp29293_c0_seq1.p1	sp|P28769|TCPA_ARATH_T-complex_protein_1_subunit_alpha_OS=Arabidopsis_thaliana_GN=CCT1_PE=2_SV=1	0	[illegible]	[illegible]
comp29293_c0_seq3.p1	sp|P28769|TCPA_ARATH_T-complex_protein_1_subunit_alpha_OS=Arabidopsis_thaliana_GN=CCT1_PE=2_SV=1	0	[illegible]	[illegible]
comp29293_c0_seq3.p2				
comp29293_c0_seq3.p3	sp|Q8LB17|Y3846_ARATH_Uncharacterized_protein_At3g58460_OS=Arabidopsis_thaliana_GN=At3g58460_PE=1_SV=1	1.00E-30	GO:0004252,GO:0006508,GO:0016020,GO:0016020,GO:0016021,GO:0016021	[illegible]
comp29294_c0_seq2.p1	sp|Q1RJR2|Y321_RICBR_Uncharacterized_RNA_pseudouridine_synthase_RBE_0321_OS=Rickettsia_bellii_(strain_RML369-C)_GN=RBE_0321_PE=3_SV=1	3.00E-42	GO:0001522,GO:0003723,GO:0003723,GO:0009451,GO:0009982,GO:0016853,GO:0016866	[illegible]
comp29295_c0_seq1.p2				
comp29295_c0_seq3.p1	sp|Q0V9G6|INSI1_XENTR_Insulin-induced_gene_1_protein_OS=Xenopus_tropicalis_GN=insig1_PE=2_SV=1	1.00E-10	GO:0005783,GO:0005789,GO:0006629,GO:0008202,GO:0008203,GO:0008203,GO:0016020,GO:0016021	[illegible]
comp29295_c1_seq1.p1				
comp29296_c0_seq2.p1	sp|P52551|MYBB_XENLA_Myb-related_protein_B_OS=Xenopus_laevis_GN=mybl2_PE=2_SV=2	8.00E-39	GO:0003677,GO:0003677,GO:0003682,GO:0003700,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0007049	[illegible]
comp29297_c0_seq1.p1				
comp29297_c0_seq1.p6				
comp29297_c0_seq1.p8	sp|Q54Z01|TBCB_DICDI_Tubulin-specific_chaperone_B_OS=Dictyostelium_discoideum_GN=tbcb_PE=3_SV=1	4.00E-11	GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005874	[illegible]
comp29297_c0_seq2.p1				
comp29297_c0_seq2.p7	sp|Q54Z01|TBCB_DICDI_Tubulin-specific_chaperone_B_OS=Dictyostelium_discoideum_GN=tbcb_PE=3_SV=1	4.00E-11	GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005874	[illegible]
comp29297_c0_seq6.p1	sp|Q54Z01|TBCB_DICDI_Tubulin-specific_chaperone_B_OS=Dictyostelium_discoideum_GN=tbcb_PE=3_SV=1	5.00E-30	GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005874	[illegible]
comp29298_c0_seq1.p1	sp|Q641Z6|EHD1_RAT_EH_domain-containing_protein_1_OS=Rattus_norvegicus_GN=Ehd1_PE=1_SV=1	1.00E-56	[illegible]	[illegible]
comp29298_c0_seq2.p1	sp|Q641Z6|EHD1_RAT_EH_domain-containing_protein_1_OS=Rattus_norvegicus_GN=Ehd1_PE=1_SV=1	4.00E-57	[illegible]	[illegible]
comp29298_c0_seq3.p1	sp|Q641Z6|EHD1_RAT_EH_domain-containing_protein_1_OS=Rattus_norvegicus_GN=Ehd1_PE=1_SV=1	6.00E-44	[illegible]	[illegible]
comp29298_c0_seq4.p1	sp|Q641Z6|EHD1_RAT_EH_domain-containing_protein_1_OS=Rattus_norvegicus_GN=Ehd1_PE=1_SV=1	6.00E-43	[illegible]	[illegible]
comp29300_c0_seq2.p1				
comp29302_c0_seq1.p1				
comp29304_c0_seq1.p1	sp|P40387|TPS1_SCHPO_Alpha,alpha-trehalose-phosphate_synthase_[UDP-forming]_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=tps1_PE=1_SV=2	3.00E-115	[illegible]	[illegible]
comp29304_c0_seq2.p1	sp|Q54K57|TPSA_DICDI_Alpha,alpha-trehalose-phosphate_synthase_[UDP-forming]_A_OS=Dictyostelium_discoideum_GN=tpsA_PE=2_SV=1	6.00E-134	GO:0003824,GO:0003825,GO:0003825,GO:0005575,GO:0005975,GO:0005992,GO:0016740,GO:0016757	[illegible]
comp29305_c0_seq2.p1	sp|O88491|NSD1_MOUSE_Histone-lysine_N-methyltransferase,_H3_lysine-36_and_H4_lysine-20_specific_OS=Mus_musculus_GN=Nsd1_PE=1_SV=1	2.00E-43	[illegible]	[illegible]
comp29305_c0_seq2.p2				
comp29305_c0_seq4.p1				
comp29305_c0_seq5.p1	sp|O88491|NSD1_MOUSE_Histone-lysine_N-methyltransferase,_H3_lysine-36_and_H4_lysine-20_specific_OS=Mus_musculus_GN=Nsd1_PE=1_SV=1	4.00E-44	[illegible]	[illegible]
comp29305_c0_seq5.p2				
comp29305_c0_seq5.p6				
comp29307_c0_seq2.p1				
comp29308_c0_seq2.p1	sp|A7HHM9|URED_ANADF_Urease_accessory_protein_UreD_OS=Anaeromyxobacter_sp._(strain_Fw109-5)_GN=ureD_PE=3_SV=1	6.00E-30	GO:0005737,GO:0005737,GO:0005737,GO:0006807,GO:0016151,GO:0016151	[illegible]
comp29309_c0_seq1.p1	sp|Q9P4S5|CCA1_CANGA_CCA_tRNA_nucleotidyltransferase,_mitochondrial_OS=Candida_glabrata_(strain_ATCC_2001_/_CBS_138_/_JCM_3761_/_NBRC_0622_/_NRRL_Y-65)_GN=CCA1_PE=1_SV=2	6.00E-66	[illegible]	[illegible]
comp29311_c0_seq2.p1	sp|Q17770|PDI2_CAEEL_Protein_disulfide-isomerase_2_OS=Caenorhabditis_elegans_GN=pdi-2_PE=1_SV=1	2.00E-61	[illegible]	[illegible]
comp29312_c0_seq1.p1	sp|Q8GXU8|LPAT1_ARATH_1-acyl-sn-glycerol-3-phosphate_acyltransferase_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=LPAT1_PE=1_SV=1	6.00E-28	[illegible]	[illegible]
comp29312_c0_seq2.p1	sp|Q8GXU8|LPAT1_ARATH_1-acyl-sn-glycerol-3-phosphate_acyltransferase_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=LPAT1_PE=1_SV=1	2.00E-19	[illegible]	[illegible]
comp29312_c0_seq3.p1	sp|Q9LLY4|LPAT1_BRANA_1-acyl-sn-glycerol-3-phosphate_acyltransferase_1,_chloroplastic_OS=Brassica_napus_GN=LPAT1_PE=2_SV=1	4.00E-11	[illegible]	[illegible]
comp29313_c0_seq2.p1				
comp29314_c0_seq1.p1	sp|P16692|PHNP_ECOLI_Protein_phnP_OS=Escherichia_coli_(strain_K12)_GN=phnP_PE=1_SV=1	2.00E-12	GO:0008081,GO:0008081,GO:0016787,GO:0019700,GO:0019700,GO:0030145,GO:0046872	[illegible]
comp29314_c1_seq1.p1	sp|P16692|PHNP_ECOLI_Protein_phnP_OS=Escherichia_coli_(strain_K12)_GN=phnP_PE=1_SV=1	1.00E-75	GO:0008081,GO:0008081,GO:0016787,GO:0019700,GO:0019700,GO:0030145,GO:0046872	[illegible]
comp29315_c0_seq1.p1				
comp29315_c0_seq1.p2	sp|Q24799|MYPH_ECHGR_Myophilin_OS=Echinococcus_granulosus_PE=2_SV=1	2.00E-32		
comp29321_c0_seq1.p1				
comp29321_c1_seq2.p1	sp|P74518|LRTA_SYNY3_Light-repressed_protein_A_homolog_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=lrtA_PE=3_SV=1	2.00E-48	GO:0044238	[illegible]
comp29322_c0_seq1.p1				
comp29322_c0_seq1.p2				
comp29322_c0_seq3.p1				
comp29323_c0_seq1.p1				
comp29323_c0_seq2.p1				
comp29323_c1_seq1.p1	sp|Q9JJI6|PIGO_MOUSE_GPI_ethanolamine_phosphate_transferase_3_OS=Mus_musculus_GN=Pigo_PE=1_SV=2	9.00E-11	[illegible]	[illegible]
comp29324_c0_seq4.p1	sp|Q9NTK5|OLA1_HUMAN_Obg-like_ATPase_1_OS=Homo_sapiens_GN=OLA1_PE=1_SV=2	6.00E-142	[illegible]	[illegible]
comp29324_c0_seq4.p2				
comp29327_c0_seq1.p1				
comp29328_c1_seq1.p1				
comp29329_c0_seq1.p1	sp|P82887|H2B_OLILU_Histone_H2B_OS=Olisthodiscus_luteus_PE=1_SV=2	1.00E-51	GO:0000786,GO:0000786,GO:0003677,GO:0003677,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0046982	[illegible]
comp29329_c0_seq3.p1	sp|P82887|H2B_OLILU_Histone_H2B_OS=Olisthodiscus_luteus_PE=1_SV=2	1.00E-51	GO:0000786,GO:0000786,GO:0003677,GO:0003677,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0046982	[illegible]
comp29329_c0_seq4.p1	sp|P82887|H2B_OLILU_Histone_H2B_OS=Olisthodiscus_luteus_PE=1_SV=2	1.00E-51	GO:0000786,GO:0000786,GO:0003677,GO:0003677,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0046982	[illegible]
comp29330_c0_seq5.p1				
comp29330_c0_seq5.p2	sp|P08452|Y1174_SYNP6_Uncharacterized_lipoprotein_syc1174_c_OS=Synechococcus_sp._(strain_ATCC_27144_/_PCC_6301_/_SAUG_1402/1)_GN=syc1174_c_PE=4_SV=2	1.00E-45	GO:0005886,GO:0005886,GO:0016020	[illegible]
comp29330_c0_seq5.p3	sp|P08452|Y1174_SYNP6_Uncharacterized_lipoprotein_syc1174_c_OS=Synechococcus_sp._(strain_ATCC_27144_/_PCC_6301_/_SAUG_1402/1)_GN=syc1174_c_PE=4_SV=2	2.00E-26	GO:0005886,GO:0005886,GO:0016020	[illegible]
comp29330_c0_seq6.p1	sp|P08452|Y1174_SYNP6_Uncharacterized_lipoprotein_syc1174_c_OS=Synechococcus_sp._(strain_ATCC_27144_/_PCC_6301_/_SAUG_1402/1)_GN=syc1174_c_PE=4_SV=2	1.00E-92	GO:0005886,GO:0005886,GO:0016020	[illegible]
comp29330_c0_seq6.p2				
comp29332_c0_seq1.p1				
comp29332_c0_seq4.p1				
comp29333_c1_seq1.p1	sp|Q7K4Q5|Y0417_DROME_Probable_protein_phosphatase_CG10417_OS=Drosophila_melanogaster_GN=CG10417_PE=1_SV=1	2.00E-54	GO:0003824,GO:0004721,GO:0004721,GO:0004722,GO:0004722,GO:0006470,GO:0006470,GO:0016787,GO:0046872	[illegible]
comp29336_c0_seq5.p1	sp|Q0P4K0|OSGP2_XENTR_Probable_tRNA_threonylcarbamoyladenosine_biosynthesis_protein_osgepl1_OS=Xenopus_tropicalis_GN=osgepl1_PE=2_SV=2	7.00E-33	GO:0005739,GO:0005739,GO:0005739,GO:0008033,GO:0016740,GO:0016746,GO:0016747,GO:0046872,GO:0070526	[illegible]
comp29336_c0_seq5.p2				
comp29337_c0_seq1.p1				
comp29337_c0_seq2.p1				
comp29338_c0_seq2.p1				
comp29338_c0_seq2.p3				
comp29339_c0_seq2.p1				
comp29339_c0_seq3.p1				
comp29340_c0_seq1.p1				
comp29340_c0_seq10.p1				
comp29340_c0_seq11.p1				
comp29340_c0_seq13.p1				
comp29340_c0_seq2.p1				
comp29340_c0_seq3.p1				
comp29340_c0_seq4.p1				
comp29340_c0_seq6.p1				
comp29341_c0_seq1.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	1.00E-18	GO:0005576,GO:0005618,GO:0005618,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0019867	[illegible]
comp29341_c0_seq2.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	2.00E-18	GO:0005576,GO:0005618,GO:0005618,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0019867	[illegible]
comp29341_c0_seq3.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	2.00E-15	GO:0005576,GO:0005618,GO:0005618,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0019867	[illegible]
comp29343_c0_seq1.p1	sp|Q5ZMA6|NADE_CHICK_Glutamine-dependent_NAD(+)_synthetase_OS=Gallus_gallus_GN=NADSYN1_PE=2_SV=1	5.00E-106	GO:0000166,GO:0003952,GO:0003952,GO:0005524,GO:0005524,GO:0006807,GO:0009435,GO:0009435,GO:0016810,GO:0016874	[illegible]
comp29343_c0_seq1.p2	sp|Q54ML1|NADE_DICDI_Glutamine-dependent_NAD(+)_synthetase_OS=Dictyostelium_discoideum_GN=nadsyn1_PE=3_SV=1	5.00E-105	[illegible]	[illegible]
comp29345_c0_seq5.p1				
comp29345_c0_seq5.p2				
comp29345_c0_seq5.p4				
comp29346_c0_seq1.p1				
comp29347_c0_seq2.p1	sp|Q9SZR9|AB9G_ARATH_ABC_transporter_G_family_member_9_OS=Arabidopsis_thaliana_GN=ABCG9_PE=2_SV=2	7.00E-49	GO:0000166,GO:0005524,GO:0005524,GO:0006200,GO:0006810,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016887	[illegible]
comp29348_c0_seq1.p1				
comp29348_c0_seq2.p1				
comp29349_c0_seq13.p1				
comp29349_c0_seq14.p1				
comp29349_c0_seq15.p1				
comp29349_c0_seq15.p2				
comp29349_c0_seq16.p1				
comp29349_c0_seq16.p3	sp|Q5R723|PPIE_PONAB_Peptidyl-prolyl_cis-trans_isomerase_E_OS=Pongo_abelii_GN=PPIE_PE=2_SV=1	5.00E-34	[illegible]	[illegible]
comp29349_c0_seq3.p1				
comp29349_c0_seq3.p2				
comp29349_c0_seq3.p3	sp|Q5R723|PPIE_PONAB_Peptidyl-prolyl_cis-trans_isomerase_E_OS=Pongo_abelii_GN=PPIE_PE=2_SV=1	5.00E-34	[illegible]	[illegible]
comp29349_c0_seq5.p1				
comp29349_c0_seq5.p2				
comp29349_c0_seq5.p3	sp|Q5R723|PPIE_PONAB_Peptidyl-prolyl_cis-trans_isomerase_E_OS=Pongo_abelii_GN=PPIE_PE=2_SV=1	5.00E-34	[illegible]	[illegible]
comp29349_c0_seq8.p1				
comp29349_c0_seq8.p3	sp|Q5R723|PPIE_PONAB_Peptidyl-prolyl_cis-trans_isomerase_E_OS=Pongo_abelii_GN=PPIE_PE=2_SV=1	5.00E-34	[illegible]	[illegible]
comp29350_c0_seq1.p1				
comp29350_c0_seq2.p1				
comp29351_c0_seq1.p1				
comp29351_c0_seq1.p2	sp|Q1RJ69|FER2_RICBR_2Fe-2S_ferredoxin_OS=Rickettsia_bellii_(strain_RML369-C)_GN=fdxB_PE=3_SV=1	3.00E-31	GO:0009055,GO:0046872,GO:0051536,GO:0051536,GO:0051537,GO:0051537,GO:0055114	[illegible]
comp29352_c0_seq1.p1				
comp29353_c0_seq1.p1				
comp29353_c0_seq2.p1	sp|A7HAB8|MUTS2_ANADF_MutS2_protein_OS=Anaeromyxobacter_sp._(strain_Fw109-5)_GN=mutS2_PE=3_SV=1	5.00E-90	[illegible]	[illegible]
comp29354_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	4.00E-34		
comp29354_c0_seq1.p2	sp|Q39613|CYPH_CATRO_Peptidyl-prolyl_cis-trans_isomerase_OS=Catharanthus_roseus_GN=PCKR1_PE=2_SV=1	3.00E-57	GO:0000413,GO:0003755,GO:0003755,GO:0003755,GO:0005737,GO:0006457,GO:0016853,GO:0042277	[illegible]
comp29354_c0_seq1.p3				
comp29355_c0_seq2.p1				
comp29355_c0_seq3.p1	sp|P21837|CRYS_DICDI_Crystal_protein_OS=Dictyostelium_discoideum_GN=cryS_PE=1_SV=1	9.00E-31	GO:0008152,GO:0008152,GO:0008152,GO:0016020,GO:0016787,GO:0031410,GO:0033118,GO:0052689,GO:0052689	[illegible]
comp29355_c0_seq4.p1	sp|P21837|CRYS_DICDI_Crystal_protein_OS=Dictyostelium_discoideum_GN=cryS_PE=1_SV=1	9.00E-61	GO:0008152,GO:0008152,GO:0008152,GO:0016020,GO:0016787,GO:0031410,GO:0033118,GO:0052689,GO:0052689	[illegible]
comp29356_c0_seq1.p1				
comp29356_c0_seq2.p1				
comp29357_c0_seq2.p1				
comp29362_c0_seq1.p1	sp|P49596|PP2C2_CAEEL_Probable_protein_phosphatase_2C_T23F11.1_OS=Caenorhabditis_elegans_GN=T23F11.1_PE=2_SV=2	2.00E-42	GO:0003824,GO:0004721,GO:0004721,GO:0004722,GO:0006470,GO:0016787,GO:0046872,GO:0048786	[illegible]
comp29363_c0_seq1.p1	sp|P80874|GS69_BACSU_General_stress_protein_69_OS=Bacillus_subtilis_GN=yhdN_PE=1_SV=2	2.00E-17	GO:0016491,GO:0016491,GO:0055114,GO:0055114	[illegible]
comp29363_c0_seq2.p1				
comp29363_c0_seq3.p1				
comp29364_c0_seq4.p1				
comp29365_c0_seq1.p1	sp|P73354|HTRA_SYNY3_Putative_serine_protease_HtrA_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=htrA_PE=1_SV=1	1.00E-44	GO:0003824,GO:0004252,GO:0006508,GO:0006508,GO:0008233,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0016787	[illegible]
comp29365_c0_seq1.p6				

comp29367_c0_seq1.p1				
comp29368_c0_seq5.p1	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	7.00E-29	GO:0000281,GO:0000281,GO:0005200,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005764,GO:0005764,GO:0005783,GO:0005794,GO:0005794,GO:0005856,GO:0005856,GO:0005886,GO:0005886,GO:0005886,GO:0007009,GO:0007016,GO:0007165,GO:0007409,GO:0007409,GO:0007411,GO:0007528,GO:0008092,GO:0009986,GO:0010628,GO:0010650,GO:0010765,GO:0014704,GO:0014704,GO:0014704,GO:0014731,GO:0016020,GO:0016020,GO:0016323,GO:0016328,GO:0016529,GO:0019228,GO:0030018,GO:0030054,GO:0030315,GO:0030424,GO:0030424,GO:0030425,GO:0030507,GO:0030674,GO:0031594,GO:0033268,GO:0033268,GO:0033268,GO:0033270,GO:0034112,GO:0042383,GO:0042383,GO:0042995,GO:0043001,GO:0043005,GO:0043034,GO:0043194,GO:0043194,GO:0043194,GO:0043266,GO:0044325,GO:0045184,GO:0045202,GO:0045202,GO:0045211,GO:0045211,GO:0045211,GO:0045296,GO:0045838,GO:0050808,GO:0071709,GO:0071709,GO:0072659,GO:0072659,GO:0072659,GO:0072660,GO:0072661,GO:0072661,GO:0090314,GO:1900827,GO:2000651,GO:0005923,GO:0009925	[illegible]
comp29369_c0_seq2.p1				
comp29369_c0_seq3.p1				
comp29369_c0_seq3.p4				
comp29370_c0_seq1.p1	sp|Q9VGR2|MIDA_DROME_Protein_midA_homolog,_mitochondrial_OS=Drosophila_melanogaster_GN=CG17726_PE=1_SV=1	4.00E-60	GO:0003674,GO:0005575,GO:0005739,GO:0005739,GO:0005739,GO:0008150,GO:0032981	[illegible]
comp29370_c0_seq1.p2				
comp29371_c0_seq1.p1				
comp29371_c0_seq2.p1				
comp29371_c0_seq6.p1				
comp29371_c0_seq7.p2				
comp29372_c0_seq1.p1	sp|Q8T1E3|DCAM_DICDI_S-adenosylmethionine_decarboxylase_proenzyme_OS=Dictyostelium_discoideum_GN=amd1_PE=3_SV=3	3.00E-58	GO:0004014,GO:0004014,GO:0004014,GO:0005575,GO:0006557,GO:0006596,GO:0006597,GO:0008295,GO:0008295,GO:0016829,GO:0016831	[illegible]
comp29372_c0_seq2.p1	sp|Q8T1E3|DCAM_DICDI_S-adenosylmethionine_decarboxylase_proenzyme_OS=Dictyostelium_discoideum_GN=amd1_PE=3_SV=3	3.00E-75	GO:0004014,GO:0004014,GO:0004014,GO:0005575,GO:0006557,GO:0006596,GO:0006597,GO:0008295,GO:0008295,GO:0016829,GO:0016831	[illegible]
comp29372_c0_seq3.p1	sp|Q8T1E3|DCAM_DICDI_S-adenosylmethionine_decarboxylase_proenzyme_OS=Dictyostelium_discoideum_GN=amd1_PE=3_SV=3	1.00E-80	GO:0004014,GO:0004014,GO:0004014,GO:0005575,GO:0006557,GO:0006596,GO:0006597,GO:0008295,GO:0008295,GO:0016829,GO:0016831	[illegible]
comp29374_c0_seq1.p1				
comp29374_c1_seq3.p1	sp|Q5W6H5|CHLG_ORYSJ_Chlorophyll_synthase,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=CHLG_PE=2_SV=1	3.00E-155	GO:0004659,GO:0004659,GO:0006098,GO:0006364,GO:0009073,GO:0009507,GO:0009507,GO:0009534,GO:0009536,GO:0009536,GO:0009902,GO:0009965,GO:0010027,GO:0015995,GO:0015995,GO:0015995,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016117,GO:0016740,GO:0016740,GO:0019288,GO:0019344,GO:0030154,GO:0031969,GO:0031969,GO:0034660,GO:0042793,GO:0045893,GO:0046408,GO:0046408,GO:0046408	[illegible]
comp29374_c1_seq4.p1	sp|Q9UPZ9|ICK_HUMAN_Serine/threonine-protein_kinase_ICK_OS=Homo_sapiens_GN=ICK_PE=1_SV=1	2.00E-118	GO:0000166,GO:0000287,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004693,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005737,GO:0005829,GO:0006468,GO:0006468,GO:0007165,GO:0007275,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0035556,GO:0036064,GO:0042073,GO:0042384,GO:0046872,GO:0051726,GO:0097542	[illegible]
comp29375_c0_seq2.p1				
comp29376_c0_seq1.p1	sp|Q38931|FKB62_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP62_OS=Arabidopsis_thaliana_GN=FKBP62_PE=1_SV=2	5.00E-12	GO:0000413,GO:0000413,GO:0003755,GO:0003755,GO:0005515,GO:0005515,GO:0005515,GO:0005516,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006457,GO:0016853,GO:0070370	[illegible]
comp29376_c0_seq1.p2				
comp29376_c0_seq2.p1	sp|Q38931|FKB62_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP62_OS=Arabidopsis_thaliana_GN=FKBP62_PE=1_SV=2	5.00E-12	GO:0000413,GO:0000413,GO:0003755,GO:0003755,GO:0005515,GO:0005515,GO:0005515,GO:0005516,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006457,GO:0016853,GO:0070370	[illegible]
comp29376_c0_seq3.p1				
comp29377_c0_seq2.p1	sp|Q7TMS5|ABCG2_MOUSE_ATP-binding_cassette_sub-family_G_member_2_OS=Mus_musculus_GN=Abcg2_PE=2_SV=1	1.00E-49	GO:0000166,GO:0005524,GO:0005524,GO:0005634,GO:0005739,GO:0005886,GO:0005886,GO:0005886,GO:0006200,GO:0006810,GO:0006855,GO:0008559,GO:0010039,GO:0015238,GO:0015893,GO:0016020,GO:0016020,GO:0016021,GO:0016324,GO:0016887,GO:0031966,GO:0042908,GO:0046618,GO:0046983,GO:0051593,GO:0060136,GO:0071549	[illegible]
comp29378_c0_seq1.p1	sp|Q8BGX3|LRTM2_MOUSE_Leucine-rich_repeat_and_transmembrane_domain-containing_protein_2_OS=Mus_musculus_GN=Lrtm2_PE=2_SV=1	3.00E-11	GO:0003674,GO:0005575,GO:0008150,GO:0016020,GO:0016020,GO:0016021	[illegible]
comp29378_c0_seq2.p1				
comp29378_c0_seq3.p1				
comp29379_c0_seq2.p1				
comp29379_c1_seq1.p1	sp|Q8VZG8|Y4885_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At4g08850_OS=Arabidopsis_thaliana_GN=At4g08850_PE=1_SV=3	3.00E-32	GO:0000166,GO:0004672,GO:0004674,GO:0005524,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006468,GO:0006857,GO:0006995,GO:0009506,GO:0009627,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0031347	[illegible]
comp29380_c0_seq2.p1	sp|Q53NI2|NADK2_ORYSJ_Probable_NAD_kinase_2,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=Os11g0191400_PE=2_SV=1	6.00E-82	GO:0000166,GO:0003951,GO:0003951,GO:0003951,GO:0005516,GO:0005524,GO:0006741,GO:0006741,GO:0008152,GO:0008152,GO:0009507,GO:0009507,GO:0009536,GO:0016301,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0019674,GO:0019674	[illegible]
comp29380_c0_seq3.p1	sp|O95544|NADK_HUMAN_NAD_kinase_OS=Homo_sapiens_GN=NADK_PE=1_SV=1	1.00E-10	GO:0000166,GO:0003951,GO:0003951,GO:0003951,GO:0003951,GO:0005524,GO:0005829,GO:0005829,GO:0006741,GO:0006766,GO:0006767,GO:0008152,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0019674,GO:0019674,GO:0044281,GO:0046034,GO:0046872	[illegible]
comp29381_c0_seq2.p1	sp|Q84JC0|RRP8_ARATH_Ribosomal_RNA-processing_protein_8_OS=Arabidopsis_thaliana_GN=At5g40530_PE=2_SV=1	2.00E-59	GO:0000183,GO:0005634,GO:0005677,GO:0005730,GO:0005730,GO:0006351,GO:0006355,GO:0006364,GO:0008168,GO:0008168,GO:0016568,GO:0016740,GO:0032259,GO:0033553,GO:0035064	[illegible]
comp29381_c0_seq2.p4				
comp29381_c0_seq4.p1	sp|Q84JC0|RRP8_ARATH_Ribosomal_RNA-processing_protein_8_OS=Arabidopsis_thaliana_GN=At5g40530_PE=2_SV=1	2.00E-59	GO:0000183,GO:0005634,GO:0005677,GO:0005730,GO:0005730,GO:0006351,GO:0006355,GO:0006364,GO:0008168,GO:0008168,GO:0016568,GO:0016740,GO:0032259,GO:0033553,GO:0035064	[illegible]
comp29381_c0_seq6.p2				
comp29381_c0_seq7.p1				
comp29382_c0_seq3.p1	sp|P14735|IDE_HUMAN_Insulin-degrading_enzyme_OS=Homo_sapiens_GN=IDE_PE=1_SV=4	6.00E-180	[illegible]	[illegible]
comp29382_c0_seq4.p1	sp|P14735|IDE_HUMAN_Insulin-degrading_enzyme_OS=Homo_sapiens_GN=IDE_PE=1_SV=4	7.00E-162	[illegible]	[illegible]
comp29383_c0_seq2.p1	sp|Q92621|NU205_HUMAN_Nuclear_pore_complex_protein_Nup205_OS=Homo_sapiens_GN=NUP205_PE=1_SV=3	7.00E-11	[illegible]	[illegible]
comp29384_c0_seq1.p1				
comp29384_c0_seq3.p1				
comp29384_c0_seq3.p2	sp|Q9UKJ3|GPTC8_HUMAN_G_patch_domain-containing_protein_8_OS=Homo_sapiens_GN=GPATCH8_PE=1_SV=2	2.00E-21	[illegible]	[illegible]
comp29385_c0_seq1.p1				
comp29386_c0_seq1.p1				
comp29386_c0_seq2.p1	sp|Q5E9T8|KIME_BOVIN_Mevalonate_kinase_OS=Bos_taurus_GN=MVK_PE=2_SV=1	5.00E-35	[illegible]	[illegible]
comp29386_c0_seq3.p1	sp|Q03426|KIME_HUMAN_Mevalonate_kinase_OS=Homo_sapiens_GN=MVK_PE=1_SV=1	8.00E-30	[illegible]	[illegible]
comp29386_c0_seq3.p2				
comp29387_c0_seq3.p1				
comp29387_c0_seq4.p1				
comp2939_c0_seq1.p2				
comp29390_c0_seq2.p1	sp|A2AV36|ANM7_DANRE_Protein_arginine_N-methyltransferase_7_OS=Danio_rerio_GN=prmt7_PE=2_SV=1	2.00E-38	[illegible]	[illegible]
comp29392_c0_seq3.p1	sp|Q4KM74|SC22B_RAT_Vesicle-trafficking_protein_SEC22b_OS=Rattus_norvegicus_GN=Sec22b_PE=1_SV=3	2.00E-31	[illegible]	[illegible]
comp29392_c0_seq4.p1	sp|Q94AU2|SEC22_ARATH_25.3_kDa_vesicle_transport_protein_OS=Arabidopsis_thaliana_GN=SEC22_PE=2_SV=1	2.00E-55	[illegible]	[illegible]
comp29393_c0_seq3.p1				
comp29395_c0_seq1.p1				
comp29395_c0_seq2.p2				
comp29396_c0_seq2.p1	sp|Q54I18|SMEK_DICDI_Suppressor_of_Mek1_OS=Dictyostelium_discoideum_GN=smkA_PE=1_SV=1	3.00E-63	[illegible]	[illegible]
comp29397_c0_seq1.p1				
comp29397_c0_seq3.p1				
comp29397_c0_seq3.p3				
comp29397_c0_seq5.p1	sp|Q8VBV4|FBXW7_MOUSE_F-box/WD_repeat-containing_protein_7_OS=Mus_musculus_GN=Fbxw7_PE=1_SV=1	1.00E-23	[illegible]	[illegible]
comp29397_c0_seq5.p2				
comp29397_c0_seq6.p1				
comp29397_c0_seq7.p1				
comp29398_c0_seq2.p1	sp|Q8NBN7|RDH13_HUMAN_Retinol_dehydrogenase_13_OS=Homo_sapiens_GN=RDH13_PE=1_SV=2	2.00E-16	[illegible]	[illegible]
comp29398_c0_seq3.p1	sp|Q96NR8|RDH12_HUMAN_Retinol_dehydrogenase_12_OS=Homo_sapiens_GN=RDH12_PE=1_SV=3	1.00E-20	[illegible]	[illegible]
comp29398_c0_seq4.p1				
comp29398_c0_seq5.p1				
comp29399_c0_seq2.p1	sp|P57370|SOHB_BUCAI_Probable_protease_sohB_OS=Buchnera_aphidicola_subsp._Acyrthosiphon_pisum_(strain_APS)_GN=sohB_PE=3_SV=1	2.00E-43	[illegible]	[illegible]
comp29400_c0_seq1.p1	sp|P22467|MYOA_DICDI_Myosin_IA_heavy_chain_OS=Dictyostelium_discoideum_GN=myoA_PE=4_SV=2	5.00E-145	[illegible]	[illegible]
comp29401_c0_seq2.p1				
comp29402_c0_seq4.p1				
comp29403_c0_seq2.p1				
comp29403_c0_seq2.p2	sp|O13792|SUB2_SCHPO_ATP-dependent_RNA_helicase_uap56_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=uap56_PE=1_SV=3	2.00E-78	[illegible]	[illegible]
comp29403_c0_seq2.p3				
comp29403_c0_seq3.p1				
comp29403_c0_seq3.p2	sp|O13792|SUB2_SCHPO_ATP-dependent_RNA_helicase_uap56_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=uap56_PE=1_SV=3	2.00E-79	[illegible]	[illegible]
comp29403_c0_seq3.p3				
comp29403_c0_seq5.p1	sp|Q5JK84|RH15_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_15_OS=Oryza_sativa_subsp._japonica_GN=Os01g0550000_PE=2_SV=1	0	[illegible]	[illegible]
comp29403_c0_seq5.p2				
comp29404_c0_seq2.p1				
comp29406_c0_seq3.p1				
comp29406_c0_seq4.p1				
comp29406_c0_seq5.p1				
comp29406_c0_seq6.p1				
comp29407_c0_seq3.p1	sp|A8KBH6|KPCB_XENTR_Protein_kinase_C_beta_type_OS=Xenopus_tropicalis_GN=prkcb_PE=2_SV=1	7.00E-13	[illegible]	[illegible]
comp29407_c0_seq4.p1	sp|A8KBH6|KPCB_XENTR_Protein_kinase_C_beta_type_OS=Xenopus_tropicalis_GN=prkcb_PE=2_SV=1	7.00E-12	[illegible]	[illegible]
comp29409_c0_seq2.p1				
comp29409_c0_seq3.p1				
comp29409_c0_seq3.p3				
comp29410_c1_seq4.p1	sp|Q99685|MGLL_HUMAN_Monoglyceride_lipase_OS=Homo_sapiens_GN=MGLL_PE=1_SV=2	9.00E-25	[illegible]	[illegible]
comp29411_c0_seq10.p1	sp|Q8K4F5|ABHDB_MOUSE_Abhydrolase_domain-containing_protein_11_OS=Mus_musculus_GN=Abhd11_PE=2_SV=1	2.00E-36	[illegible]	[illegible]
comp29411_c0_seq10.p2	sp|Q9FZ62|PPSP2_ARATH_Inorganic_pyrophosphatase_2_OS=Arabidopsis_thaliana_GN=At1g17710_PE=2_SV=1	1.00E-33	[illegible]	[illegible]
comp29411_c0_seq10.p5				
comp29411_c0_seq12.p2	sp|Q9FZ62|PPSP2_ARATH_Inorganic_pyrophosphatase_2_OS=Arabidopsis_thaliana_GN=At1g17710_PE=2_SV=1	3.00E-24	[illegible]	[illegible]
comp29411_c0_seq23.p1	sp|Q2TAP9|ABHDB_XENLA_Abhydrolase_domain-containing_protein_11_OS=Xenopus_laevis_GN=abhd11_PE=2_SV=1	5.00E-29	GO:0008152,GO:0016787	[illegible]
comp29411_c0_seq3.p2				
comp29411_c0_seq30.p1	sp|Q2TAP9|ABHDB_XENLA_Abhydrolase_domain-containing_protein_11_OS=Xenopus_laevis_GN=abhd11_PE=2_SV=1	2.00E-43	GO:0008152,GO:0016787	[illegible]
comp29411_c0_seq30.p2	sp|Q9FZ62|PPSP2_ARATH_Inorganic_pyrophosphatase_2_OS=Arabidopsis_thaliana_GN=At1g17710_PE=2_SV=1	1.00E-33	[illegible]	[illegible]
comp29411_c0_seq44.p1	sp|Q2TAP9|ABHDB_XENLA_Abhydrolase_domain-containing_protein_11_OS=Xenopus_laevis_GN=abhd11_PE=2_SV=1	9.00E-22	GO:0008152,GO:0016787	[illegible]
comp29411_c0_seq44.p4				
comp29413_c0_seq1.p1	sp|P05128|KPCG_BOVIN_Protein_kinase_C_gamma_type_(Fragment)_OS=Bos_taurus_GN=PRKCG_PE=2_SV=1	1.00E-11	[illegible]	[illegible]
comp29415_c0_seq2.p1	sp|Q7TNH6|NPHP3_MOUSE_Nephrocystin-3_OS=Mus_musculus_GN=Nphp3_PE=1_SV=2	2.00E-37	[illegible]	[illegible]
comp29416_c0_seq3.p1				
comp29419_c0_seq3.p1				
comp29419_c0_seq4.p1				
comp29419_c0_seq5.p1				
comp29420_c0_seq1.p1	sp|O07051|LTAA_AERJA_L-allo-threonine_aldolase_OS=Aeromonas_jandaei_GN=ltaA_PE=1_SV=1	1.00E-86	[illegible]	[illegible]
comp29420_c0_seq2.p1	sp|O07051|LTAA_AERJA_L-allo-threonine_aldolase_OS=Aeromonas_jandaei_GN=ltaA_PE=1_SV=1	6.00E-12	[illegible]	[illegible]
comp29420_c0_seq3.p2	sp|O07051|LTAA_AERJA_L-allo-threonine_aldolase_OS=Aeromonas_jandaei_GN=ltaA_PE=1_SV=1	1.00E-42	[illegible]	[illegible]
comp29420_c0_seq3.p4	sp|O07051|LTAA_AERJA_L-allo-threonine_aldolase_OS=Aeromonas_jandaei_GN=ltaA_PE=1_SV=1	7.00E-27	[illegible]	[illegible]
comp29421_c0_seq1.p1	sp|Q0SQ51|SYN_CLOPS_Asparagine--tRNA_ligase_OS=Clostridium_perfringens_(strain_SM101_/_Type_A)_GN=asnS_PE=3_SV=1	3.00E-80	[illegible]	[illegible]
comp29421_c0_seq1.p3				
comp29421_c1_seq1.p1	sp|Q6MEC9|SYN_PARUW_Asparagine--tRNA_ligase_OS=Protochlamydia_amoebophila_(strain_UWE25)_GN=asnS_PE=3_SV=1	8.00E-84	[illegible]	[illegible]
comp29421_c1_seq2.p1	sp|Q6MEC9|SYN_PARUW_Asparagine--tRNA_ligase_OS=Protochlamydia_amoebophila_(strain_UWE25)_GN=asnS_PE=3_SV=1	2.00E-42	[illegible]	[illegible]
comp29424_c0_seq1.p1				
comp29425_c0_seq2.p1	sp|Q8JZW4|CPNE5_MOUSE_Copine-5_OS=Mus_musculus_GN=Cpne5_PE=2_SV=1	4.00E-107	[illegible]	[illegible]
comp29426_c0_seq2.p1	sp|P76043|YCJQ_ECOLI_Uncharacterized_zinc-type_alcohol_dehydrogenase-like_protein_YcjQ_OS=Escherichia_coli_(strain_K12)_GN=ycjQ_PE=3_SV=1	4.00E-14	[illegible]	[illegible]
comp29427_c0_seq1.p1				
comp29428_c2_seq2.p1	sp|Q9C641|EFGM_ARATH_Elongation_factor_G,_mitochondrial_OS=Arabidopsis_thaliana_GN=At1g45332_PE=1_SV=1	0	[illegible]	[illegible]
comp29429_c1_seq2.p1	sp|Q5RAD5|RTF1_PONAB_RNA_polymerase-associated_protein_RTF1_homolog_(Fragment)_OS=Pongo_abelii_GN=RTF1_PE=2_SV=2	2.00E-24	[illegible]	[illegible]
comp29430_c1_seq1.p1				
comp29431_c0_seq2.p1				
comp29433_c0_seq1.p1				
comp29433_c1_seq3.p1	sp|Q3B7H2|TAM41_DANRE_Mitochondrial_translocator_assembly_and_maintenance_protein_41_homolog_OS=Danio_rerio_GN=tamm41_PE=2_SV=1	1.00E-33	[illegible]	[illegible]
comp29433_c1_seq3.p2				
comp29433_c1_seq6.p1	sp|Q8INF2|TAM41_DROME_Mitochondrial_translocator_assembly_and_maintenance_protein_41_homolog_OS=Drosophila_melanogaster_GN=CG33331_PE=2_SV=1	1.00E-52	[illegible]	[illegible]
comp29433_c1_seq6.p2				
comp29433_c1_seq6.p3				
comp29434_c0_seq1.p1				
comp29434_c0_seq4.p1				
comp29434_c1_seq1.p1	sp|Q9LS42|CASP_ARATH_Protein_CASP_OS=Arabidopsis_thaliana_GN=CASP_PE=1_SV=2	5.00E-34	[illegible]	[illegible]
comp29434_c4_seq1.p1				
comp29435_c0_seq1.p1				
comp29435_c0_seq2.p2				
comp29436_c0_seq1.p1				
comp29436_c0_seq1.p5				
comp29437_c0_seq3.p1	sp|Q05090|KLC_STRPU_Kinesin_light_chain_OS=Strongylocentrotus_purpuratus_PE=2_SV=1	2.00E-43	[illegible]	[illegible]
comp29438_c0_seq1.p1				
comp29438_c0_seq2.p1				
comp29439_c0_seq1.p1				
comp29439_c0_seq3.p1				
comp29440_c0_seq1.p1				
comp29440_c0_seq2.p1				
comp29440_c0_seq3.p1				
comp29440_c0_seq5.p1				
comp29441_c0_seq1.p1	sp|Q3B7M6|NEDD1_BOVIN_Protein_NEDD1_OS=Bos_taurus_GN=NEDD1_PE=2_SV=1	5.00E-21	[illegible]	[illegible]
comp29441_c0_seq3.p1				
comp29441_c0_seq4.p1	sp|Q9Y2Z9|COQ6_HUMAN_Ubiquinone_biosynthesis_monooxygenase_COQ6_OS=Homo_sapiens_GN=COQ6_PE=1_SV=2	3.00E-28	[illegible]	[illegible]
comp29442_c0_seq1.p1				
comp29444_c0_seq3.p1				
comp29444_c0_seq4.p1	sp|Q9R1C7|PR40A_MOUSE_Pre-mRNA-processing_factor_40_homolog_A_OS=Mus_musculus_GN=Prpf40a_PE=1_SV=1	2.00E-17	[illegible]	[illegible]
comp29445_c0_seq1.p1	sp|O15865|CDPK2_PLAFK_Calcium-dependent_protein_kinase_2_OS=Plasmodium_falciparum_(isolate_K1_/_Thailand)_GN=CPK2_PE=1_SV=3	1.00E-66	[illegible]	[illegible]
comp29447_c0_seq3.p1				
comp29448_c0_seq1.p1				
comp29449_c0_seq1.p2				
comp29449_c0_seq2.p1				
comp29450_c0_seq2.p1	sp|Q9V3A4|CSUP_DROME_Protein_catecholamines_up_OS=Drosophila_melanogaster_GN=Catsup_PE=2_SV=1	5.00E-36	[illegible]	[illegible]
comp29450_c0_seq5.p1				
comp29450_c0_seq6.p1				
comp29452_c0_seq2.p1				
comp29452_c1_seq1.p1				
comp29453_c0_seq1.p1	sp|A5PK43|ERAL1_BOVIN_GTPase_Era,_mitochondrial_OS=Bos_taurus_GN=ERAL1_PE=2_SV=1	6.00E-32	[illegible]	[illegible]
comp29454_c0_seq1.p1	sp|B3DNN5|CDC16_ARATH_Anaphase-promoting_complex_subunit_6_OS=Arabidopsis_thaliana_GN=APC6_PE=2_SV=1	3.00E-107	[illegible]	[illegible]
comp29455_c0_seq1.p1	sp|Q9V6G5|TAZ_DROME_Tafazzin_homolog_OS=Drosophila_melanogaster_GN=Taz_PE=2_SV=2	3.00E-35	[illegible]	[illegible]
comp29455_c0_seq3.p1	sp|Q9V6G5|TAZ_DROME_Tafazzin_homolog_OS=Drosophila_melanogaster_GN=Taz_PE=2_SV=2	6.00E-35	[illegible]	[illegible]
comp29456_c0_seq1.p2				
comp29457_c0_seq2.p1				
comp29457_c0_seq2.p2	sp|Q50EK1|C16B1_PICSI_Cytochrome_P450_716B1_OS=Picea_sitchensis_GN=CYP716B1_PE=2_SV=1	2.00E-17	[illegible]	[illegible]
comp29459_c0_seq2.p1	sp|Q8L850|PI5K9_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_9_OS=Arabidopsis_thaliana_GN=PIP5K9_PE=1_SV=2	5.00E-19	[illegible]	[illegible]
comp29459_c0_seq3.p1	sp|Q8L850|PI5K9_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_9_OS=Arabidopsis_thaliana_GN=PIP5K9_PE=1_SV=2	3.00E-19	[illegible]	[illegible]
comp29461_c0_seq5.p1	sp|Q5UNY5|YR727_MIMIV_Uncharacterized_protein_R727_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R727_PE=1_SV=1	6.00E-11	GO:0019012,GO:0019012	[illegible]
comp29461_c1_seq1.p1				
comp29462_c0_seq2.p1	sp|Q55680|Y005_SYNY3_Uncharacterized_protein_sll0005_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll0005_PE=3_SV=1	6.00E-103	[illegible]	[illegible]
comp29462_c0_seq2.p2	sp|Q5ZIH2|MON1A_CHICK_Vacuolar_fusion_protein_MON1_homolog_A_OS=Gallus_gallus_GN=MON1A_PE=2_SV=1	6.00E-22		
comp29463_c0_seq1.p1	sp|Q8IY18|SMC5_HUMAN_Structural_maintenance_of_chromosomes_protein_5_OS=Homo_sapiens_GN=SMC5_PE=1_SV=2	6.00E-106	[illegible]	[illegible]
comp29464_c0_seq1.p1				
comp29464_c0_seq2.p1				
comp29464_c0_seq2.p2	sp|Q08603|PGTB2_RAT_Geranylgeranyl_transferase_type-2_subunit_beta_OS=Rattus_norvegicus_GN=Rabggtb_PE=1_SV=1	3.00E-120	[illegible]	[illegible]
comp29465_c0_seq1.p1	sp|Q0VCN3|IFT27_BOVIN_Intraflagellar_transport_protein_27_homolog_OS=Bos_taurus_GN=IFT27_PE=2_SV=1	2.00E-27	[illegible]	[illegible]
comp29465_c0_seq3.p1	sp|Q9BW83|IFT27_HUMAN_Intraflagellar_transport_protein_27_homolog_OS=Homo_sapiens_GN=IFT27_PE=1_SV=1	2.00E-17	[illegible]	[illegible]
comp29466_c0_seq1.p1				
comp29466_c0_seq2.p1				
comp29468_c0_seq2.p1	sp|Q56Y85|AMP2B_ARATH_Methionine_aminopeptidase_2B_OS=Arabidopsis_thaliana_GN=MAP2B_PE=2_SV=2	2.00E-174	[illegible]	[illegible]
comp29468_c0_seq3.p1	sp|Q56Y85|AMP2B_ARATH_Methionine_aminopeptidase_2B_OS=Arabidopsis_thaliana_GN=MAP2B_PE=2_SV=2	2.00E-177	[illegible]	[illegible]
comp29469_c0_seq1.p1				
comp29469_c0_seq3.p1				
comp29469_c2_seq1.p1				
comp29469_c2_seq2.p1				
comp29470_c0_seq1.p1	sp|Q9MA15|Y1960_ARATH_Uncharacterized_aarF_domain-containing_protein_kinase_At1g79600,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g79600_PE=1_SV=1	8.00E-18	[illegible]	[illegible]
comp29470_c0_seq2.p1	sp|Q9MA15|Y1960_ARATH_Uncharacterized_aarF_domain-containing_protein_kinase_At1g79600,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g79600_PE=1_SV=1	6.00E-128	[illegible]	[illegible]
comp29470_c0_seq3.p1				
comp29471_c0_seq2.p1	sp|Q15751|HERC1_HUMAN_Probable_E3_ubiquitin-protein_ligase_HERC1_OS=Homo_sapiens_GN=HERC1_PE=1_SV=2	7.00E-16	[illegible]	[illegible]
comp29471_c0_seq3.p1				
comp29472_c0_seq3.p1				
comp29473_c0_seq1.p1				
comp29473_c0_seq2.p1				
comp29473_c0_seq4.p1				
comp29473_c0_seq5.p1				
comp29473_c0_seq8.p1				
comp29474_c0_seq1.p1				
comp29474_c0_seq4.p1				
comp29475_c0_seq1.p1				
comp29475_c0_seq1.p3				
comp29476_c0_seq1.p1	sp|Q9USN5|DHE2_SCHPO_Putative_NAD-specific_glutamate_dehydrogenase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC132.04c_PE=2_SV=1	3.00E-71	[illegible]	[illegible]
comp29477_c0_seq1.p1	sp|Q9LVQ8|P2C80_ARATH_Probable_protein_phosphatase_2C_80_OS=Arabidopsis_thaliana_GN=At5g66720_PE=2_SV=1	1.00E-28	[illegible]	[illegible]
comp29477_c0_seq1.p2				
comp29478_c0_seq3.p1	sp|Q54DF7|Y2354_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0292354_OS=Dictyostelium_discoideum_GN=DDB_G0292354_PE=3_SV=1	1.00E-40	[illegible]	[illegible]
comp29479_c0_seq1.p1	sp|Q9ULJ6|ZMIZ1_HUMAN_Zinc_finger_MIZ_domain-containing_protein_1_OS=Homo_sapiens_GN=ZMIZ1_PE=1_SV=3	5.00E-13	[illegible]	[illegible]
comp29479_c0_seq1.p5				
comp29479_c0_seq2.p1	sp|Q9ULJ6|ZMIZ1_HUMAN_Zinc_finger_MIZ_domain-containing_protein_1_OS=Homo_sapiens_GN=ZMIZ1_PE=1_SV=3	5.00E-13	[illegible]	[illegible]
comp29479_c0_seq2.p5				
comp29479_c0_seq3.p1	sp|Q9ULJ6|ZMIZ1_HUMAN_Zinc_finger_MIZ_domain-containing_protein_1_OS=Homo_sapiens_GN=ZMIZ1_PE=1_SV=3	1.00E-12	[illegible]	[illegible]
comp29479_c0_seq4.p1				
comp29479_c0_seq5.p1	sp|Q9ULJ6|ZMIZ1_HUMAN_Zinc_finger_MIZ_domain-containing_protein_1_OS=Homo_sapiens_GN=ZMIZ1_PE=1_SV=3	1.00E-12	[illegible]	[illegible]
comp29480_c0_seq3.p1	sp|Q9QUQ5|TRPC4_MOUSE_Short_transient_receptor_potential_channel_4_OS=Mus_musculus_GN=Trpc4_PE=1_SV=1	5.00E-15	[illegible]	[illegible]
comp29481_c0_seq2.p1	sp|Q54XA2|Y9099_DICDI_DEP_domain-containing_protein_DDB_G0279099_OS=Dictyostelium_discoideum_GN=DDB_G0279099_PE=3_SV=1	6.00E-47	[illegible]	[illegible]
comp29482_c0_seq1.p1	sp|Q0WMY5|PP365_ARATH_Pentatricopeptide_repeat-containing_protein_At5g04810,_chloroplastic_OS=Arabidopsis_thaliana_GN=PPR4_PE=1_SV=1	7.00E-21	[illegible]	[illegible]
comp29482_c0_seq2.p1				
comp29483_c0_seq1.p1	sp|Q9QX72|SEBP2_RAT_Selenocysteine_insertion_sequence-binding_protein_2_OS=Rattus_norvegicus_GN=Secisbp2_PE=1_SV=1	4.00E-26	[illegible]	[illegible]
comp29484_c0_seq3.p1	sp|Q5N863|BGL04_ORYSJ_Beta-glucosidase_4_OS=Oryza_sativa_subsp._japonica_GN=BGLU4_PE=2_SV=1	5.00E-138	[illegible]	[illegible]
comp29485_c0_seq1.p1	sp|Q8L7J2|BGL06_ORYSJ_Beta-glucosidase_6_OS=Oryza_sativa_subsp._japonica_GN=BGLU6_PE=1_SV=1	3.00E-110	[illegible]	[illegible]
comp29485_c0_seq1.p4	sp|Q5Z9Z0|BGL24_ORYSJ_Beta-glucosidase_24_OS=Oryza_sativa_subsp._japonica_GN=BGLU24_PE=2_SV=1	5.00E-14	[illegible]	[illegible]
comp29485_c0_seq3.p1	sp|Q8L7J2|BGL06_ORYSJ_Beta-glucosidase_6_OS=Oryza_sativa_subsp._japonica_GN=BGLU6_PE=1_SV=1	5.00E-157	[illegible]	[illegible]
comp29486_c0_seq2.p1				
comp29486_c1_seq1.p1	sp|B5DE69|CHD8_XENTR_Chromodomain-helicase-DNA-binding_protein_8_OS=Xenopus_tropicalis_GN=chd8_PE=2_SV=2	2.00E-84	[illegible]	[illegible]
comp29487_c0_seq1.p1	sp|O43772|MCAT_HUMAN_Mitochondrial_carnitine/acylcarnitine_carrier_protein_OS=Homo_sapiens_GN=SLC25A20_PE=1_SV=1	5.00E-37	[illegible]	[illegible]
comp29487_c0_seq3.p3				
comp29487_c0_seq4.p1				
comp29488_c0_seq1.p1	sp|P07850|SUOX_CHICK_Sulfite_oxidase_OS=Gallus_gallus_GN=SUOX_PE=1_SV=3	2.00E-147	[illegible]	[illegible]
comp29488_c0_seq1.p2				
comp29491_c0_seq1.p1				
comp29492_c0_seq1.p1	sp|P54453|YQEH_BACSU_Uncharacterized_protein_yqeH_OS=Bacillus_subtilis_GN=yqeH_PE=1_SV=1	8.00E-54	[illegible]	[illegible]
comp29492_c0_seq2.p1				
comp29493_c0_seq2.p1	sp|Q0J8G4|SCRK2_ORYSJ_Fructokinase-2_OS=Oryza_sativa_subsp._japonica_GN=FRK2_PE=1_SV=1	4.00E-30	[illegible]	[illegible]
comp29494_c0_seq3.p1				
comp29495_c0_seq1.p1				
comp29495_c0_seq2.p1				
comp29496_c0_seq2.p1				
comp29496_c0_seq2.p2	sp|A5DB51|RISA_PICGU_Riboflavin_synthase_alpha_chain_OS=Meyerozyma_guilliermondii_(strain_ATCC_6260_/_CBS_566_/_DSM_6381_/_JCM_1539_/_NBRC_10279_/_NRRL_Y-324)_GN=RIB5_PE=2_SV=3	8.00E-52	[illegible]	[illegible]
comp29496_c0_seq2.p3	sp|Q54GD9|ARV1_DICDI_Protein_arv1_homolog_OS=Dictyostelium_discoideum_GN=arv1_PE=3_SV=1	5.00E-20	[illegible]	[illegible]
comp29496_c0_seq3.p1				
comp29496_c0_seq3.p2	sp|A5DB51|RISA_PICGU_Riboflavin_synthase_alpha_chain_OS=Meyerozyma_guilliermondii_(strain_ATCC_6260_/_CBS_566_/_DSM_6381_/_JCM_1539_/_NBRC_10279_/_NRRL_Y-324)_GN=RIB5_PE=2_SV=3	8.00E-52	[illegible]	[illegible]
comp29496_c0_seq3.p3	sp|Q54GD9|ARV1_DICDI_Protein_arv1_homolog_OS=Dictyostelium_discoideum_GN=arv1_PE=3_SV=1	5.00E-20	[illegible]	[illegible]
comp29496_c0_seq5.p1				
comp29496_c0_seq5.p2				
comp29497_c0_seq1.p1	sp|P0CX09|YN073_YEAST_Mannitol_dehydrogenase_YNR073C_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YNR073C_PE=3_SV=1	2.00E-99	[illegible]	[illegible]
comp29497_c1_seq1.p1				
comp29498_c0_seq2.p1	sp|Q67XX3|FB252_ARATH_F-box_protein_At5g06550_OS=Arabidopsis_thaliana_GN=At5g06550_PE=2_SV=1	2.00E-15	[illegible]	[illegible]
comp29499_c0_seq1.p1				
comp29499_c0_seq5.p1				
comp29500_c0_seq1.p1				
comp29500_c0_seq1.p2				
comp29500_c0_seq2.p1	sp|B2FQP3|ASPN_STRMK_Peptidyl-Asp_metalloendopeptidase_OS=Stenotrophomonas_maltophilia_(strain_K279a)_GN=Smlt0970_PE=3_SV=1	1.00E-14	[illegible]	[illegible]
comp29501_c0_seq2.p1	sp|O18866|KCMA1_PIG_Calcium-activated_potassium_channel_subunit_alpha-1_(Fragment)_OS=Sus_scrofa_GN=KCNMA1_PE=2_SV=2	2.00E-18	[illegible]	[illegible]
comp29503_c0_seq4.p2				
comp29504_c0_seq2.p1				
comp29504_c0_seq4.p1				
comp29505_c0_seq3.p1				
comp29505_c0_seq5.p1				
comp29505_c0_seq6.p1				
comp29506_c0_seq1.p1				
comp29507_c0_seq1.p1				
comp29508_c0_seq1.p1				
comp29508_c0_seq2.p1	sp|O97341|CALM_SUBDO_Calmodulin_OS=Suberites_domuncula_PE=2_SV=3	9.00E-33	GO:0005509,GO:0046872	[illegible]
comp29509_c0_seq2.p1				
comp29512_c0_seq3.p2				
comp29514_c0_seq2.p3				
comp29515_c1_seq2.p1	sp|Q8BMB3|IF4E2_MOUSE_Eukaryotic_translation_initiation_factor_4E_type_2_OS=Mus_musculus_GN=Eif4e2_PE=1_SV=1	5.00E-35	[illegible]	[illegible]
comp29517_c0_seq1.p1	sp|Q61316|HSP74_MOUSE_Heat_shock_70_kDa_protein_4_OS=Mus_musculus_GN=Hspa4_PE=1_SV=1	2.00E-69	[illegible]	[illegible]
comp29518_c0_seq4.p1				
comp29520_c0_seq1.p1	sp|Q55BU7|UBXN7_DICDI_UBX_domain-containing_protein_7_homolog_OS=Dictyostelium_discoideum_GN=ubxd7_PE=4_SV=1	4.00E-21	[illegible]	[illegible]
comp29521_c0_seq1.p1				
comp29521_c0_seq2.p1				
comp29524_c0_seq1.p1				
comp29525_c0_seq1.p1	sp|Q9W3V8|ALG8_DROME_Probable_dolichyl_pyrophosphate_Glc1Man9GlcNAc2_alpha-1,3-glucosyltransferase_OS=Drosophila_melanogaster_GN=CG4542_PE=2_SV=1	7.00E-48	[illegible]	[illegible]
comp29525_c0_seq1.p2	sp|B2RX14|TUT4_MOUSE_Terminal_uridylyltransferase_4_OS=Mus_musculus_GN=Zcchc11_PE=1_SV=2	4.00E-14	[illegible]	[illegible]
comp29525_c0_seq1.p3				
comp29525_c0_seq11.p1	sp|B2RX14|TUT4_MOUSE_Terminal_uridylyltransferase_4_OS=Mus_musculus_GN=Zcchc11_PE=1_SV=2	1.00E-13	[illegible]	[illegible]
comp29525_c0_seq11.p2	sp|O80505|ALG8_ARATH_Probable_dolichyl_pyrophosphate_Glc1Man9GlcNAc2_alpha-1,3-glucosyltransferase_OS=Arabidopsis_thaliana_GN=At2g44660_PE=2_SV=3	1.00E-28	[illegible]	[illegible]
comp29525_c0_seq12.p1	sp|B2RX14|TUT4_MOUSE_Terminal_uridylyltransferase_4_OS=Mus_musculus_GN=Zcchc11_PE=1_SV=2	1.00E-13	[illegible]	[illegible]
comp29525_c0_seq12.p2	sp|O80505|ALG8_ARATH_Probable_dolichyl_pyrophosphate_Glc1Man9GlcNAc2_alpha-1,3-glucosyltransferase_OS=Arabidopsis_thaliana_GN=At2g44660_PE=2_SV=3	1.00E-28	[illegible]	[illegible]
comp29525_c0_seq13.p1	sp|B2RX14|TUT4_MOUSE_Terminal_uridylyltransferase_4_OS=Mus_musculus_GN=Zcchc11_PE=1_SV=2	4.00E-14	[illegible]	[illegible]
comp29525_c0_seq13.p2	sp|O80505|ALG8_ARATH_Probable_dolichyl_pyrophosphate_Glc1Man9GlcNAc2_alpha-1,3-glucosyltransferase_OS=Arabidopsis_thaliana_GN=At2g44660_PE=2_SV=3	1.00E-28	[illegible]	[illegible]
comp29525_c0_seq13.p3				
comp29525_c0_seq3.p1	sp|B2RX14|TUT4_MOUSE_Terminal_uridylyltransferase_4_OS=Mus_musculus_GN=Zcchc11_PE=1_SV=2	4.00E-14	[illegible]	[illegible]
comp29525_c0_seq3.p2	sp|O80505|ALG8_ARATH_Probable_dolichyl_pyrophosphate_Glc1Man9GlcNAc2_alpha-1,3-glucosyltransferase_OS=Arabidopsis_thaliana_GN=At2g44660_PE=2_SV=3	1.00E-28	[illegible]	[illegible]
comp29525_c0_seq3.p3				
comp29525_c0_seq4.p1	sp|B2RX14|TUT4_MOUSE_Terminal_uridylyltransferase_4_OS=Mus_musculus_GN=Zcchc11_PE=1_SV=2	1.00E-13	[illegible]	[illegible]
comp29525_c0_seq4.p2	sp|Q9W3V8|ALG8_DROME_Probable_dolichyl_pyrophosphate_Glc1Man9GlcNAc2_alpha-1,3-glucosyltransferase_OS=Drosophila_melanogaster_GN=CG4542_PE=2_SV=1	7.00E-48	[illegible]	[illegible]
comp29525_c0_seq5.p1	sp|Q9W3V8|ALG8_DROME_Probable_dolichyl_pyrophosphate_Glc1Man9GlcNAc2_alpha-1,3-glucosyltransferase_OS=Drosophila_melanogaster_GN=CG4542_PE=2_SV=1	7.00E-48	[illegible]	[illegible]

comp29525_c0_seq5.p2	sp|B2RX14|TUT4_MOUSE_Terminal_uridylyltransferase_4_OS=Mus_musculus_GN=Zcchc11_PE=1_SV=2	4.00E-14	GO:0001816,GO:0003676,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0008270,GO:0010586,GO:0010587,GO:0016740,GO:0016779,GO:0016779,GO:0019827,GO:0031047,GO:0031054,GO:0031123,GO:0031664,GO:0032088,GO:0032755,GO:0046872,GO:0050265,GO:0050265,GO:0070102,GO:0071044	cytokine production,nucleic acid binding,protein binding,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,cytoplasm,zinc ion binding,miRNA metabolic process,miRNA catabolic process,transferase activity,nucleotidyltransferase activity,nucleotidyltransferase activity,stem cell maintenance,gene silencing by RNA,pre-miRNA processing,RNA 3'-end processing,regulation of lipopolysaccharide-mediated signaling pathway,negative regulation of NF-kappaB transcription factor activity,positive regulation of interleukin-6 production,metal ion binding,RNA uridylyltransferase activity,RNA uridylyltransferase activity,interleukin-6-mediated signaling pathway,histone mRNA catabolic process
comp29525_c0_seq5.p3				
comp29525_c0_seq8.p1	sp|B2RX14|TUT4_MOUSE_Terminal_uridylyltransferase_4_OS=Mus_musculus_GN=Zcchc11_PE=1_SV=2	1.00E-13	GO:0001816,GO:0003676,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0008270,GO:0010586,GO:0010587,GO:0016740,GO:0016779,GO:0016779,GO:0019827,GO:0031047,GO:0031054,GO:0031123,GO:0031664,GO:0032088,GO:0032755,GO:0046872,GO:0050265,GO:0050265,GO:0070102,GO:0071044	cytokine production,nucleic acid binding,protein binding,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,cytoplasm,zinc ion binding,miRNA metabolic process,miRNA catabolic process,transferase activity,nucleotidyltransferase activity,nucleotidyltransferase activity,stem cell maintenance,gene silencing by RNA,pre-miRNA processing,RNA 3'-end processing,regulation of lipopolysaccharide-mediated signaling pathway,negative regulation of NF-kappaB transcription factor activity,positive regulation of interleukin-6 production,metal ion binding,RNA uridylyltransferase activity,RNA uridylyltransferase activity,interleukin-6-mediated signaling pathway,histone mRNA catabolic process
comp29525_c0_seq8.p2	sp|Q9W3V8|ALG8_DROME_Probable_dolichyl_pyrophosphate_Glc1Man9GlcNAc2_alpha-1,3-glucosyltransferase_OS=Drosophila_melanogaster_GN=CG4542_PE=2_SV=1	7.00E-48	GO:0003384,GO:0005783,GO:0005783,GO:0005789,GO:0005789,GO:0005789,GO:0006486,GO:0006486,GO:0006487,GO:0006487,GO:0006490,GO:0007377,GO:0016020,GO:0016021,GO:0016740,GO:0016757,GO:0016758,GO:0042281,GO:0042283	apical constriction involved in gastrulation,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,endoplasmic reticulum membrane,endoplasmic reticulum membrane,protein glycosylation,protein glycosylation,protein N-linked glycosylation,protein N-linked glycosylation,oligosaccharide-lipid intermediate biosynthetic process,germ-band extension,membrane,integral component of membrane,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups,dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity,dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase activity
comp29526_c0_seq3.p1	sp|Q9U2R0|BIN3D_CAEEL_Probable_methyltransferase_Y17G7B.18_OS=Caenorhabditis_elegans_GN=Y17G7B.18_PE=2_SV=1	2.00E-21	GO:0008168,GO:0008168,GO:0016740,GO:0032259	methyltransferase activity,methyltransferase activity,transferase activity,methylation
comp29528_c0_seq1.p2				
comp29528_c0_seq2.p1				
comp29529_c0_seq1.p1				
comp29529_c0_seq3.p1				
comp29530_c0_seq2.p1				
comp29530_c0_seq3.p1				
comp29531_c0_seq1.p1				
comp29532_c0_seq2.p1	sp|Q9VAN6|SLBP_DROME_Histone_RNA_hairpin-binding_protein_OS=Drosophila_melanogaster_GN=Slbp_PE=1_SV=1	8.00E-13	GO:0003723,GO:0003723,GO:0003729,GO:0005515,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006397,GO:0006398,GO:0006398,GO:0006398,GO:0006398,GO:0006398,GO:0006398,GO:0007076,GO:0007275,GO:0035613,GO:0035613	RNA binding,RNA binding,mRNA binding,protein binding,nucleus,nucleus,cytoplasm,cytoplasm,mRNA processing,histone mRNA 3'-end processing,histone mRNA 3'-end processing,histone mRNA 3'-end processing,histone mRNA 3'-end processing,histone mRNA 3'-end processing,histone mRNA 3'-end processing,mitotic chromosome condensation,multicellular organismal development,RNA stem-loop binding,RNA stem-loop binding
comp29533_c0_seq2.p1	sp|Q86JM3|RPC6_DICDI_DNA-directed_RNA_polymerase_III_subunit_rpc6_OS=Dictyostelium_discoideum_GN=polr3f_PE=3_SV=1	9.00E-15	GO:0003677,GO:0003899,GO:0003899,GO:0003899,GO:0005634,GO:0005634,GO:0005666,GO:0005666,GO:0006351,GO:0006383,GO:0044351,GO:0001056	DNA binding,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,nucleus,nucleus,DNA-directed RNA polymerase III complex,DNA-directed RNA polymerase III complex,transcription, DNA-templated,transcription from RNA polymerase III promoter,macropinocytosis,RNA polymerase III activity
comp29533_c0_seq3.p1	sp|Q86JM3|RPC6_DICDI_DNA-directed_RNA_polymerase_III_subunit_rpc6_OS=Dictyostelium_discoideum_GN=polr3f_PE=3_SV=1	2.00E-19	GO:0003677,GO:0003899,GO:0003899,GO:0003899,GO:0005634,GO:0005634,GO:0005666,GO:0005666,GO:0006351,GO:0006383,GO:0044351,GO:0001056	DNA binding,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,nucleus,nucleus,DNA-directed RNA polymerase III complex,DNA-directed RNA polymerase III complex,transcription, DNA-templated,transcription from RNA polymerase III promoter,macropinocytosis,RNA polymerase III activity
comp29533_c0_seq4.p1	sp|Q9FZ36|M3K2_ARATH_Mitogen-activated_protein_kinase_kinase_kinase_2_OS=Arabidopsis_thaliana_GN=ANP2_PE=2_SV=1	3.00E-58	GO:0000165,GO:0000166,GO:0000186,GO:0004672,GO:0004674,GO:0004674,GO:0004709,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005874,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0043622	MAPK cascade,nucleotide binding,activation of MAPKK activity,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,MAP kinase kinase kinase activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,microtubule,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,cortical microtubule organization
comp29533_c0_seq4.p2	sp|Q86JM3|RPC6_DICDI_DNA-directed_RNA_polymerase_III_subunit_rpc6_OS=Dictyostelium_discoideum_GN=polr3f_PE=3_SV=1	2.00E-47	GO:0003677,GO:0003899,GO:0003899,GO:0003899,GO:0005634,GO:0005634,GO:0005666,GO:0005666,GO:0006351,GO:0006383,GO:0044351,GO:0001056	DNA binding,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,nucleus,nucleus,DNA-directed RNA polymerase III complex,DNA-directed RNA polymerase III complex,transcription, DNA-templated,transcription from RNA polymerase III promoter,macropinocytosis,RNA polymerase III activity
comp29534_c1_seq1.p1	sp|Q9RC92|UGL_BACGL_Unsaturated_glucuronyl_hydrolase_OS=Bacillus_sp._(strain_GL1)_GN=ugl_PE=1_SV=1	1.00E-33	GO:0000272,GO:0003824,GO:0005737,GO:0005737,GO:0005975,GO:0008152,GO:0016787,GO:0016798	polysaccharide catabolic process,catalytic activity,cytoplasm,cytoplasm,carbohydrate metabolic process,metabolic process,hydrolase activity,hydrolase activity, acting on glycosyl bonds
comp29534_c1_seq2.p1	sp|Q9RC92|UGL_BACGL_Unsaturated_glucuronyl_hydrolase_OS=Bacillus_sp._(strain_GL1)_GN=ugl_PE=1_SV=1	2.00E-33	GO:0000272,GO:0003824,GO:0005737,GO:0005737,GO:0005975,GO:0008152,GO:0016787,GO:0016798	polysaccharide catabolic process,catalytic activity,cytoplasm,cytoplasm,carbohydrate metabolic process,metabolic process,hydrolase activity,hydrolase activity, acting on glycosyl bonds
comp29535_c0_seq4.p1				
comp29535_c0_seq5.p1				
comp29535_c0_seq8.p1				
comp29536_c0_seq1.p1	sp|Q503I8|NGLY1_DANRE_Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine_amidase_OS=Danio_rerio_GN=ngly1_PE=2_SV=1	4.00E-71	GO:0000224,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006516,GO:0006516,GO:0016787,GO:0046872	peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase activity,cytoplasm,cytoplasm,cytoplasm,cytoplasm,glycoprotein catabolic process,glycoprotein catabolic process,hydrolase activity,metal ion binding
comp29539_c0_seq2.p1	sp|C0SPB2|YWTG_BACSU_Putative_metabolite_transport_protein_ywtG_OS=Bacillus_subtilis_GN=ywtG_PE=3_SV=1	1.00E-63	GO:0005215,GO:0005886,GO:0005886,GO:0006810,GO:0006810,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0022857,GO:0022891,GO:0055085	transporter activity,plasma membrane,plasma membrane,transport,transport,membrane,membrane,integral component of membrane,integral component of membrane,transmembrane transporter activity,substrate-specific transmembrane transporter activity,transmembrane transport
comp29539_c0_seq2.p2				
comp29539_c0_seq5.p1	sp|Q32NG5|GTR12_XENLA_Solute_carrier_family_2,_facilitated_glucose_transporter_member_12_OS=Xenopus_laevis_GN=slc2a12_PE=2_SV=1	6.00E-32	GO:0005215,GO:0006810,GO:0006810,GO:0008643,GO:0012505,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0022857,GO:0022891,GO:0055085	transporter activity,transport,transport,carbohydrate transport,endomembrane system,membrane,membrane,integral component of membrane,integral component of membrane,transmembrane transporter activity,substrate-specific transmembrane transporter activity,transmembrane transport
comp29540_c0_seq1.p1				
comp29540_c0_seq3.p1				
comp29542_c0_seq1.p1				
comp29542_c0_seq4.p1				
comp29543_c0_seq1.p1	sp|Q8YSU5|Y2987_NOSS1_UPF0187_protein_alr2987_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=alr2987_PE=3_SV=1	6.00E-21	GO:0005886,GO:0005886,GO:0016020,GO:0016021	plasma membrane,plasma membrane,membrane,integral component of membrane
comp29544_c0_seq1.p1				
comp29544_c1_seq2.p1	sp|Q99ME9|NOG1_MOUSE_Nucleolar_GTP-binding_protein_1_OS=Mus_musculus_GN=Gtpbp4_PE=2_SV=3	0	GO:0000079,GO:0000079,GO:0000166,GO:0001649,GO:0003924,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0005634,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0005730,GO:0005737,GO:0005737,GO:0005794,GO:0006184,GO:0008156,GO:0008156,GO:0008285,GO:0008285,GO:0016020,GO:0022408,GO:0022408,GO:0030336,GO:0030336,GO:0031397,GO:0031397,GO:0031965,GO:0033342,GO:0033342,GO:0042254,GO:0044822,GO:0048471,GO:0048471,GO:0050821,GO:0050821	regulation of cyclin-dependent protein serine/threonine kinase activity,regulation of cyclin-dependent protein serine/threonine kinase activity,nucleotide binding,osteoblast differentiation,GTPase activity,GTPase activity,GTP binding,GTP binding,GTP binding,nucleus,nucleus,nucleus,nucleolus,nucleolus,nucleolus,cytoplasm,cytoplasm,Golgi apparatus,GTP catabolic process,negative regulation of DNA replication,negative regulation of DNA replication,negative regulation of cell proliferation,negative regulation of cell proliferation,membrane,negative regulation of cell-cell adhesion,negative regulation of cell-cell adhesion,negative regulation of cell migration,negative regulation of cell migration,negative regulation of protein ubiquitination,negative regulation of protein ubiquitination,nuclear membrane,negative regulation of collagen binding,negative regulation of collagen binding,ribosome biogenesis,poly(A) RNA binding,perinuclear region of cytoplasm,perinuclear region of cytoplasm,protein stabilization,protein stabilization
comp29545_c0_seq1.p1	sp|Q5ZMM1|NO66_CHICK_Lysine-specific_demethylase_NO66_OS=Gallus_gallus_GN=NO66_PE=2_SV=1	1.00E-17	GO:0005506,GO:0005634,GO:0005634,GO:0005654,GO:0005730,GO:0006351,GO:0006355,GO:0016491,GO:0016568,GO:0016706,GO:0032453,GO:0034720,GO:0045668,GO:0045892,GO:0046872,GO:0051213,GO:0051864,GO:0051864,GO:0055114,GO:0070544	iron ion binding,nucleus,nucleus,nucleoplasm,nucleolus,transcription, DNA-templated,regulation of transcription, DNA-templated,oxidoreductase activity,chromatin modification,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,histone demethylase activity (H3-K4 specific),histone H3-K4 demethylation,negative regulation of osteoblast differentiation,negative regulation of transcription, DNA-templated,metal ion binding,dioxygenase activity,histone demethylase activity (H3-K36 specific),histone demethylase activity (H3-K36 specific),oxidation-reduction process,histone H3-K36 demethylation
comp29546_c0_seq1.p1				
comp29547_c0_seq1.p1				
comp29548_c0_seq3.p1	sp|P36412|RB11A_DICDI_Ras-related_protein_Rab-11A_OS=Dictyostelium_discoideum_GN=rab11A_PE=1_SV=1	7.00E-41	GO:0000166,GO:0000166,GO:0000331,GO:0003924,GO:0005515,GO:0005515,GO:0005525,GO:0005525,GO:0005525,GO:0005773,GO:0006184,GO:0006810,GO:0006886,GO:0006887,GO:0007231,GO:0007231,GO:0007264,GO:0007264,GO:0015031,GO:0015031,GO:0016020,GO:0017112,GO:0019003,GO:0031164,GO:0031164,GO:0031164,GO:0032482,GO:0032794,GO:0032794,GO:0032851,GO:0034394,GO:0044351,GO:0045335,GO:0055037,GO:0071476	nucleotide binding,nucleotide binding,contractile vacuole,GTPase activity,protein binding,protein binding,GTP binding,GTP binding,GTP binding,vacuole,GTP catabolic process,transport,intracellular protein transport,exocytosis,osmosensory signaling pathway,osmosensory signaling pathway,small GTPase mediated signal transduction,small GTPase mediated signal transduction,protein transport,protein transport,membrane,Rab guanyl-nucleotide exchange factor activity,GDP binding,contractile vacuolar membrane,contractile vacuolar membrane,contractile vacuolar membrane,Rab protein signal transduction,GTPase activating protein binding,GTPase activating protein binding,positive regulation of Rab GTPase activity,protein localization to cell surface,macropinocytosis,phagocytic vesicle,recycling endosome,cellular hypotonic response
comp29548_c0_seq3.p3				
comp29549_c1_seq1.p1				
comp29550_c0_seq2.p1				
comp29551_c0_seq4.p1				
comp29551_c0_seq5.p1				
comp29551_c0_seq5.p2				
comp29551_c0_seq6.p1				
comp29551_c0_seq7.p1				
comp29552_c1_seq2.p1				
comp29552_c1_seq2.p2	sp|P31584|YPTV1_VOLCA_GTP-binding_protein_yptV1_OS=Volvox_carteri_GN=YPTV1_PE=3_SV=1	7.00E-16	GO:0000166,GO:0005525,GO:0005525,GO:0005886,GO:0005886,GO:0006810,GO:0007264,GO:0015031,GO:0015031,GO:0016020	nucleotide binding,GTP binding,GTP binding,plasma membrane,plasma membrane,transport,small GTPase mediated signal transduction,protein transport,protein transport,membrane
comp29553_c0_seq1.p1				
comp29554_c0_seq1.p1				
comp29554_c0_seq1.p2				
comp29555_c0_seq1.p1	sp|Q9M9U9|RKD1_ARATH_Protein_RKD1_OS=Arabidopsis_thaliana_GN=RKD1_PE=3_SV=1	2.00E-12	GO:0003677,GO:0003700,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0006355,GO:0051302	DNA binding,sequence-specific DNA binding transcription factor activity,nucleus,nucleus,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of cell division
comp29556_c1_seq1.p1				
comp29556_c2_seq2.p1				
comp29557_c0_seq1.p1				
comp29558_c0_seq1.p1				
comp29558_c0_seq2.p1				
comp29558_c1_seq2.p1	sp|Q69ZL1|FGD6_MOUSE_FYVE,_RhoGEF_and_PH_domain-containing_protein_6_OS=Mus_musculus_GN=Fgd6_PE=1_SV=2	2.00E-24	GO:0003674,GO:0005085,GO:0005089,GO:0005575,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0008150,GO:0032321,GO:0035023,GO:0043547,GO:0046872,GO:0046872	molecular_function,guanyl-nucleotide exchange factor activity,Rho guanyl-nucleotide exchange factor activity,cellular_component,cytoplasm,cytoplasm,cytoskeleton,cytoskeleton,biological_process,positive regulation of Rho GTPase activity,regulation of Rho protein signal transduction,positive regulation of GTPase activity,metal ion binding,metal ion binding
comp29558_c1_seq3.p1				
comp29560_c0_seq1.p1				
comp29560_c0_seq2.p1				
comp29565_c0_seq1.p1				
comp29566_c0_seq1.p1				
comp29566_c0_seq1.p2				
comp29566_c0_seq5.p1				
comp29567_c0_seq12.p1				
comp29567_c0_seq12.p3	sp|O81769|DPH5_ARATH_Probable_diphthine_synthase_OS=Arabidopsis_thaliana_GN=At4g31790_PE=2_SV=1	3.00E-58	GO:0004164,GO:0004164,GO:0004164,GO:0008152,GO:0008168,GO:0008168,GO:0009220,GO:0016740,GO:0017183,GO:0017183,GO:0017183,GO:0032259	diphthine synthase activity,diphthine synthase activity,diphthine synthase activity,metabolic process,methyltransferase activity,methyltransferase activity,pyrimidine ribonucleotide biosynthetic process,transferase activity,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,methylation
comp29567_c0_seq12.p5				
comp29567_c0_seq14.p1	sp|O81769|DPH5_ARATH_Probable_diphthine_synthase_OS=Arabidopsis_thaliana_GN=At4g31790_PE=2_SV=1	3.00E-109	GO:0004164,GO:0004164,GO:0004164,GO:0008152,GO:0008168,GO:0008168,GO:0009220,GO:0016740,GO:0017183,GO:0017183,GO:0017183,GO:0032259	diphthine synthase activity,diphthine synthase activity,diphthine synthase activity,metabolic process,methyltransferase activity,methyltransferase activity,pyrimidine ribonucleotide biosynthetic process,transferase activity,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,methylation
comp29567_c0_seq14.p2				
comp29567_c0_seq14.p3				
comp29567_c0_seq14.p6				
comp29567_c0_seq3.p1	sp|O81769|DPH5_ARATH_Probable_diphthine_synthase_OS=Arabidopsis_thaliana_GN=At4g31790_PE=2_SV=1	3.00E-109	GO:0004164,GO:0004164,GO:0004164,GO:0008152,GO:0008168,GO:0008168,GO:0009220,GO:0016740,GO:0017183,GO:0017183,GO:0017183,GO:0032259	diphthine synthase activity,diphthine synthase activity,diphthine synthase activity,metabolic process,methyltransferase activity,methyltransferase activity,pyrimidine ribonucleotide biosynthetic process,transferase activity,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,methylation
comp29567_c0_seq3.p2				
comp29567_c0_seq3.p3				
comp29567_c0_seq7.p1				
comp29567_c0_seq7.p3	sp|O81769|DPH5_ARATH_Probable_diphthine_synthase_OS=Arabidopsis_thaliana_GN=At4g31790_PE=2_SV=1	3.00E-58	GO:0004164,GO:0004164,GO:0004164,GO:0008152,GO:0008168,GO:0008168,GO:0009220,GO:0016740,GO:0017183,GO:0017183,GO:0017183,GO:0032259	diphthine synthase activity,diphthine synthase activity,diphthine synthase activity,metabolic process,methyltransferase activity,methyltransferase activity,pyrimidine ribonucleotide biosynthetic process,transferase activity,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,peptidyl-diphthamide biosynthetic process from peptidyl-histidine,methylation
comp29568_c0_seq1.p4				
comp29568_c0_seq2.p1				
comp29568_c0_seq5.p4				
comp29569_c0_seq2.p2				
comp29569_c0_seq3.p1				
comp29570_c0_seq5.p1	sp|O59258|UPPS_PYRHO_Tritrans,polycis-undecaprenyl-diphosphate_synthase_(GGDP_specific)_OS=Pyrococcus_horikoshii_(strain_ATCC_700860_/_DSM_12428_/_JCM_9974_/_NBRC_100139_/_OT-3)_GN=uppS_PE=3_SV=1	2.00E-63	GO:0000287,GO:0004659,GO:0008152,GO:0008152,GO:0008152,GO:0016740,GO:0016765,GO:0046872	magnesium ion binding,prenyltransferase activity,metabolic process,metabolic process,metabolic process,transferase activity,transferase activity, transferring alkyl or aryl (other than methyl) groups,metal ion binding
comp29570_c0_seq7.p1				
comp29570_c0_seq8.p1	sp|Q5JGE1|UPPS_PYRKO_Tritrans,polycis-undecaprenyl-diphosphate_synthase_(GGDP_specific)_OS=Pyrococcus_kodakaraensis_(strain_ATCC_BAA-918_/_JCM_12380_/_KOD1)_GN=uppS_PE=3_SV=1	6.00E-34	GO:0000287,GO:0004659,GO:0008152,GO:0008152,GO:0008152,GO:0016740,GO:0016765,GO:0046872	magnesium ion binding,prenyltransferase activity,metabolic process,metabolic process,metabolic process,transferase activity,transferase activity, transferring alkyl or aryl (other than methyl) groups,metal ion binding
comp29571_c0_seq1.p1				
comp29572_c0_seq1.p1				
comp29572_c0_seq2.p1				
comp29572_c0_seq4.p1				
comp29573_c0_seq3.p1				
comp29573_c0_seq4.p1				
comp29575_c0_seq1.p1				
comp29575_c0_seq2.p1	sp|Q9NP64|NO40_HUMAN_Nucleolar_protein_of_40_kDa_OS=Homo_sapiens_GN=ZCCHC17_PE=1_SV=1	3.00E-27	GO:0003676,GO:0003723,GO:0005515,GO:0005634,GO:0005634,GO:0005730,GO:0008270,GO:0030529,GO:0043231,GO:0044822,GO:0044822,GO:0045111,GO:0046872	nucleic acid binding,RNA binding,protein binding,nucleus,nucleus,nucleolus,zinc ion binding,ribonucleoprotein complex,intracellular membrane-bounded organelle,poly(A) RNA binding,poly(A) RNA binding,intermediate filament cytoskeleton,metal ion binding
comp29577_c0_seq1.p1				
comp29577_c0_seq2.p1				
comp29577_c0_seq3.p2				
comp29577_c2_seq1.p1	sp|Q5RBG1|RAB5B_PONAB_Ras-related_protein_Rab-5B_OS=Pongo_abelii_GN=RAB5B_PE=2_SV=1	8.00E-81	GO:0000166,GO:0005525,GO:0005525,GO:0005768,GO:0005768,GO:0005886,GO:0005886,GO:0006810,GO:0007032,GO:0007264,GO:0015031,GO:0015031,GO:0016020,GO:0019003,GO:0019003,GO:0019882,GO:0030100,GO:0030139,GO:0030742,GO:0031901,GO:0042470,GO:0070062	nucleotide binding,GTP binding,GTP binding,endosome,endosome,plasma membrane,plasma membrane,transport,endosome organization,small GTPase mediated signal transduction,protein transport,protein transport,membrane,GDP binding,GDP binding,antigen processing and presentation,regulation of endocytosis,endocytic vesicle,GTP-dependent protein binding,early endosome membrane,melanosome,extracellular vesicular exosome
comp29579_c0_seq1.p1	sp|Q15397|K0020_HUMAN_Pumilio_domain-containing_protein_KIAA0020_OS=Homo_sapiens_GN=KIAA0020_PE=1_SV=3	3.00E-36	GO:0003723,GO:0003723,GO:0003729,GO:0005634,GO:0005730,GO:0005730,GO:0005783,GO:0006417,GO:0044822,GO:0044822	RNA binding,RNA binding,mRNA binding,nucleus,nucleolus,nucleolus,endoplasmic reticulum,regulation of translation,poly(A) RNA binding,poly(A) RNA binding
comp29581_c0_seq1.p2				
comp29581_c0_seq2.p1				
comp29581_c0_seq4.p2				
comp29581_c0_seq7.p2				
comp29582_c0_seq1.p1				
comp29582_c0_seq2.p1				
comp29582_c0_seq2.p2				
comp29582_c0_seq3.p1				
comp29583_c0_seq1.p1				
comp29584_c0_seq7.p2				
comp29584_c0_seq9.p2				
comp29585_c0_seq1.p1				
comp29585_c0_seq2.p1				
comp29585_c0_seq4.p1				
comp29588_c0_seq4.p1				
comp29589_c0_seq1.p1	sp|P44094|Y1014_HAEIN_Uncharacterized_protein_HI_1014_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=HI_1014_PE=4_SV=1	7.00E-27	GO:0003824,GO:0008152,GO:0050662	catalytic activity,metabolic process,coenzyme binding
comp29590_c0_seq12.p1				
comp29590_c0_seq5.p1				
comp29591_c0_seq2.p1	sp|B1AY13|UBP24_MOUSE_Ubiquitin_carboxyl-terminal_hydrolase_24_OS=Mus_musculus_GN=Usp24_PE=1_SV=1	1.00E-50	GO:0004197,GO:0004221,GO:0004843,GO:0005575,GO:0006508,GO:0006511,GO:0008233,GO:0008234,GO:0016579,GO:0016787,GO:0036459,GO:0043161,GO:0061136	cysteine-type endopeptidase activity,ubiquitin thiolesterase activity,ubiquitin-specific protease activity,cellular_component,proteolysis,ubiquitin-dependent protein catabolic process,peptidase activity,cysteine-type peptidase activity,protein deubiquitination,hydrolase activity,ubiquitinyl hydrolase activity,proteasome-mediated ubiquitin-dependent protein catabolic process,regulation of proteasomal protein catabolic process
comp29592_c0_seq3.p1	sp|Q2N806|KATG_ERYLH_Catalase-peroxidase_OS=Erythrobacter_litoralis_(strain_HTCC2594)_GN=katG_PE=3_SV=1	5.00E-122	GO:0004096,GO:0004096,GO:0004601,GO:0004601,GO:0004601,GO:0004601,GO:0006979,GO:0016491,GO:0020037,GO:0042744,GO:0046872,GO:0055114,GO:0055114	catalase activity,catalase activity,peroxidase activity,peroxidase activity,peroxidase activity,peroxidase activity,response to oxidative stress,oxidoreductase activity,heme binding,hydrogen peroxide catabolic process,metal ion binding,oxidation-reduction process,oxidation-reduction process
comp29592_c0_seq4.p1	sp|Q3IQZ9|KATG_NATPD_Catalase-peroxidase_OS=Natronomonas_pharaonis_(strain_DSM_2160_/_ATCC_35678)_GN=katG_PE=3_SV=1	7.00E-80	GO:0004096,GO:0004096,GO:0004601,GO:0004601,GO:0004601,GO:0004601,GO:0006979,GO:0016491,GO:0020037,GO:0042744,GO:0046872,GO:0055114,GO:0055114	catalase activity,catalase activity,peroxidase activity,peroxidase activity,peroxidase activity,peroxidase activity,response to oxidative stress,oxidoreductase activity,heme binding,hydrogen peroxide catabolic process,metal ion binding,oxidation-reduction process,oxidation-reduction process
comp29593_c0_seq3.p1	sp|Q9S1G2|DPO1_RHILE_DNA_polymerase_I_OS=Rhizobium_leguminosarum_GN=polA_PE=3_SV=1	5.00E-48	GO:0003676,GO:0003677,GO:0003677,GO:0003824,GO:0003887,GO:0003887,GO:0003887,GO:0004518,GO:0004527,GO:0004527,GO:0006139,GO:0006260,GO:0006260,GO:0006261,GO:0006281,GO:0006281,GO:0006974,GO:0008408,GO:0016740,GO:0016779,GO:0016787,GO:0071897,GO:0071897,GO:0071897,GO:0090305,GO:0090305,GO:0090305,GO:0090305	nucleic acid binding,DNA binding,DNA binding,catalytic activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,nuclease activity,exonuclease activity,exonuclease activity,nucleobase-containing compound metabolic process,DNA replication,DNA replication,DNA-dependent DNA replication,DNA repair,DNA repair,cellular response to DNA damage stimulus,3'-5' exonuclease activity,transferase activity,nucleotidyltransferase activity,hydrolase activity,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp29594_c0_seq3.p1				
comp29595_c0_seq1.p1				
comp29596_c0_seq1.p1	sp|P10242|MYB_HUMAN_Transcriptional_activator_Myb_OS=Homo_sapiens_GN=MYB_PE=1_SV=2	1.00E-52	GO:0000082,GO:0000122,GO:0000978,GO:0000978,GO:0001077,GO:0001077,GO:0001701,GO:0003677,GO:0003677,GO:0003677,GO:0003682,GO:0003700,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0006338,GO:0006351,GO:0006355,GO:0006355,GO:0006355,GO:0006355,GO:0006816,GO:0007596,GO:0010468,GO:0016363,GO:0030183,GO:0045624,GO:0045892,GO:0045893,GO:0045893,GO:0045893,GO:0045944,GO:0045944,GO:0045944,GO:0045944,GO:0048538,GO:0048566,GO:0048872,GO:0051571,GO:0051574	G1/S transition of mitotic cell cycle,negative regulation of transcription from RNA polymerase II promoter,RNA polymerase II core promoter proximal region sequence-specific DNA binding,RNA polymerase II core promoter proximal region sequence-specific DNA binding,RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription,RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription,in utero embryonic development,DNA binding,DNA binding,DNA binding,chromatin binding,sequence-specific DNA binding transcription factor activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,chromatin remodeling,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,calcium ion transport,blood coagulation,regulation of gene expression,nuclear matrix,B cell differentiation,positive regulation of T-helper cell differentiation,negative regulation of transcription, DNA-templated,positive regulation of transcription, DNA-templated,positive regulation of transcription, DNA-templated,positive regulation of transcription, DNA-templated,positive regulation of transcription from RNA polymerase II promoter,positive regulation of transcription from RNA polymerase II promoter,positive regulation of transcription from RNA polymerase II promoter,positive regulation of transcription from RNA polymerase II promoter,thymus development,embryonic digestive tract development,homeostasis of number of cells,positive regulation of histone H3-K4 methylation,positive regulation of histone H3-K9 methylation
comp29597_c0_seq1.p2				
comp29600_c0_seq4.p1	sp|Q9ET64|NSMA_RAT_Sphingomyelin_phosphodiesterase_2_OS=Rattus_norvegicus_GN=Smpd2_PE=1_SV=1	2.00E-23	GO:0004767,GO:0004767,GO:0004767,GO:0004767,GO:0005886,GO:0005886,GO:0005901,GO:0006629,GO:0006665,GO:0006665,GO:0009612,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016787,GO:0035556,GO:0046513,GO:0046872	sphingomyelin phosphodiesterase activity,sphingomyelin phosphodiesterase activity,sphingomyelin phosphodiesterase activity,sphingomyelin phosphodiesterase activity,plasma membrane,plasma membrane,caveola,lipid metabolic process,sphingolipid metabolic process,sphingolipid metabolic process,response to mechanical stimulus,membrane,membrane,membrane,integral component of membrane,hydrolase activity,intracellular signal transduction,ceramide biosynthetic process,metal ion binding
comp29601_c0_seq1.p1				
comp29601_c0_seq2.p1				
comp29602_c0_seq1.p1				
comp29603_c0_seq3.p2				
comp29603_c0_seq4.p1				
comp29604_c0_seq1.p1				
comp29604_c0_seq2.p1				
comp29604_c0_seq3.p1				
comp29605_c0_seq3.p1	sp|P0CN90|ATG26_CRYNJ_Sterol_3-beta-glucosyltransferase_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=ATG26_PE=3_SV=1	8.00E-14	GO:0005737,GO:0005737,GO:0005975,GO:0006629,GO:0006694,GO:0006810,GO:0006914,GO:0008152,GO:0008202,GO:0015031,GO:0016020,GO:0016020,GO:0016126,GO:0016740,GO:0016757,GO:0016758,GO:0016906,GO:0030259	cytoplasm,cytoplasm,carbohydrate metabolic process,lipid metabolic process,steroid biosynthetic process,transport,autophagy,metabolic process,steroid metabolic process,protein transport,membrane,membrane,sterol biosynthetic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups,sterol 3-beta-glucosyltransferase activity,lipid glycosylation
comp29605_c0_seq3.p2				
comp29605_c0_seq4.p1				
comp29605_c0_seq4.p2	sp|P0CN90|ATG26_CRYNJ_Sterol_3-beta-glucosyltransferase_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=ATG26_PE=3_SV=1	8.00E-14	GO:0005737,GO:0005737,GO:0005975,GO:0006629,GO:0006694,GO:0006810,GO:0006914,GO:0008152,GO:0008202,GO:0015031,GO:0016020,GO:0016020,GO:0016126,GO:0016740,GO:0016757,GO:0016758,GO:0016906,GO:0030259	cytoplasm,cytoplasm,carbohydrate metabolic process,lipid metabolic process,steroid biosynthetic process,transport,autophagy,metabolic process,steroid metabolic process,protein transport,membrane,membrane,sterol biosynthetic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring hexosyl groups,sterol 3-beta-glucosyltransferase activity,lipid glycosylation
comp29606_c0_seq1.p1	sp|B7G3Y9|LIPA2_PHATC_Lipoyl_synthase_2,_mitochondrial_OS=Phaeodactylum_tricornutum_(strain_CCAP_1055/1)_GN=PHATRDRAFT_28652_PE=3_SV=1	3.00E-138	GO:0003824,GO:0005739,GO:0005739,GO:0005739,GO:0009107,GO:0009107,GO:0009249,GO:0016740,GO:0016783,GO:0016992,GO:0016992,GO:0016992,GO:0046872,GO:0051536,GO:0051536,GO:0051539,GO:0051539,GO:0051539,GO:0051539	catalytic activity,mitochondrion,mitochondrion,mitochondrion,lipoate biosynthetic process,lipoate biosynthetic process,protein lipoylation,transferase activity,sulfurtransferase activity,lipoate synthase activity,lipoate synthase activity,lipoate synthase activity,metal ion binding,iron-sulfur cluster binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp29606_c0_seq2.p1	sp|B3L8F2|LIPA_PLAKH_Lipoyl_synthase,_apicoplast_OS=Plasmodium_knowlesi_(strain_H)_GN=lipA_PE=3_SV=1	5.00E-37	GO:0003824,GO:0009107,GO:0009107,GO:0009249,GO:0009536,GO:0016740,GO:0016783,GO:0016992,GO:0016992,GO:0016992,GO:0020011,GO:0020011,GO:0020011,GO:0046872,GO:0051536,GO:0051536,GO:0051539,GO:0051539,GO:0051539,GO:0051539	catalytic activity,lipoate biosynthetic process,lipoate biosynthetic process,protein lipoylation,plastid,transferase activity,sulfurtransferase activity,lipoate synthase activity,lipoate synthase activity,lipoate synthase activity,apicoplast,apicoplast,apicoplast,metal ion binding,iron-sulfur cluster binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp29606_c0_seq3.p1	sp|B3L8F2|LIPA_PLAKH_Lipoyl_synthase,_apicoplast_OS=Plasmodium_knowlesi_(strain_H)_GN=lipA_PE=3_SV=1	8.00E-67	GO:0003824,GO:0009107,GO:0009107,GO:0009249,GO:0009536,GO:0016740,GO:0016783,GO:0016992,GO:0016992,GO:0016992,GO:0020011,GO:0020011,GO:0020011,GO:0046872,GO:0051536,GO:0051536,GO:0051539,GO:0051539,GO:0051539,GO:0051539	catalytic activity,lipoate biosynthetic process,lipoate biosynthetic process,protein lipoylation,plastid,transferase activity,sulfurtransferase activity,lipoate synthase activity,lipoate synthase activity,lipoate synthase activity,apicoplast,apicoplast,apicoplast,metal ion binding,iron-sulfur cluster binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp29606_c0_seq5.p1	sp|B7G3Y9|LIPA2_PHATC_Lipoyl_synthase_2,_mitochondrial_OS=Phaeodactylum_tricornutum_(strain_CCAP_1055/1)_GN=PHATRDRAFT_28652_PE=3_SV=1	7.00E-69	GO:0003824,GO:0005739,GO:0005739,GO:0005739,GO:0009107,GO:0009107,GO:0009249,GO:0016740,GO:0016783,GO:0016992,GO:0016992,GO:0016992,GO:0046872,GO:0051536,GO:0051536,GO:0051539,GO:0051539,GO:0051539,GO:0051539	catalytic activity,mitochondrion,mitochondrion,mitochondrion,lipoate biosynthetic process,lipoate biosynthetic process,protein lipoylation,transferase activity,sulfurtransferase activity,lipoate synthase activity,lipoate synthase activity,lipoate synthase activity,metal ion binding,iron-sulfur cluster binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp29606_c0_seq5.p2	sp|B3L8F2|LIPA_PLAKH_Lipoyl_synthase,_apicoplast_OS=Plasmodium_knowlesi_(strain_H)_GN=lipA_PE=3_SV=1	5.00E-37	GO:0003824,GO:0009107,GO:0009107,GO:0009249,GO:0009536,GO:0016740,GO:0016783,GO:0016992,GO:0016992,GO:0016992,GO:0020011,GO:0020011,GO:0020011,GO:0046872,GO:0051536,GO:0051536,GO:0051539,GO:0051539,GO:0051539,GO:0051539	catalytic activity,lipoate biosynthetic process,lipoate biosynthetic process,protein lipoylation,plastid,transferase activity,sulfurtransferase activity,lipoate synthase activity,lipoate synthase activity,lipoate synthase activity,apicoplast,apicoplast,apicoplast,metal ion binding,iron-sulfur cluster binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp29606_c0_seq7.p1	sp|Q5U4W6|INT6B_XENLA_Integrator_complex_subunit_6-B_OS=Xenopus_laevis_GN=ints6-b_PE=2_SV=1	1.00E-15	GO:0005634,GO:0005634	nucleus,nucleus
comp29607_c0_seq3.p1	sp|Q58630|Y1233_METJA_Uncharacterized_protein_MJ1233_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ1233_PE=4_SV=1	3.00E-33		
comp29607_c0_seq3.p5				
comp29608_c0_seq1.p1	sp|Q54PK4|SMC2_DICDI_Structural_maintenance_of_chromosomes_protein_2_OS=Dictyostelium_discoideum_GN=smc2_PE=3_SV=1	0	GO:0000166,GO:0000796,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0007049,GO:0007067,GO:0007076,GO:0007076,GO:0030261,GO:0044351,GO:0051276,GO:0051301	nucleotide binding,condensin complex,ATP binding,ATP binding,nucleus,nucleus,nucleus,chromosome,cell cycle,mitotic nuclear division,mitotic chromosome condensation,mitotic chromosome condensation,chromosome condensation,macropinocytosis,chromosome organization,cell division
comp29608_c0_seq1.p6				
comp29608_c0_seq2.p1				
comp29609_c0_seq2.p1				
comp29609_c0_seq2.p2				
comp29609_c0_seq3.p1				
comp29611_c0_seq1.p1	sp|Q6ZDY8|DHSA_ORYSJ_Succinate_dehydrogenase_[ubiquinone]_flavoprotein_subunit,_mitochondrial_OS=Oryza_sativa_subsp._japonica_GN=SDH1_PE=2_SV=1	5.00E-81	GO:0005739,GO:0005743,GO:0005743,GO:0006099,GO:0006099,GO:0006099,GO:0008177,GO:0016020,GO:0016491,GO:0016491,GO:0016627,GO:0022900,GO:0050660,GO:0055114,GO:0055114,GO:0055114	mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,tricarboxylic acid cycle,tricarboxylic acid cycle,tricarboxylic acid cycle,succinate dehydrogenase (ubiquinone) activity,membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-CH group of donors,electron transport chain,flavin adenine dinucleotide binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp29611_c0_seq3.p1	sp|O82663|DHSA1_ARATH_Succinate_dehydrogenase_[ubiquinone]_flavoprotein_subunit_1,_mitochondrial_OS=Arabidopsis_thaliana_GN=SDH1-1_PE=1_SV=1	0	GO:0000104,GO:0005524,GO:0005618,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005749,GO:0005749,GO:0006099,GO:0006099,GO:0006099,GO:0006121,GO:0008177,GO:0016020,GO:0016491,GO:0016491,GO:0016627,GO:0022900,GO:0050660,GO:0050897,GO:0055114,GO:0055114,GO:0055114,GO:0005794	succinate dehydrogenase activity,ATP binding,cell wall,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial respiratory chain complex II,mitochondrial respiratory chain complex II,tricarboxylic acid cycle,tricarboxylic acid cycle,tricarboxylic acid cycle,mitochondrial electron transport, succinate to ubiquinone,succinate dehydrogenase (ubiquinone) activity,membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-CH group of donors,electron transport chain,flavin adenine dinucleotide binding,cobalt ion binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,Golgi apparatus
comp29611_c0_seq4.p1	sp|O82663|DHSA1_ARATH_Succinate_dehydrogenase_[ubiquinone]_flavoprotein_subunit_1,_mitochondrial_OS=Arabidopsis_thaliana_GN=SDH1-1_PE=1_SV=1	3.00E-179	GO:0000104,GO:0005524,GO:0005618,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005749,GO:0005749,GO:0006099,GO:0006099,GO:0006099,GO:0006121,GO:0008177,GO:0016020,GO:0016491,GO:0016491,GO:0016627,GO:0022900,GO:0050660,GO:0050897,GO:0055114,GO:0055114,GO:0055114,GO:0005794	succinate dehydrogenase activity,ATP binding,cell wall,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial respiratory chain complex II,mitochondrial respiratory chain complex II,tricarboxylic acid cycle,tricarboxylic acid cycle,tricarboxylic acid cycle,mitochondrial electron transport, succinate to ubiquinone,succinate dehydrogenase (ubiquinone) activity,membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-CH group of donors,electron transport chain,flavin adenine dinucleotide binding,cobalt ion binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,Golgi apparatus
comp29612_c0_seq1.p1				
comp29614_c0_seq4.p2				
comp29614_c0_seq5.p1				
comp29614_c0_seq7.p1	sp|Q03720|SLO_DROME_Calcium-activated_potassium_channel_slowpoke_OS=Drosophila_melanogaster_GN=slo_PE=1_SV=3	2.00E-12	GO:0005216,GO:0005244,GO:0005249,GO:0005267,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005886,GO:0006810,GO:0006811,GO:0006811,GO:0006813,GO:0006813,GO:0006813,GO:0006813,GO:0006813,GO:0006813,GO:0006813,GO:0007623,GO:0008076,GO:0015269,GO:0015269,GO:0015269,GO:0015269,GO:0015269,GO:0015269,GO:0015269,GO:0016020,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0034765,GO:0042493,GO:0043005,GO:0043025,GO:0045433,GO:0045433,GO:0045433,GO:0048512,GO:0055085,GO:0060072,GO:0060072,GO:0071805,GO:0071805	ion channel activity,voltage-gated ion channel activity,voltage-gated potassium channel activity,potassium channel activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,plasma membrane,transport,ion transport,ion transport,potassium ion transport,potassium ion transport,potassium ion transport,potassium ion transport,potassium ion transport,potassium ion transport,potassium ion transport,circadian rhythm,voltage-gated potassium channel complex,calcium-activated potassium channel activity,calcium-activated potassium channel activity,calcium-activated potassium channel activity,calcium-activated potassium channel activity,calcium-activated potassium channel activity,calcium-activated potassium channel activity,calcium-activated potassium channel activity,membrane,membrane,membrane,membrane,integral component of membrane,regulation of ion transmembrane transport,response to drug,neuron projection,neuronal cell body,male courtship behavior, veined wing generated song production,male courtship behavior, veined wing generated song production,male courtship behavior, veined wing generated song production,circadian behavior,transmembrane transport,large conductance calcium-activated potassium channel activity,large conductance calcium-activated potassium channel activity,potassium ion transmembrane transport,potassium ion transmembrane transport
comp29614_c0_seq8.p1	sp|Q03720|SLO_DROME_Calcium-activated_potassium_channel_slowpoke_OS=Drosophila_melanogaster_GN=slo_PE=1_SV=3	3.00E-12	GO:0005216,GO:0005244,GO:0005249,GO:0005267,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005886,GO:0006810,GO:0006811,GO:0006811,GO:0006813,GO:0006813,GO:0006813,GO:0006813,GO:0006813,GO:0006813,GO:0006813,GO:0007623,GO:0008076,GO:0015269,GO:0015269,GO:0015269,GO:0015269,GO:0015269,GO:0015269,GO:0015269,GO:0016020,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0034765,GO:0042493,GO:0043005,GO:0043025,GO:0045433,GO:0045433,GO:0045433,GO:0048512,GO:0055085,GO:0060072,GO:0060072,GO:0071805,GO:0071805	ion channel activity,voltage-gated ion channel activity,voltage-gated potassium channel activity,potassium channel activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,plasma membrane,transport,ion transport,ion transport,potassium ion transport,potassium ion transport,potassium ion transport,potassium ion transport,potassium ion transport,potassium ion transport,potassium ion transport,circadian rhythm,voltage-gated potassium channel complex,calcium-activated potassium channel activity,calcium-activated potassium channel activity,calcium-activated potassium channel activity,calcium-activated potassium channel activity,calcium-activated potassium channel activity,calcium-activated potassium channel activity,calcium-activated potassium channel activity,membrane,membrane,membrane,membrane,integral component of membrane,regulation of ion transmembrane transport,response to drug,neuron projection,neuronal cell body,male courtship behavior, veined wing generated song production,male courtship behavior, veined wing generated song production,male courtship behavior, veined wing generated song production,circadian behavior,transmembrane transport,large conductance calcium-activated potassium channel activity,large conductance calcium-activated potassium channel activity,potassium ion transmembrane transport,potassium ion transmembrane transport
comp29616_c0_seq1.p1	sp|Q9XGM8|MGAT1_ARATH_Alpha-1,3-mannosyl-glycoprotein_2-beta-N-acetylglucosaminyltransferase_OS=Arabidopsis_thaliana_GN=GNTI_PE=1_SV=1	8.00E-41	GO:0000139,GO:0003827,GO:0003827,GO:0005768,GO:0005794,GO:0005794,GO:0005794,GO:0005794,GO:0005794,GO:0005794,GO:0005802,GO:0006486,GO:0006486,GO:0006486,GO:0006487,GO:0006491,GO:0006972,GO:0008375,GO:0016020,GO:0016021,GO:0016262,GO:0016740,GO:0016757,GO:0016757,GO:0019344,GO:0046872	Golgi membrane,alpha-1,3-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity,alpha-1,3-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity,endosome,Golgi apparatus,Golgi apparatus,Golgi apparatus,Golgi apparatus,Golgi apparatus,Golgi apparatus,trans-Golgi network,protein glycosylation,protein glycosylation,protein glycosylation,protein N-linked glycosylation,N-glycan processing,hyperosmotic response,acetylglucosaminyltransferase activity,membrane,integral component of membrane,protein N-acetylglucosaminyltransferase activity,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring glycosyl groups,cysteine biosynthetic process,metal ion binding
comp29617_c0_seq1.p1	sp|Q054K1|Y674_LEPBL_UPF0176_protein_LBL_0674_OS=Leptospira_borgpetersenii_serovar_Hardjo-bovis_(strain_L550)_GN=LBL_0674_PE=3_SV=1	7.00E-14		
comp29617_c0_seq2.p1	sp|A8GCZ9|Y1886_SERP5_UPF0176_protein_Spro_1886_OS=Serratia_proteamaculans_(strain_568)_GN=Spro_1886_PE=3_SV=1	1.00E-63		
comp29618_c0_seq10.p1	sp|Q86U06|RBM23_HUMAN_Probable_RNA-binding_protein_23_OS=Homo_sapiens_GN=RBM23_PE=1_SV=1	1.00E-27	GO:0000166,GO:0003676,GO:0003723,GO:0003723,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0006397,GO:0016020	nucleotide binding,nucleic acid binding,RNA binding,RNA binding,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,mRNA processing,membrane
comp29618_c0_seq10.p4				
comp29618_c0_seq12.p1	sp|Q86U06|RBM23_HUMAN_Probable_RNA-binding_protein_23_OS=Homo_sapiens_GN=RBM23_PE=1_SV=1	2.00E-20	GO:0000166,GO:0003676,GO:0003723,GO:0003723,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0006397,GO:0016020	nucleotide binding,nucleic acid binding,RNA binding,RNA binding,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,mRNA processing,membrane
comp29618_c0_seq12.p3				
comp29618_c0_seq15.p1	sp|Q86U06|RBM23_HUMAN_Probable_RNA-binding_protein_23_OS=Homo_sapiens_GN=RBM23_PE=1_SV=1	3.00E-23	GO:0000166,GO:0003676,GO:0003723,GO:0003723,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0006397,GO:0016020	nucleotide binding,nucleic acid binding,RNA binding,RNA binding,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,mRNA processing,membrane
comp29618_c0_seq15.p3				
comp29618_c0_seq2.p1				
comp29618_c0_seq3.p1	sp|Q86U06|RBM23_HUMAN_Probable_RNA-binding_protein_23_OS=Homo_sapiens_GN=RBM23_PE=1_SV=1	5.00E-25	GO:0000166,GO:0003676,GO:0003723,GO:0003723,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0006397,GO:0016020	nucleotide binding,nucleic acid binding,RNA binding,RNA binding,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,mRNA processing,membrane
comp29618_c0_seq3.p4				
comp29619_c0_seq1.p1				
comp29619_c0_seq3.p1				
comp29620_c0_seq3.p1	sp|Q64152|BTF3_MOUSE_Transcription_factor_BTF3_OS=Mus_musculus_GN=Btf3_PE=2_SV=3	2.00E-26	GO:0001701,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0006810,GO:0015031,GO:0044822	in utero embryonic development,nucleus,nucleus,cytoplasm,cytoplasm,transcription, DNA-templated,regulation of transcription, DNA-templated,transport,protein transport,poly(A) RNA binding
comp29621_c0_seq1.p1	sp|Q54T82|Y1931_DICDI_Putative_leucine-rich_repeat-containing_protein_DDB_G0281931_OS=Dictyostelium_discoideum_GN=DDB_G0281931_PE=4_SV=1	1.00E-13	GO:0003674,GO:0005575,GO:0008150,GO:0016020,GO:0016020,GO:0016021	molecular_function,cellular_component,biological_process,membrane,membrane,integral component of membrane
comp29621_c0_seq1.p2				
comp29621_c0_seq2.p1				
comp29621_c0_seq2.p2				
comp29622_c0_seq1.p1	sp|Q9CR50|ZN363_MOUSE_RING_finger_and_CHY_zinc_finger_domain-containing_protein_1_OS=Mus_musculus_GN=Rchy1_PE=1_SV=1	3.00E-64	GO:0000151,GO:0000151,GO:0002039,GO:0004842,GO:0004842,GO:0005102,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0008270,GO:0016567,GO:0016567,GO:0016567,GO:0016607,GO:0016874,GO:0031398,GO:0031398,GO:0032436,GO:0032436,GO:0042787,GO:0042787,GO:0042803,GO:0046872,GO:0051865,GO:0051865	ubiquitin ligase complex,ubiquitin ligase complex,p53 binding,ubiquitin-protein transferase activity,ubiquitin-protein transferase activity,receptor binding,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,zinc ion binding,protein ubiquitination,protein ubiquitination,protein ubiquitination,nuclear speck,ligase activity,positive regulation of protein ubiquitination,positive regulation of protein ubiquitination,positive regulation of proteasomal ubiquitin-dependent protein catabolic process,positive regulation of proteasomal ubiquitin-dependent protein catabolic process,protein ubiquitination involved in ubiquitin-dependent protein catabolic process,protein ubiquitination involved in ubiquitin-dependent protein catabolic process,protein homodimerization activity,metal ion binding,protein autoubiquitination,protein autoubiquitination
comp29623_c0_seq1.p1				
comp29623_c1_seq1.p1				
comp29623_c2_seq1.p1				
comp29624_c0_seq1.p1				
comp29626_c0_seq3.p1	sp|Q9SZR1|ACA10_ARATH_Calcium-transporting_ATPase_10,_plasma_membrane-type_OS=Arabidopsis_thaliana_GN=ACA10_PE=1_SV=2	9.00E-166	GO:0000166,GO:0000166,GO:0005388,GO:0005388,GO:0005388,GO:0005388,GO:0005516,GO:0005516,GO:0005524,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006811,GO:0006812,GO:0006816,GO:0006816,GO:0006882,GO:0008152,GO:0009506,GO:0009624,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016787,GO:0019829,GO:0046872,GO:0046872,GO:0070588	nucleotide binding,nucleotide binding,calcium-transporting ATPase activity,calcium-transporting ATPase activity,calcium-transporting ATPase activity,calcium-transporting ATPase activity,calmodulin binding,calmodulin binding,ATP binding,ATP binding,plasma membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,transport,ion transport,cation transport,calcium ion transport,calcium ion transport,cellular zinc ion homeostasis,metabolic process,plasmodesma,response to nematode,membrane,membrane,membrane,integral component of membrane,integral component of membrane,hydrolase activity,cation-transporting ATPase activity,metal ion binding,metal ion binding,calcium ion transmembrane transport
comp29627_c0_seq1.p1	sp|P53500|ACT_CYAME_Actin_OS=Cyanidioschyzon_merolae_PE=3_SV=1	1.00E-68	GO:0000166,GO:0005524,GO:0005737,GO:0005856,GO:0005856	nucleotide binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton
comp29627_c0_seq2.p1				
comp29627_c0_seq2.p4				
comp29627_c0_seq4.p1	sp|P53500|ACT_CYAME_Actin_OS=Cyanidioschyzon_merolae_PE=3_SV=1	2.00E-68	GO:0000166,GO:0005524,GO:0005737,GO:0005856,GO:0005856	nucleotide binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton
comp29627_c0_seq5.p1	sp|P53487|ARP2_ACACA_Actin-related_protein_2_OS=Acanthamoeba_castellanii_GN=arp2_PE=2_SV=1	2.00E-136	GO:0000166,GO:0003779,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0042995,GO:0042995	nucleotide binding,actin binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,cell projection,cell projection
comp29627_c0_seq5.p2				
comp29627_c0_seq6.p1	sp|Q56A35|ARP2B_DANRE_Actin-related_protein_2-B_OS=Danio_rerio_GN=actr2b_PE=2_SV=1	6.00E-167	GO:0000166,GO:0003779,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0042995,GO:0042995	nucleotide binding,actin binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,cell projection,cell projection
comp29627_c0_seq6.p2				
comp29629_c0_seq2.p1				
comp29629_c0_seq2.p5				
comp29630_c0_seq2.p1				
comp29630_c0_seq2.p5				
comp29630_c0_seq4.p1				
comp29631_c0_seq1.p1				
comp29631_c0_seq6.p1				
comp29632_c0_seq1.p1				
comp29632_c0_seq2.p1				
comp29632_c0_seq3.p1				
comp29632_c0_seq4.p1				
comp29632_c0_seq6.p1				
comp29632_c0_seq7.p1				
comp29633_c1_seq1.p1				
comp29633_c1_seq2.p1				
comp29634_c0_seq2.p1	sp|Q9ASU1|DGAT2_ARATH_Diacylglycerol_O-acyltransferase_2_OS=Arabidopsis_thaliana_GN=DGAT2_PE=2_SV=1	1.00E-27	GO:0004144,GO:0004144,GO:0005783,GO:0005789,GO:0006071,GO:0006629,GO:0016020,GO:0016021,GO:0016740,GO:0016746,GO:0016747,GO:0019432,GO:0019432	diacylglycerol O-acyltransferase activity,diacylglycerol O-acyltransferase activity,endoplasmic reticulum,endoplasmic reticulum membrane,glycerol metabolic process,lipid metabolic process,membrane,integral component of membrane,transferase activity,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups other than amino-acyl groups,triglyceride biosynthetic process,triglyceride biosynthetic process
comp29634_c0_seq2.p2	sp|Q50568|FDHC_METTF_Probable_formate_transporter_OS=Methanobacterium_thermoformicicum_GN=fdhC_PE=3_SV=1	1.00E-45	GO:0005215,GO:0005886,GO:0005886,GO:0006810,GO:0006810,GO:0016020,GO:0016020,GO:0016021	transporter activity,plasma membrane,plasma membrane,transport,transport,membrane,membrane,integral component of membrane
comp29635_c0_seq1.p1				
comp29635_c0_seq2.p1				
comp29636_c0_seq5.p1	sp|Q6A026|PDS5A_MOUSE_Sister_chromatid_cohesion_protein_PDS5_homolog_A_OS=Mus_musculus_GN=Pds5a_PE=2_SV=3	2.00E-55	GO:0005634,GO:0005634,GO:0007049,GO:0007067,GO:0008156,GO:0051301	nucleus,nucleus,cell cycle,mitotic nuclear division,negative regulation of DNA replication,cell division
comp29637_c0_seq2.p1				
comp29637_c1_seq2.p1				
comp29638_c0_seq1.p1	sp|B4NBL6|PTC71_DROWI_Protein_phosphatase_PTC7_homolog_fig_OS=Drosophila_willistoni_GN=fig_PE=3_SV=1	7.00E-30	GO:0003824,GO:0004721,GO:0004721,GO:0004722,GO:0005575,GO:0016311,GO:0016787,GO:0046872	catalytic activity,phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,protein serine/threonine phosphatase activity,cellular_component,dephosphorylation,hydrolase activity,metal ion binding
comp29640_c0_seq1.p1				
comp29640_c0_seq3.p1				
comp29641_c0_seq1.p1				
comp29641_c0_seq2.p1				
comp29642_c0_seq2.p1	sp|Q8BT60|CPNE3_MOUSE_Copine-3_OS=Mus_musculus_GN=Cpne3_PE=1_SV=2	1.00E-11	GO:0004674,GO:0004674,GO:0005829,GO:0005829,GO:0006468,GO:0044822,GO:0070062	protein serine/threonine kinase activity,protein serine/threonine kinase activity,cytosol,cytosol,protein phosphorylation,poly(A) RNA binding,extracellular vesicular exosome
comp29642_c0_seq3.p1	sp|Q8IYJ1|CPNE9_HUMAN_Copine-9_OS=Homo_sapiens_GN=CPNE9_PE=1_SV=3	1.00E-96	GO:0005615,GO:0070062	extracellular space,extracellular vesicular exosome
comp29643_c0_seq3.p1				
comp29643_c0_seq8.p1				
comp29643_c0_seq9.p1				
comp29644_c0_seq2.p1				
comp29644_c0_seq2.p2	sp|Q82UC1|APAG_NITEU_Protein_ApaG_OS=Nitrosomonas_europaea_(strain_ATCC_19718_/_NBRC_14298)_GN=apaG_PE=3_SV=1	3.00E-12		
comp29644_c0_seq3.p1				
comp29645_c0_seq2.p1				
comp29646_c0_seq1.p1				
comp29646_c0_seq3.p1				
comp29648_c0_seq2.p1	sp|Q08759|MYB_XENLA_Transcriptional_activator_Myb_OS=Xenopus_laevis_GN=myb_PE=2_SV=1	5.00E-25	GO:0003677,GO:0003677,GO:0003682,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0006355	DNA binding,DNA binding,chromatin binding,nucleus,nucleus,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated
comp29649_c0_seq1.p1	sp|Q96EN8|MOCOS_HUMAN_Molybdenum_cofactor_sulfurase_OS=Homo_sapiens_GN=MOCOS_PE=1_SV=2	8.00E-99	GO:0003824,GO:0005575,GO:0005829,GO:0006766,GO:0006767,GO:0006777,GO:0006777,GO:0006777,GO:0008152,GO:0008265,GO:0008265,GO:0008265,GO:0008265,GO:0016740,GO:0016829,GO:0030151,GO:0030151,GO:0030170,GO:0030170,GO:0032324,GO:0043545,GO:0044281	catalytic activity,cellular_component,cytosol,vitamin metabolic process,water-soluble vitamin metabolic process,Mo-molybdopterin cofactor biosynthetic process,Mo-molybdopterin cofactor biosynthetic process,Mo-molybdopterin cofactor biosynthetic process,metabolic process,Mo-molybdopterin cofactor sulfurase activity,Mo-molybdopterin cofactor sulfurase activity,Mo-molybdopterin cofactor sulfurase activity,Mo-molybdopterin cofactor sulfurase activity,transferase activity,lyase activity,molybdenum ion binding,molybdenum ion binding,pyridoxal phosphate binding,pyridoxal phosphate binding,molybdopterin cofactor biosynthetic process,molybdopterin cofactor metabolic process,small molecule metabolic process
comp29649_c0_seq2.p1	sp|Q14CH1|MOCOS_MOUSE_Molybdenum_cofactor_sulfurase_OS=Mus_musculus_GN=Mocos_PE=2_SV=1	3.00E-67	GO:0003824,GO:0005575,GO:0006777,GO:0006777,GO:0006777,GO:0008152,GO:0008265,GO:0008265,GO:0008265,GO:0008265,GO:0016740,GO:0016829,GO:0030151,GO:0030151,GO:0030170,GO:0030170,GO:0043545,GO:0043545	catalytic activity,cellular_component,Mo-molybdopterin cofactor biosynthetic process,Mo-molybdopterin cofactor biosynthetic process,Mo-molybdopterin cofactor biosynthetic process,metabolic process,Mo-molybdopterin cofactor sulfurase activity,Mo-molybdopterin cofactor sulfurase activity,Mo-molybdopterin cofactor sulfurase activity,Mo-molybdopterin cofactor sulfurase activity,transferase activity,lyase activity,molybdenum ion binding,molybdenum ion binding,pyridoxal phosphate binding,pyridoxal phosphate binding,molybdopterin cofactor metabolic process,molybdopterin cofactor metabolic process
comp29650_c0_seq1.p1				
comp29650_c1_seq1.p1	sp|Q9C0V4|YOM2_SCHPO_Uncharacterized_protein_PB7E8.02_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBPB7E8.02_PE=2_SV=1	2.00E-28	GO:0003674,GO:0005737,GO:0005739,GO:0008150	molecular_function,cytoplasm,mitochondrion,biological_process
comp29651_c0_seq1.p1	sp|P54638|ARGE_DICDI_Acetylornithine_deacetylase_OS=Dictyostelium_discoideum_GN=argE_PE=1_SV=2	4.00E-144	GO:0005615,GO:0006526,GO:0006526,GO:0008152,GO:0008652,GO:0008777,GO:0016787,GO:0016787,GO:0044351,GO:0045335,GO:0045335,GO:0046872	extracellular space,arginine biosynthetic process,arginine biosynthetic process,metabolic process,cellular amino acid biosynthetic process,acetylornithine deacetylase activity,hydrolase activity,hydrolase activity,macropinocytosis,phagocytic vesicle,phagocytic vesicle,metal ion binding
comp29651_c0_seq1.p2	sp|O67469|RUVX_AQUAE_Putative_Holliday_junction_resolvase_OS=Aquifex_aeolicus_(strain_VF5)_GN=aq_1498_PE=3_SV=1	6.00E-12	GO:0003676,GO:0004518,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006139,GO:0006281,GO:0006281,GO:0006281,GO:0006310,GO:0006310,GO:0006310,GO:0006974,GO:0006974,GO:0016787,GO:0016788,GO:0016788,GO:0090305	nucleic acid binding,nuclease activity,cytoplasm,cytoplasm,cytoplasm,cytoplasm,nucleobase-containing compound metabolic process,DNA repair,DNA repair,DNA repair,DNA recombination,DNA recombination,DNA recombination,cellular response to DNA damage stimulus,cellular response to DNA damage stimulus,hydrolase activity,hydrolase activity, acting on ester bonds,hydrolase activity, acting on ester bonds,nucleic acid phosphodiester bond hydrolysis
comp29651_c0_seq3.p1	sp|O67469|RUVX_AQUAE_Putative_Holliday_junction_resolvase_OS=Aquifex_aeolicus_(strain_VF5)_GN=aq_1498_PE=3_SV=1	6.00E-12	GO:0003676,GO:0004518,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006139,GO:0006281,GO:0006281,GO:0006281,GO:0006310,GO:0006310,GO:0006310,GO:0006974,GO:0006974,GO:0016787,GO:0016788,GO:0016788,GO:0090305	nucleic acid binding,nuclease activity,cytoplasm,cytoplasm,cytoplasm,cytoplasm,nucleobase-containing compound metabolic process,DNA repair,DNA repair,DNA repair,DNA recombination,DNA recombination,DNA recombination,cellular response to DNA damage stimulus,cellular response to DNA damage stimulus,hydrolase activity,hydrolase activity, acting on ester bonds,hydrolase activity, acting on ester bonds,nucleic acid phosphodiester bond hydrolysis
comp29652_c0_seq1.p1	sp|Q6P3W7|SCYL2_HUMAN_SCY1-like_protein_2_OS=Homo_sapiens_GN=SCYL2_PE=1_SV=1	1.00E-49	GO:0002092,GO:0004672,GO:0005102,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005737,GO:0005768,GO:0005794,GO:0005794,GO:0006468,GO:0008333,GO:0010008,GO:0016020,GO:0016772,GO:0030136,GO:0031410,GO:0048471,GO:0090090,GO:2000286,GO:2000370	positive regulation of receptor internalization,protein kinase activity,receptor binding,protein binding,protein binding,protein binding,ATP binding,cytoplasm,endosome,Golgi apparatus,Golgi apparatus,protein phosphorylation,endosome to lysosome transport,endosome membrane,membrane,transferase activity, transferring phosphorus-containing groups,clathrin-coated vesicle,cytoplasmic vesicle,perinuclear region of cytoplasm,negative regulation of canonical Wnt signaling pathway,receptor internalization involved in canonical Wnt signaling pathway,positive regulation of clathrin-mediated endocytosis
comp29652_c0_seq1.p2				
comp29653_c0_seq1.p1	sp|Q8CCB4|VPS53_MOUSE_Vacuolar_protein_sorting-associated_protein_53_homolog_OS=Mus_musculus_GN=Vps53_PE=2_SV=1	1.00E-114	GO:0000938,GO:0000938,GO:0005768,GO:0005794,GO:0005794,GO:0006810,GO:0010008,GO:0015031,GO:0016020,GO:0042147	GARP complex,GARP complex,endosome,Golgi apparatus,Golgi apparatus,transport,endosome membrane,protein transport,membrane,retrograde transport, endosome to Golgi
comp29653_c0_seq1.p2	sp|P43619|NADC_YEAST_Nicotinate-nucleotide_pyrophosphorylase_[carboxylating]_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=BNA6_PE=1_SV=1	1.00E-92	GO:0003824,GO:0004514,GO:0004514,GO:0004514,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0009435,GO:0009435,GO:0016740,GO:0016757,GO:0016763,GO:0019363,GO:0019363,GO:0034354,GO:0042802,GO:0042802,GO:0042802	catalytic activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nucleus,nucleus,cytoplasm,cytoplasm,NAD biosynthetic process,NAD biosynthetic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring pentosyl groups,pyridine nucleotide biosynthetic process,pyridine nucleotide biosynthetic process,'de novo' NAD biosynthetic process from tryptophan,identical protein binding,identical protein binding,identical protein binding
comp29653_c0_seq2.p1	sp|Q8CCB4|VPS53_MOUSE_Vacuolar_protein_sorting-associated_protein_53_homolog_OS=Mus_musculus_GN=Vps53_PE=2_SV=1	1.00E-114	GO:0000938,GO:0000938,GO:0005768,GO:0005794,GO:0005794,GO:0006810,GO:0010008,GO:0015031,GO:0016020,GO:0042147	GARP complex,GARP complex,endosome,Golgi apparatus,Golgi apparatus,transport,endosome membrane,protein transport,membrane,retrograde transport, endosome to Golgi
comp29653_c0_seq2.p3	sp|P43619|NADC_YEAST_Nicotinate-nucleotide_pyrophosphorylase_[carboxylating]_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=BNA6_PE=1_SV=1	2.00E-48	GO:0003824,GO:0004514,GO:0004514,GO:0004514,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0009435,GO:0009435,GO:0016740,GO:0016757,GO:0016763,GO:0019363,GO:0019363,GO:0034354,GO:0042802,GO:0042802,GO:0042802	catalytic activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nucleus,nucleus,cytoplasm,cytoplasm,NAD biosynthetic process,NAD biosynthetic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring pentosyl groups,pyridine nucleotide biosynthetic process,pyridine nucleotide biosynthetic process,'de novo' NAD biosynthetic process from tryptophan,identical protein binding,identical protein binding,identical protein binding
comp29653_c0_seq2.p5	sp|A7SG73|NADC_NEMVE_Nicotinate-nucleotide_pyrophosphorylase_[carboxylating]_(Fragment)_OS=Nematostella_vectensis_GN=qprt_PE=3_SV=1	2.00E-30	GO:0003824,GO:0004514,GO:0004514,GO:0009435,GO:0009435,GO:0016740,GO:0016757,GO:0016763,GO:0019363,GO:0019363	catalytic activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,NAD biosynthetic process,NAD biosynthetic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring pentosyl groups,pyridine nucleotide biosynthetic process,pyridine nucleotide biosynthetic process
comp29653_c0_seq4.p1	sp|Q5VIR6|VPS53_HUMAN_Vacuolar_protein_sorting-associated_protein_53_homolog_OS=Homo_sapiens_GN=VPS53_PE=1_SV=1	1.00E-92	GO:0000938,GO:0005515,GO:0005515,GO:0005768,GO:0005794,GO:0005794,GO:0005794,GO:0006810,GO:0010008,GO:0015031,GO:0016020,GO:0042147,GO:0048471	GARP complex,protein binding,protein binding,endosome,Golgi apparatus,Golgi apparatus,Golgi apparatus,transport,endosome membrane,protein transport,membrane,retrograde transport, endosome to Golgi,perinuclear region of cytoplasm
comp29653_c0_seq4.p2	sp|Q8CCB4|VPS53_MOUSE_Vacuolar_protein_sorting-associated_protein_53_homolog_OS=Mus_musculus_GN=Vps53_PE=2_SV=1	3.00E-25	GO:0000938,GO:0000938,GO:0005768,GO:0005794,GO:0005794,GO:0006810,GO:0010008,GO:0015031,GO:0016020,GO:0042147	GARP complex,GARP complex,endosome,Golgi apparatus,Golgi apparatus,transport,endosome membrane,protein transport,membrane,retrograde transport, endosome to Golgi
comp29653_c0_seq4.p3	sp|A7SG73|NADC_NEMVE_Nicotinate-nucleotide_pyrophosphorylase_[carboxylating]_(Fragment)_OS=Nematostella_vectensis_GN=qprt_PE=3_SV=1	1.00E-33	GO:0003824,GO:0004514,GO:0004514,GO:0009435,GO:0009435,GO:0016740,GO:0016757,GO:0016763,GO:0019363,GO:0019363	catalytic activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,NAD biosynthetic process,NAD biosynthetic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring pentosyl groups,pyridine nucleotide biosynthetic process,pyridine nucleotide biosynthetic process
comp29653_c0_seq5.p1	sp|Q5VIR6|VPS53_HUMAN_Vacuolar_protein_sorting-associated_protein_53_homolog_OS=Homo_sapiens_GN=VPS53_PE=1_SV=1	1.00E-92	GO:0000938,GO:0005515,GO:0005515,GO:0005768,GO:0005794,GO:0005794,GO:0005794,GO:0006810,GO:0010008,GO:0015031,GO:0016020,GO:0042147,GO:0048471	GARP complex,protein binding,protein binding,endosome,Golgi apparatus,Golgi apparatus,Golgi apparatus,transport,endosome membrane,protein transport,membrane,retrograde transport, endosome to Golgi,perinuclear region of cytoplasm
comp29653_c0_seq5.p3	sp|Q8CCB4|VPS53_MOUSE_Vacuolar_protein_sorting-associated_protein_53_homolog_OS=Mus_musculus_GN=Vps53_PE=2_SV=1	3.00E-25	GO:0000938,GO:0000938,GO:0005768,GO:0005794,GO:0005794,GO:0006810,GO:0010008,GO:0015031,GO:0016020,GO:0042147	GARP complex,GARP complex,endosome,Golgi apparatus,Golgi apparatus,transport,endosome membrane,protein transport,membrane,retrograde transport, endosome to Golgi
comp29653_c0_seq5.p4	sp|P43619|NADC_YEAST_Nicotinate-nucleotide_pyrophosphorylase_[carboxylating]_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=BNA6_PE=1_SV=1	2.00E-48	GO:0003824,GO:0004514,GO:0004514,GO:0004514,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0009435,GO:0009435,GO:0016740,GO:0016757,GO:0016763,GO:0019363,GO:0019363,GO:0034354,GO:0042802,GO:0042802,GO:0042802	catalytic activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nucleus,nucleus,cytoplasm,cytoplasm,NAD biosynthetic process,NAD biosynthetic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring pentosyl groups,pyridine nucleotide biosynthetic process,pyridine nucleotide biosynthetic process,'de novo' NAD biosynthetic process from tryptophan,identical protein binding,identical protein binding,identical protein binding
comp29653_c0_seq5.p6	sp|A7SG73|NADC_NEMVE_Nicotinate-nucleotide_pyrophosphorylase_[carboxylating]_(Fragment)_OS=Nematostella_vectensis_GN=qprt_PE=3_SV=1	2.00E-30	GO:0003824,GO:0004514,GO:0004514,GO:0009435,GO:0009435,GO:0016740,GO:0016757,GO:0016763,GO:0019363,GO:0019363	catalytic activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,NAD biosynthetic process,NAD biosynthetic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring pentosyl groups,pyridine nucleotide biosynthetic process,pyridine nucleotide biosynthetic process
comp29653_c0_seq7.p1	sp|Q8CCB4|VPS53_MOUSE_Vacuolar_protein_sorting-associated_protein_53_homolog_OS=Mus_musculus_GN=Vps53_PE=2_SV=1	1.00E-114	GO:0000938,GO:0000938,GO:0005768,GO:0005794,GO:0005794,GO:0006810,GO:0010008,GO:0015031,GO:0016020,GO:0042147	GARP complex,GARP complex,endosome,Golgi apparatus,Golgi apparatus,transport,endosome membrane,protein transport,membrane,retrograde transport, endosome to Golgi
comp29653_c0_seq7.p2	sp|A7SG73|NADC_NEMVE_Nicotinate-nucleotide_pyrophosphorylase_[carboxylating]_(Fragment)_OS=Nematostella_vectensis_GN=qprt_PE=3_SV=1	1.00E-33	GO:0003824,GO:0004514,GO:0004514,GO:0009435,GO:0009435,GO:0016740,GO:0016757,GO:0016763,GO:0019363,GO:0019363	catalytic activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,NAD biosynthetic process,NAD biosynthetic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring pentosyl groups,pyridine nucleotide biosynthetic process,pyridine nucleotide biosynthetic process
comp29653_c0_seq9.p1	sp|Q5VIR6|VPS53_HUMAN_Vacuolar_protein_sorting-associated_protein_53_homolog_OS=Homo_sapiens_GN=VPS53_PE=1_SV=1	1.00E-92	GO:0000938,GO:0005515,GO:0005515,GO:0005768,GO:0005794,GO:0005794,GO:0005794,GO:0006810,GO:0010008,GO:0015031,GO:0016020,GO:0042147,GO:0048471	GARP complex,protein binding,protein binding,endosome,Golgi apparatus,Golgi apparatus,Golgi apparatus,transport,endosome membrane,protein transport,membrane,retrograde transport, endosome to Golgi,perinuclear region of cytoplasm
comp29653_c0_seq9.p2	sp|P43619|NADC_YEAST_Nicotinate-nucleotide_pyrophosphorylase_[carboxylating]_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=BNA6_PE=1_SV=1	1.00E-92	GO:0003824,GO:0004514,GO:0004514,GO:0004514,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0009435,GO:0009435,GO:0016740,GO:0016757,GO:0016763,GO:0019363,GO:0019363,GO:0034354,GO:0042802,GO:0042802,GO:0042802	catalytic activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate-nucleotide diphosphorylase (carboxylating) activity,nucleus,nucleus,cytoplasm,cytoplasm,NAD biosynthetic process,NAD biosynthetic process,transferase activity,transferase activity, transferring glycosyl groups,transferase activity, transferring pentosyl groups,pyridine nucleotide biosynthetic process,pyridine nucleotide biosynthetic process,'de novo' NAD biosynthetic process from tryptophan,identical protein binding,identical protein binding,identical protein binding
comp29653_c0_seq9.p3	sp|Q8CCB4|VPS53_MOUSE_Vacuolar_protein_sorting-associated_protein_53_homolog_OS=Mus_musculus_GN=Vps53_PE=2_SV=1	3.00E-25	GO:0000938,GO:0000938,GO:0005768,GO:0005794,GO:0005794,GO:0006810,GO:0010008,GO:0015031,GO:0016020,GO:0042147	GARP complex,GARP complex,endosome,Golgi apparatus,Golgi apparatus,transport,endosome membrane,protein transport,membrane,retrograde transport, endosome to Golgi
comp29656_c0_seq1.p1				
comp29660_c0_seq1.p1				
comp29660_c0_seq2.p2				
comp29661_c0_seq1.p1				
comp29662_c0_seq1.p1	sp|Q558Z3|SSU72_DICDI_RNA_polymerase_II_subunit_A_C-terminal_domain_phosphatase_SSU72_OS=Dictyostelium_discoideum_GN=ssu72_PE=3_SV=1	3.00E-27	GO:0004721,GO:0004721,GO:0004721,GO:0005634,GO:0005634,GO:0005634,GO:0006397,GO:0006397,GO:0016311,GO:0016311,GO:0016311,GO:0016787	phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,nucleus,nucleus,nucleus,mRNA processing,mRNA processing,dephosphorylation,dephosphorylation,dephosphorylation,hydrolase activity
comp29662_c0_seq4.p1	sp|Q558Z3|SSU72_DICDI_RNA_polymerase_II_subunit_A_C-terminal_domain_phosphatase_SSU72_OS=Dictyostelium_discoideum_GN=ssu72_PE=3_SV=1	2.00E-41	GO:0004721,GO:0004721,GO:0004721,GO:0005634,GO:0005634,GO:0005634,GO:0006397,GO:0006397,GO:0016311,GO:0016311,GO:0016311,GO:0016787	phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,nucleus,nucleus,nucleus,mRNA processing,mRNA processing,dephosphorylation,dephosphorylation,dephosphorylation,hydrolase activity
comp29663_c0_seq3.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	8.00E-45	GO:0003674,GO:0005576,GO:0005576,GO:0008150,GO:0070062,GO:0072562	molecular_function,extracellular region,extracellular region,biological_process,extracellular vesicular exosome,blood microparticle
comp29663_c0_seq5.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	3.00E-40	GO:0003674,GO:0005576,GO:0005576,GO:0008150,GO:0070062,GO:0072562	molecular_function,extracellular region,extracellular region,biological_process,extracellular vesicular exosome,blood microparticle
comp29663_c0_seq7.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	4.00E-45	GO:0003674,GO:0005576,GO:0005576,GO:0008150,GO:0070062,GO:0072562	molecular_function,extracellular region,extracellular region,biological_process,extracellular vesicular exosome,blood microparticle
comp29663_c0_seq8.p1	sp|P22792|CPN2_HUMAN_Carboxypeptidase_N_subunit_2_OS=Homo_sapiens_GN=CPN2_PE=1_SV=3	1.00E-39	GO:0005576,GO:0005576,GO:0005576,GO:0030234,GO:0050790,GO:0050821,GO:0070062,GO:0070062,GO:0072562	extracellular region,extracellular region,extracellular region,enzyme regulator activity,regulation of catalytic activity,protein stabilization,extracellular vesicular exosome,extracellular vesicular exosome,blood microparticle
comp29664_c0_seq3.p1	sp|Q9CD72|PCRA_MYCLE_ATP-dependent_DNA_helicase_pcrA_OS=Mycobacterium_leprae_GN=pcrA_PE=3_SV=1	2.00E-97	GO:0000166,GO:0003677,GO:0003677,GO:0004003,GO:0004386,GO:0005524,GO:0005524,GO:0006281,GO:0006974,GO:0016787,GO:0016787,GO:0032508	nucleotide binding,DNA binding,DNA binding,ATP-dependent DNA helicase activity,helicase activity,ATP binding,ATP binding,DNA repair,cellular response to DNA damage stimulus,hydrolase activity,hydrolase activity,DNA duplex unwinding
comp29664_c0_seq3.p2				
comp29665_c0_seq1.p1	sp|B7K5H5|SYI_CYAP8_Isoleucine--tRNA_ligase_OS=Cyanothece_sp._(strain_PCC_8801)_GN=ileS_PE=3_SV=1	0	GO:0000166,GO:0000166,GO:0002161,GO:0003824,GO:0004812,GO:0004812,GO:0004822,GO:0004822,GO:0004822,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006418,GO:0006428,GO:0006428,GO:0006450,GO:0008270,GO:0016874,GO:0046872	nucleotide binding,nucleotide binding,aminoacyl-tRNA editing activity,catalytic activity,aminoacyl-tRNA ligase activity,aminoacyl-tRNA ligase activity,isoleucine-tRNA ligase activity,isoleucine-tRNA ligase activity,isoleucine-tRNA ligase activity,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,translation,tRNA aminoacylation for protein translation,isoleucyl-tRNA aminoacylation,isoleucyl-tRNA aminoacylation,regulation of translational fidelity,zinc ion binding,ligase activity,metal ion binding
comp29665_c0_seq1.p2	sp|Q92M71|SUHB_RHIME_Inositol-1-monophosphatase_OS=Rhizobium_meliloti_(strain_1021)_GN=suhB_PE=3_SV=1	1.00E-49	GO:0008934,GO:0008934,GO:0016787,GO:0046854,GO:0046855,GO:0046872,GO:0052832,GO:0052833,GO:0052834	inositol monophosphate 1-phosphatase activity,inositol monophosphate 1-phosphatase activity,hydrolase activity,phosphatidylinositol phosphorylation,inositol phosphate dephosphorylation,metal ion binding,inositol monophosphate 3-phosphatase activity,inositol monophosphate 4-phosphatase activity,inositol monophosphate phosphatase activity
comp29666_c0_seq3.p1	sp|P22983|PPDK_CLOSY_Pyruvate,_phosphate_dikinase_OS=Clostridium_symbiosum_GN=ppdK_PE=1_SV=5	0	GO:0000166,GO:0003824,GO:0005524,GO:0005524,GO:0006090,GO:0016301,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0046872,GO:0050242,GO:0050242	nucleotide binding,catalytic activity,ATP binding,ATP binding,pyruvate metabolic process,kinase activity,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,metal ion binding,pyruvate, phosphate dikinase activity,pyruvate, phosphate dikinase activity
comp29667_c0_seq1.p1				
comp29667_c0_seq2.p1	sp|Q2HJG5|VPS35_BOVIN_Vacuolar_protein_sorting-associated_protein_35_OS=Bos_taurus_GN=VPS35_PE=2_SV=1	1.00E-118	GO:0005737,GO:0005737,GO:0005765,GO:0005768,GO:0005768,GO:0005770,GO:0005829,GO:0006810,GO:0006886,GO:0008565,GO:0015031,GO:0015031,GO:0016020,GO:0016020,GO:0030904,GO:0030904,GO:0042147,GO:0042147,GO:0042147,GO:0045056,GO:0070062,GO:0097422,GO:1990126	cytoplasm,cytoplasm,lysosomal membrane,endosome,endosome,late endosome,cytosol,transport,intracellular protein transport,protein transporter activity,protein transport,protein transport,membrane,membrane,retromer complex,retromer complex,retrograde transport, endosome to Golgi,retrograde transport, endosome to Golgi,retrograde transport, endosome to Golgi,transcytosis,extracellular vesicular exosome,tubular endosome,retrograde transport, endosome to plasma membrane
comp29668_c0_seq2.p1	sp|Q54YG5|TPPC5_DICDI_Trafficking_protein_particle_complex_subunit_5_OS=Dictyostelium_discoideum_GN=trappc5_PE=3_SV=1	2.00E-48	GO:0005783,GO:0005783,GO:0005794,GO:0005794,GO:0006810,GO:0016192,GO:0044351	endoplasmic reticulum,endoplasmic reticulum,Golgi apparatus,Golgi apparatus,transport,vesicle-mediated transport,macropinocytosis
comp29670_c0_seq2.p1				
comp29670_c0_seq3.p2				
comp29670_c0_seq5.p1				
comp29672_c0_seq5.p1	sp|Q53RK8|RH21_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_21_OS=Oryza_sativa_subsp._japonica_GN=Os03g0708600_PE=2_SV=1	1.00E-170	GO:0000166,GO:0003676,GO:0003723,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006200,GO:0006397,GO:0008026,GO:0008380,GO:0016787	nucleotide binding,nucleic acid binding,RNA binding,helicase activity,ATP binding,ATP binding,nucleus,nucleus,cytoplasm,cytoplasm,ATP catabolic process,mRNA processing,ATP-dependent helicase activity,RNA splicing,hydrolase activity
comp29673_c0_seq1.p1				
comp29673_c0_seq3.p1				
comp29675_c0_seq1.p1				
comp29675_c0_seq4.p1				
comp29677_c0_seq1.p1	sp|P01104|MYB_AVIMB_Transforming_protein_Myb_OS=Avian_myeloblastosis_virus_GN=V-MYB_PE=1_SV=2	1.00E-14	GO:0003677,GO:0003677,GO:0003682,GO:0006355,GO:0042025,GO:0042025	DNA binding,DNA binding,chromatin binding,regulation of transcription, DNA-templated,host cell nucleus,host cell nucleus
comp29680_c0_seq2.p1	sp|Q2XVR6|SC4AB_TAKRU_Sodium_channel_protein_type_4_subunit_alpha_B_OS=Takifugu_rubripes_GN=scn4ab_PE=3_SV=1	4.00E-100	GO:0001518,GO:0005216,GO:0005244,GO:0005248,GO:0005272,GO:0006810,GO:0006811,GO:0006811,GO:0006814,GO:0006814,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0034220,GO:0034765,GO:0035725,GO:0035725,GO:0055085	voltage-gated sodium channel complex,ion channel activity,voltage-gated ion channel activity,voltage-gated sodium channel activity,sodium channel activity,transport,ion transport,ion transport,sodium ion transport,sodium ion transport,membrane,membrane,membrane,integral component of membrane,ion transmembrane transport,regulation of ion transmembrane transport,sodium ion transmembrane transport,sodium ion transmembrane transport,transmembrane transport
comp29682_c0_seq4.p1	sp|Q9M0Y8|NSF_ARATH_Vesicle-fusing_ATPase_OS=Arabidopsis_thaliana_GN=NSF_PE=2_SV=2	0	GO:0000166,GO:0005515,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005773,GO:0005794,GO:0005795,GO:0005886,GO:0006200,GO:0006810,GO:0006891,GO:0008152,GO:0009506,GO:0015031,GO:0016192,GO:0016787,GO:0016887,GO:0043001,GO:0046872,GO:0048211	nucleotide binding,protein binding,ATP binding,ATP binding,cytoplasm,cytoplasm,vacuole,Golgi apparatus,Golgi stack,plasma membrane,ATP catabolic process,transport,intra-Golgi vesicle-mediated transport,metabolic process,plasmodesma,protein transport,vesicle-mediated transport,hydrolase activity,ATPase activity,Golgi to plasma membrane protein transport,metal ion binding,Golgi vesicle docking
comp29682_c0_seq6.p1	sp|P54644|KRAC_DICDI_RAC_family_serine/threonine-protein_kinase_homolog_OS=Dictyostelium_discoideum_GN=pkbA_PE=1_SV=1	3.00E-114	GO:0000166,GO:0000281,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004674,GO:0004691,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005938,GO:0006468,GO:0006468,GO:0006468,GO:0006468,GO:0006935,GO:0006935,GO:0007163,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0019887,GO:0030010,GO:0031036,GO:0031154,GO:0043327,GO:0043327,GO:0044351,GO:0044351,GO:0045859,GO:0048015,GO:0050765,GO:0005829,GO:0005886	nucleotide binding,mitotic cytokinesis,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,cAMP-dependent protein kinase activity,protein binding,ATP binding,ATP binding,ATP binding,cell cortex,protein phosphorylation,protein phosphorylation,protein phosphorylation,protein phosphorylation,chemotaxis,chemotaxis,establishment or maintenance of cell polarity,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,protein kinase regulator activity,establishment of cell polarity,myosin II filament assembly,culmination involved in sorocarp development,chemotaxis to cAMP,chemotaxis to cAMP,macropinocytosis,macropinocytosis,regulation of protein kinase activity,phosphatidylinositol-mediated signaling,negative regulation of phagocytosis,cytosol,plasma membrane
comp29682_c0_seq7.p1	sp|Q9Z1M4|KS6B2_MOUSE_Ribosomal_protein_S6_kinase_beta-2_OS=Mus_musculus_GN=Rps6kb2_PE=1_SV=1	3.00E-27	GO:0000166,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0004711,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006468,GO:0006468,GO:0007165,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0042277,GO:0043491,GO:0045948	nucleotide binding,protein kinase activity,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ribosomal protein S6 kinase activity,ATP binding,ATP binding,nucleus,nucleus,cytoplasm,cytoplasm,protein phosphorylation,protein phosphorylation,signal transduction,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptide binding,protein kinase B signaling,positive regulation of translational initiation
comp29684_c0_seq1.p1	sp|Q7XJS0|ASHR1_ARATH_Histone-lysine_N-methyltransferase_ASHR1_OS=Arabidopsis_thaliana_GN=ASHR1_PE=2_SV=2	6.00E-18	GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0008168,GO:0016568,GO:0016740,GO:0018024,GO:0032259,GO:0034968,GO:0046872	nucleus,nucleus,chromosome,chromosome,methyltransferase activity,chromatin modification,transferase activity,histone-lysine N-methyltransferase activity,methylation,histone lysine methylation,metal ion binding
comp29684_c0_seq2.p1	sp|Q7XJS0|ASHR1_ARATH_Histone-lysine_N-methyltransferase_ASHR1_OS=Arabidopsis_thaliana_GN=ASHR1_PE=2_SV=2	2.00E-16	GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0008168,GO:0016568,GO:0016740,GO:0018024,GO:0032259,GO:0034968,GO:0046872	nucleus,nucleus,chromosome,chromosome,methyltransferase activity,chromatin modification,transferase activity,histone-lysine N-methyltransferase activity,methylation,histone lysine methylation,metal ion binding
comp29684_c0_seq3.p1	sp|Q7XJS0|ASHR1_ARATH_Histone-lysine_N-methyltransferase_ASHR1_OS=Arabidopsis_thaliana_GN=ASHR1_PE=2_SV=2	9.00E-18	GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0008168,GO:0016568,GO:0016740,GO:0018024,GO:0032259,GO:0034968,GO:0046872	nucleus,nucleus,chromosome,chromosome,methyltransferase activity,chromatin modification,transferase activity,histone-lysine N-methyltransferase activity,methylation,histone lysine methylation,metal ion binding
comp29684_c0_seq5.p1	sp|Q7XJS0|ASHR1_ARATH_Histone-lysine_N-methyltransferase_ASHR1_OS=Arabidopsis_thaliana_GN=ASHR1_PE=2_SV=2	1.00E-16	GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0008168,GO:0016568,GO:0016740,GO:0018024,GO:0032259,GO:0034968,GO:0046872	nucleus,nucleus,chromosome,chromosome,methyltransferase activity,chromatin modification,transferase activity,histone-lysine N-methyltransferase activity,methylation,histone lysine methylation,metal ion binding
comp29685_c0_seq2.p1				
comp29685_c0_seq3.p1				
comp29688_c0_seq3.p1	sp|Q8BW96|KCC1D_MOUSE_Calcium/calmodulin-dependent_protein_kinase_type_1D_OS=Mus_musculus_GN=Camk1d_PE=1_SV=2	1.00E-50	GO:0000166,GO:0003824,GO:0004672,GO:0004674,GO:0004674,GO:0004683,GO:0005516,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006468,GO:0006954,GO:0007399,GO:0008152,GO:0010976,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0032793,GO:0032793,GO:0043065,GO:0043066,GO:0050766,GO:0050766,GO:0050773,GO:0050773,GO:0060267,GO:0060267,GO:0071622,GO:0071622,GO:0090023	nucleotide binding,catalytic activity,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,calmodulin-dependent protein kinase activity,calmodulin binding,ATP binding,ATP binding,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,cytoplasm,protein phosphorylation,inflammatory response,nervous system development,metabolic process,positive regulation of neuron projection development,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,positive regulation of CREB transcription factor activity,positive regulation of CREB transcription factor activity,positive regulation of apoptotic process,negative regulation of apoptotic process,positive regulation of phagocytosis,positive regulation of phagocytosis,regulation of dendrite development,regulation of dendrite development,positive regulation of respiratory burst,positive regulation of respiratory burst,regulation of granulocyte chemotaxis,regulation of granulocyte chemotaxis,positive regulation of neutrophil chemotaxis
comp29688_c1_seq1.p1				
comp29690_c0_seq1.p1	sp|Q8N8A2|ANR44_HUMAN_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_B_OS=Homo_sapiens_GN=ANKRD44_PE=1_SV=3	1.00E-19	GO:0005515,GO:0005515,GO:0005515	protein binding,protein binding,protein binding
comp29690_c0_seq2.p1	sp|Q8N8A2|ANR44_HUMAN_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_B_OS=Homo_sapiens_GN=ANKRD44_PE=1_SV=3	6.00E-20	GO:0005515,GO:0005515,GO:0005515	protein binding,protein binding,protein binding
comp29690_c0_seq2.p2				
comp29691_c0_seq1.p1	sp|Q8ND76|CCNY_HUMAN_Cyclin-Y_OS=Homo_sapiens_GN=CCNY_PE=1_SV=2	1.00E-31	GO:0000079,GO:0000086,GO:0000308,GO:0000308,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0007049,GO:0016020,GO:0016055,GO:0016538,GO:0016538,GO:0019901,GO:0045737,GO:0045737,GO:0051301,GO:0060828,GO:0070062	regulation of cyclin-dependent protein serine/threonine kinase activity,G2/M transition of mitotic cell cycle,cytoplasmic cyclin-dependent protein kinase holoenzyme complex,cytoplasmic cyclin-dependent protein kinase holoenzyme complex,protein binding,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,plasma membrane,plasma membrane,plasma membrane,plasma membrane,cell cycle,membrane,Wnt signaling pathway,cyclin-dependent protein serine/threonine kinase regulator activity,cyclin-dependent protein serine/threonine kinase regulator activity,protein kinase binding,positive regulation of cyclin-dependent protein serine/threonine kinase activity,positive regulation of cyclin-dependent protein serine/threonine kinase activity,cell division,regulation of canonical Wnt signaling pathway,extracellular vesicular exosome
comp29692_c0_seq1.p1	sp|Q54G43|SHKE_DICDI_Dual_specificity_protein_kinase_shkE_OS=Dictyostelium_discoideum_GN=shkE_PE=3_SV=1	6.00E-25	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004713,GO:0005524,GO:0005524,GO:0005575,GO:0006468,GO:0016020,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0018108,GO:0051219	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein tyrosine kinase activity,ATP binding,ATP binding,cellular_component,protein phosphorylation,membrane,membrane,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-tyrosine phosphorylation,phosphoprotein binding
comp29694_c0_seq1.p1	sp|O60100|IMB4_SCHPO_Probable_importin_subunit_beta-4_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=kap123_PE=2_SV=1	1.00E-97	GO:0005634,GO:0005634,GO:0005634,GO:0005635,GO:0005635,GO:0005643,GO:0005737,GO:0005737,GO:0005829,GO:0006605,GO:0006810,GO:0006886,GO:0006913,GO:0008536,GO:0015031,GO:0031965	nucleus,nucleus,nucleus,nuclear envelope,nuclear envelope,nuclear pore,cytoplasm,cytoplasm,cytosol,protein targeting,transport,intracellular protein transport,nucleocytoplasmic transport,Ran GTPase binding,protein transport,nuclear membrane
comp29694_c0_seq2.p1	sp|Q8VI75|IPO4_MOUSE_Importin-4_OS=Mus_musculus_GN=Ipo4_PE=1_SV=1	2.00E-32	GO:0000790,GO:0005515,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006335,GO:0006336,GO:0006610,GO:0006810,GO:0006886,GO:0008536,GO:0015031,GO:0016020,GO:0042254,GO:0043234	nuclear chromatin,protein binding,nucleus,nucleus,cytoplasm,cytoplasm,DNA replication-dependent nucleosome assembly,DNA replication-independent nucleosome assembly,ribosomal protein import into nucleus,transport,intracellular protein transport,Ran GTPase binding,protein transport,membrane,ribosome biogenesis,protein complex
comp29694_c0_seq3.p1	sp|Q8VI75|IPO4_MOUSE_Importin-4_OS=Mus_musculus_GN=Ipo4_PE=1_SV=1	1.00E-48	GO:0000790,GO:0005515,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006335,GO:0006336,GO:0006610,GO:0006810,GO:0006886,GO:0008536,GO:0015031,GO:0016020,GO:0042254,GO:0043234	nuclear chromatin,protein binding,nucleus,nucleus,cytoplasm,cytoplasm,DNA replication-dependent nucleosome assembly,DNA replication-independent nucleosome assembly,ribosomal protein import into nucleus,transport,intracellular protein transport,Ran GTPase binding,protein transport,membrane,ribosome biogenesis,protein complex
comp29696_c0_seq1.p2				
comp29696_c0_seq3.p1				
comp29696_c0_seq4.p1				
comp29696_c0_seq6.p1				
comp29696_c0_seq8.p1				
comp29697_c0_seq2.p1				
comp29697_c0_seq2.p2				
comp29698_c0_seq1.p1				
comp29699_c0_seq2.p1				
comp29699_c0_seq3.p1				
comp29699_c0_seq4.p1				
comp29700_c0_seq3.p1	sp|B2HCU5|Y1059_MYCMM_Putative_S-adenosyl-L-methionine-dependent_methyltransferase_MMAR_1059_OS=Mycobacterium_marinum_(strain_ATCC_BAA-535_/_M)_GN=MMAR_1059_PE=3_SV=1	7.00E-29	GO:0008168,GO:0008168,GO:0016740,GO:0032259,GO:0032259	methyltransferase activity,methyltransferase activity,transferase activity,methylation,methylation
comp29702_c0_seq2.p1				
comp29702_c0_seq3.p1				
comp29702_c0_seq3.p2				
comp29702_c0_seq3.p7				
comp29702_c0_seq4.p3				
comp29702_c0_seq6.p2				
comp29703_c0_seq1.p1	sp|Q9Y253|POLH_HUMAN_DNA_polymerase_eta_OS=Homo_sapiens_GN=POLH_PE=1_SV=1	4.00E-55	GO:0000731,GO:0003677,GO:0003684,GO:0003684,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005654,GO:0005654,GO:0005654,GO:0005654,GO:0005654,GO:0005737,GO:0006260,GO:0006281,GO:0006281,GO:0006281,GO:0006281,GO:0006282,GO:0006290,GO:0006301,GO:0006974,GO:0010225,GO:0016740,GO:0016779,GO:0046872,GO:0071897	DNA synthesis involved in DNA repair,DNA binding,damaged DNA binding,damaged DNA binding,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,protein binding,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleoplasm,nucleoplasm,nucleoplasm,nucleoplasm,nucleoplasm,cytoplasm,DNA replication,DNA repair,DNA repair,DNA repair,DNA repair,regulation of DNA repair,pyrimidine dimer repair,postreplication repair,cellular response to DNA damage stimulus,response to UV-C,transferase activity,nucleotidyltransferase activity,metal ion binding,DNA biosynthetic process
comp29703_c0_seq2.p1	sp|O42917|ESO1_SCHPO_N-acetyltransferase_eso1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=eso1_PE=1_SV=1	1.00E-18	GO:0000790,GO:0003684,GO:0003887,GO:0003887,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0006281,GO:0006281,GO:0007049,GO:0016740,GO:0016746,GO:0018003,GO:0019985,GO:0019985,GO:0034087,GO:0034182,GO:0035861,GO:0043596,GO:0046872,GO:0052858,GO:2000720	nuclear chromatin,damaged DNA binding,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,protein binding,nucleus,nucleus,nucleus,DNA repair,DNA repair,cell cycle,transferase activity,transferase activity, transferring acyl groups,peptidyl-lysine N6-acetylation,translesion synthesis,translesion synthesis,establishment of mitotic sister chromatid cohesion,regulation of maintenance of mitotic sister chromatid cohesion,site of double-strand break,nuclear replication fork,metal ion binding,peptidyl-lysine N-acetyltransferase activity, acting on acetyl phosphate as donor,positive regulation of maintenance of mitotic sister chromatid cohesion, centromeric
comp29703_c1_seq3.p1	sp|Q54EW1|GLYC2_DICDI_Serine_hydroxymethyltransferase_2_OS=Dictyostelium_discoideum_GN=shmt2_PE=3_SV=1	0	GO:0003824,GO:0004372,GO:0004372,GO:0004372,GO:0005759,GO:0006544,GO:0006563,GO:0006730,GO:0006730,GO:0016740,GO:0030170,GO:0035999,GO:0044351	catalytic activity,glycine hydroxymethyltransferase activity,glycine hydroxymethyltransferase activity,glycine hydroxymethyltransferase activity,mitochondrial matrix,glycine metabolic process,L-serine metabolic process,one-carbon metabolic process,one-carbon metabolic process,transferase activity,pyridoxal phosphate binding,tetrahydrofolate interconversion,macropinocytosis
comp29704_c1_seq2.p1	sp|P52032|GPX1_ARATH_Phospholipid_hydroperoxide_glutathione_peroxidase_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=GPX1_PE=1_SV=2	2.00E-13	GO:0004601,GO:0004602,GO:0006979,GO:0009407,GO:0009507,GO:0009507,GO:0009507,GO:0009507,GO:0009507,GO:0009535,GO:0009536,GO:0009570,GO:0009570,GO:0009941,GO:0009941,GO:0016491,GO:0047066,GO:0055114,GO:0055114	peroxidase activity,glutathione peroxidase activity,response to oxidative stress,toxin catabolic process,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast,chloroplast thylakoid membrane,plastid,chloroplast stroma,chloroplast stroma,chloroplast envelope,chloroplast envelope,oxidoreductase activity,phospholipid-hydroperoxide glutathione peroxidase activity,oxidation-reduction process,oxidation-reduction process
comp29704_c1_seq3.p1	sp|Q02073|CH10C_SPIOL_20_kDa_chaperonin,_chloroplastic_OS=Spinacia_oleracea_GN=CPN21_PE=2_SV=1	3.00E-11	GO:0005524,GO:0005737,GO:0006457,GO:0009507,GO:0009507,GO:0009536	ATP binding,cytoplasm,protein folding,chloroplast,chloroplast,plastid
comp29705_c0_seq1.p1				
comp29705_c1_seq2.p1				
comp29705_c2_seq1.p1	sp|Q54BM5|BBP_DICDI_Branchpoint-bridging_protein_OS=Dictyostelium_discoideum_GN=sf1_PE=3_SV=1	8.00E-16	GO:0000243,GO:0000398,GO:0003676,GO:0003723,GO:0003723,GO:0003723,GO:0005634,GO:0005634,GO:0006397,GO:0008270,GO:0008380,GO:0046872	commitment complex,mRNA splicing, via spliceosome,nucleic acid binding,RNA binding,RNA binding,RNA binding,nucleus,nucleus,mRNA processing,zinc ion binding,RNA splicing,metal ion binding
comp29706_c0_seq2.p1	sp|P08440|ALF_MAIZE_Fructose-bisphosphate_aldolase,_cytoplasmic_isozyme_OS=Zea_mays_PE=2_SV=1	4.00E-99	GO:0003824,GO:0004332,GO:0004332,GO:0005737,GO:0005737,GO:0006096,GO:0006096,GO:0006096,GO:0016829	catalytic activity,fructose-bisphosphate aldolase activity,fructose-bisphosphate aldolase activity,cytoplasm,cytoplasm,glycolytic process,glycolytic process,glycolytic process,lyase activity
comp29706_c1_seq1.p1	sp|Q8BGA9|OXA1L_MOUSE_Mitochondrial_inner_membrane_protein_OXA1L_OS=Mus_musculus_GN=Oxa1l_PE=2_SV=1	2.00E-31	GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0016020,GO:0016021,GO:0016021,GO:0031966,GO:0042803,GO:0051205,GO:0051262,GO:0097031,GO:0097177	mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,membrane,integral component of membrane,integral component of membrane,mitochondrial membrane,protein homodimerization activity,protein insertion into membrane,protein tetramerization,mitochondrial respiratory chain complex I biogenesis,mitochondrial ribosome binding
comp29707_c0_seq1.p1				
comp29708_c0_seq2.p1				
comp29708_c0_seq3.p1				
comp29708_c0_seq4.p2				
comp29708_c0_seq6.p1				

comp29709_c0_seq1.p1	sp|Q8K2I9|FBX18_MOUSE_F-box_only_protein_18_OS=Mus_musculus_GN=Fbxo18_PE=2_SV=1	5.00E-49	[illegible]	[illegible]
comp29710_c0_seq1.p1	sp|Q54UC0|PRKDC_DICDI_DNA-dependent_protein_kinase_catalytic_subunit_OS=Dictyostelium_discoideum_GN=dnapkcs_PE=3_SV=2	7.00E-109	[illegible]	[illegible]
comp29710_c0_seq2.p1	sp|Q54UC0|PRKDC_DICDI_DNA-dependent_protein_kinase_catalytic_subunit_OS=Dictyostelium_discoideum_GN=dnapkcs_PE=3_SV=2	2.00E-70	[illegible]	[illegible]
comp29711_c0_seq1.p1	sp|Q6AYI2|KLDC3_RAT_Kelch_domain-containing_protein_3_OS=Rattus_norvegicus_GN=Klhdc3_PE=2_SV=1	1.00E-15	[illegible]	[illegible]
comp29711_c0_seq3.p1				
comp29711_c0_seq5.p1	sp|P87061|TEA1_SCHPO_Tip_elongation_aberrant_protein_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=tea1_PE=1_SV=1	3.00E-14	[illegible]	[illegible]
comp29712_c0_seq2.p1	sp|Q63ZG9|GGNB2_XENLA_Gametogenetin-binding_protein_2_OS=Xenopus_laevis_GN=ggnbp2_PE=2_SV=1	2.00E-12	[illegible]	[illegible]
comp29712_c0_seq2.p2	sp|Q0JL73|RH26_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_26_OS=Oryza_sativa_subsp._japonica_GN=Os01g0618500_PE=2_SV=1	1.00E-84	[illegible]	[illegible]
comp29712_c0_seq3.p1	sp|Q0JL73|RH26_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_26_OS=Oryza_sativa_subsp._japonica_GN=Os01g0618500_PE=2_SV=1	9.00E-76	[illegible]	[illegible]
comp29713_c0_seq2.p1	sp|Q76P23|PM34_DICDI_Mitochondrial_substrate_carrier_family_protein_Q_OS=Dictyostelium_discoideum_GN=mcfQ_PE=2_SV=1	5.00E-25	[illegible]	[illegible]
comp29713_c0_seq5.p1				
comp29713_c0_seq5.p2	sp|P29610|CY12_SOLTU_Cytochrome_c1-2,_heme_protein,_mitochondrial_(Fragment)_OS=Solanum_tuberosum_GN=CYCL_PE=1_SV=1	5.00E-92	[illegible]	[illegible]
comp29714_c0_seq3.p1				
comp29715_c0_seq1.p1				
comp29715_c0_seq3.p1	sp|P42696|RBM34_HUMAN_RNA-binding_protein_34_OS=Homo_sapiens_GN=RBM34_PE=1_SV=2	1.00E-26	[illegible]	[illegible]
comp29716_c0_seq1.p1	sp|P53569|CEBPZ_MOUSE_CCAAT/enhancer-binding_protein_zeta_OS=Mus_musculus_GN=Cebpz_PE=2_SV=2	2.00E-82	[illegible]	[illegible]
comp29716_c1_seq1.p1				
comp29717_c0_seq1.p1				
comp29719_c0_seq3.p1	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	4.00E-15	[illegible]	[illegible]
comp29720_c0_seq1.p1				
comp29721_c0_seq1.p1	sp|Q54CN8|TAF13_DICDI_Transcription_initiation_factor_TFIID_subunit_13_OS=Dictyostelium_discoideum_GN=taf13_PE=3_SV=1	1.00E-13	[illegible]	[illegible]
comp29722_c0_seq3.p1				
comp29723_c0_seq4.p1	sp|Q8W496|PTC52_ARATH_Protochlorophyllide-dependent_translocon_component_52,_chloroplastic_OS=Arabidopsis_thaliana_GN=PTC52_PE=2_SV=1	5.00E-70	[illegible]	[illegible]
comp29723_c0_seq5.p1	sp|Q8W496|PTC52_ARATH_Protochlorophyllide-dependent_translocon_component_52,_chloroplastic_OS=Arabidopsis_thaliana_GN=PTC52_PE=2_SV=1	2.00E-69	[illegible]	[illegible]
comp29724_c0_seq1.p1				
comp29727_c0_seq1.p1				
comp29729_c0_seq1.p1				
comp29729_c0_seq10.p1	sp|Q32LQ6|MFSD1_DANRE_Major_facilitator_superfamily_domain-containing_protein_1_OS=Danio_rerio_GN=mfsd1_PE=2_SV=1	3.00E-12	[illegible]	[illegible]
comp29729_c0_seq11.p1	sp|Q1JQC1|MFSD1_BOVIN_Major_facilitator_superfamily_domain-containing_protein_1_OS=Bos_taurus_GN=MFSD1_PE=2_SV=1	2.00E-26	[illegible]	[illegible]
comp29729_c0_seq12.p2				
comp29729_c0_seq2.p1	sp|Q1JQC1|MFSD1_BOVIN_Major_facilitator_superfamily_domain-containing_protein_1_OS=Bos_taurus_GN=MFSD1_PE=2_SV=1	7.00E-23	[illegible]	[illegible]
comp29729_c0_seq2.p2				
comp29729_c0_seq3.p3				
comp29729_c0_seq9.p1				
comp29731_c0_seq1.p1				
comp29732_c0_seq2.p1				
comp29732_c0_seq3.p1				
comp29734_c0_seq1.p1				
comp29734_c0_seq2.p1				
comp29735_c0_seq4.p1	sp|B2RYM5|BRCC3_RAT_Lys-63-specific_deubiquitinase_BRCC36_OS=Rattus_norvegicus_GN=Brcc3_PE=2_SV=1	1.00E-41	[illegible]	[illegible]
comp29735_c0_seq5.p1	sp|B2RYM5|BRCC3_RAT_Lys-63-specific_deubiquitinase_BRCC36_OS=Rattus_norvegicus_GN=Brcc3_PE=2_SV=1	1.00E-42	[illegible]	[illegible]
comp29737_c0_seq1.p1	sp|P23800|RCC1_MESAU_Regulator_of_chromosome_condensation_OS=Mesocricetus_auratus_GN=RCC1_PE=1_SV=1	1.00E-42	[illegible]	[illegible]
comp29737_c0_seq1.p5				
comp29738_c0_seq1.p1				
comp29739_c0_seq1.p1	sp|A4I7K1|SEY1_LEIIN_Protein_SEY1_homolog_OS=Leishmania_infantum_GN=LinJ32.0740_PE=3_SV=2	2.00E-22	[illegible]	[illegible]
comp29739_c0_seq3.p1				
comp29740_c0_seq1.p1	sp|P75791|YBIU_ECOLI_Uncharacterized_protein_ybiU_OS=Escherichia_coli_(strain_K12)_GN=ybiU_PE=1_SV=1	3.00E-24		
comp29740_c0_seq1.p4				
comp29741_c0_seq2.p1	sp|O15819|H33A_DICDI_Histone_H3.3_type_a_OS=Dictyostelium_discoideum_GN=H3a_PE=1_SV=1	4.00E-43	[illegible]	[illegible]
comp29741_c0_seq3.p1	sp|P08437|H3_VOLCA_Histone_H3_OS=Volvox_carteri_GN=H3-I_PE=3_SV=2	4.00E-61	[illegible]	[illegible]
comp29742_c0_seq1.p1	sp|Q9ZR37|DUS1_ARATH_Dual_specificity_protein_phosphatase_1_OS=Arabidopsis_thaliana_GN=DSPTP1_PE=1_SV=1	9.00E-22	[illegible]	[illegible]
comp29742_c0_seq2.p1	sp|Q9ZR37|DUS1_ARATH_Dual_specificity_protein_phosphatase_1_OS=Arabidopsis_thaliana_GN=DSPTP1_PE=1_SV=1	3.00E-20	[illegible]	[illegible]
comp29742_c0_seq2.p2				
comp29744_c0_seq6.p1	sp|Q84K71|MATE2_ARATH_MATE_efflux_family_protein_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=DTX44_PE=2_SV=1	1.00E-28	[illegible]	[illegible]
comp29745_c0_seq2.p1				
comp29745_c0_seq4.p1				
comp29745_c0_seq4.p4				
comp29745_c0_seq6.p1				
comp29745_c0_seq7.p2				
comp29745_c0_seq8.p1				
comp29746_c0_seq3.p1				
comp29746_c0_seq4.p1				
comp29746_c0_seq6.p1				
comp29747_c0_seq1.p1	sp|O64624|PP163_ARATH_Pentatricopeptide_repeat-containing_protein_At2g18940_OS=Arabidopsis_thaliana_GN=At2g18940_PE=2_SV=1	2.00E-44	[illegible]	[illegible]
comp29748_c0_seq1.p1	sp|P60027|TF2H4_PANTR_General_transcription_factor_IIH_subunit_4_OS=Pan_troglodytes_GN=GTF2H4_PE=3_SV=1	2.00E-61	[illegible]	[illegible]
comp29748_c0_seq1.p2				
comp29748_c0_seq4.p1				
comp29748_c0_seq4.p3				
comp29748_c0_seq5.p1	sp|P60027|TF2H4_PANTR_General_transcription_factor_IIH_subunit_4_OS=Pan_troglodytes_GN=GTF2H4_PE=3_SV=1	4.00E-61	[illegible]	[illegible]
comp29748_c0_seq5.p2				
comp29748_c0_seq6.p1				
comp29748_c0_seq6.p3				
comp29749_c0_seq1.p1				
comp29751_c0_seq2.p1	sp|Q4WJM7|HUT1_ASPFU_UDP-galactose_transporter_homolog_1_OS=Neosartorya_fumigata_(strain_ATCC_MYA-4609_/_Af293_/_CBS_101355_/_FGSC_A1100)_GN=hut1_PE=3_SV=1	8.00E-47	[illegible]	[illegible]
comp29752_c0_seq1.p1				
comp29752_c0_seq1.p2				
comp29752_c0_seq3.p1				
comp29755_c0_seq2.p1	sp|Q9LV03|GLUT1_ARATH_Glutamate_synthase_1_[NADH],_chloroplastic_OS=Arabidopsis_thaliana_GN=GLT1_PE=1_SV=2	0	[illegible]	[illegible]
comp29755_c0_seq3.p1	sp|Q0JKD0|GLT1_ORYSJ_Glutamate_synthase_1_[NADH],_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=Os01g0681900_PE=2_SV=1	0	[illegible]	[illegible]
comp29755_c0_seq3.p2				
comp29756_c0_seq1.p1				
comp29757_c0_seq2.p1				
comp29758_c0_seq1.p2				
comp29758_c0_seq3.p1				
comp29760_c0_seq1.p1	sp|Q42711|MDARS_CUCSA_Monodehydroascorbate_reductase,_seedling_isozyme_OS=Cucumis_sativus_PE=2_SV=1	2.00E-30	[illegible]	[illegible]
comp29760_c0_seq1.p4				
comp29761_c0_seq1.p1	sp|Q6H941|ALKB2_PSEAE_Alkane_1-monooxygenase_2_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=alkB2_PE=1_SV=1	1.00E-69	[illegible]	[illegible]
comp29761_c0_seq2.p1	sp|Q0VTH3|ALKB2_ALCBS_Alkane_1-monooxygenase_2_OS=Alcanivorax_borkumensis_(strain_SK2_/_ATCC_700651_/_DSM_11573)_GN=alkB2_PE=2_SV=1	2.00E-32	[illegible]	[illegible]
comp29761_c0_seq4.p1	sp|Q6H941|ALKB2_PSEAE_Alkane_1-monooxygenase_2_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=alkB2_PE=1_SV=1	1.00E-69	[illegible]	[illegible]
comp29761_c0_seq8.p1	sp|Q0VKZ3|ALKB1_ALCBS_Alkane_1-monooxygenase_1_OS=Alcanivorax_borkumensis_(strain_SK2_/_ATCC_700651_/_DSM_11573)_GN=alkB1_PE=1_SV=1	3.00E-18	[illegible]	[illegible]
comp29762_c0_seq2.p1				
comp29762_c0_seq2.p2	sp|O46431|FIBP_CHLAE_Acidic_fibroblast_growth_factor_intracellular-binding_protein_OS=Chlorocebus_aethiops_GN=FIBP_PE=2_SV=2	6.00E-21	[illegible]	[illegible]
comp29763_c0_seq1.p1				
comp29763_c0_seq2.p1				
comp29763_c0_seq3.p1				
comp29763_c0_seq3.p2				
comp29763_c0_seq4.p1				
comp29763_c0_seq4.p2				
comp29766_c0_seq1.p1				
comp29768_c0_seq1.p1	sp|Q5R581|KLC1_PONAB_Kinesin_light_chain_1_OS=Pongo_abelii_GN=KLC1_PE=2_SV=3	3.00E-28	[illegible]	[illegible]
comp29768_c0_seq3.p1	sp|Q5R581|KLC1_PONAB_Kinesin_light_chain_1_OS=Pongo_abelii_GN=KLC1_PE=2_SV=3	6.00E-21	[illegible]	[illegible]
comp29770_c0_seq1.p1	sp|Q5EE05|ABHD5_PIG_1-acylglycerol-3-phosphate_O-acyltransferase_ABHD5_OS=Sus_scrofa_GN=ABHD5_PE=2_SV=1	2.00E-35	[illegible]	[illegible]
comp29770_c0_seq2.p1	sp|Q5EE05|ABHD5_PIG_1-acylglycerol-3-phosphate_O-acyltransferase_ABHD5_OS=Sus_scrofa_GN=ABHD5_PE=2_SV=1	4.00E-37	[illegible]	[illegible]
comp29771_c0_seq2.p1	sp|P29474|NOS3_HUMAN_Nitric_oxide_synthase,_endothelial_OS=Homo_sapiens_GN=NOS3_PE=1_SV=3	5.00E-135	[illegible]	[illegible]
comp29771_c0_seq2.p2	sp|P37039|NCPR_CAVPO_NADPH--cytochrome_P450_reductase_OS=Cavia_porcellus_GN=POR_PE=2_SV=2	7.00E-20	[illegible]	[illegible]
comp29773_c0_seq1.p1	sp|Q6TMK4|POXA_DICDI_Peroxinectin_A_OS=Dictyostelium_discoideum_GN=poxA_PE=2_SV=1	9.00E-12	[illegible]	[illegible]
comp29773_c0_seq3.p1	sp|B5DG51|MCMBP_SALSA_Mini-chromosome_maintenance_complex-binding_protein_OS=Salmo_salar_GN=mcmbp_PE=2_SV=1	2.00E-65	[illegible]	[illegible]
comp29774_c0_seq11.p1				
comp29774_c0_seq7.p1	sp|B9EMY6|FEN1_SALSA_Flap_endonuclease_1_OS=Salmo_salar_GN=fen1_PE=2_SV=1	1.00E-90	[illegible]	[illegible]
comp29774_c0_seq7.p2	sp|Q43468|STIP_SOYBN_Heat_shock_protein_STI_OS=Glycine_max_GN=STI_PE=2_SV=1	5.00E-12	[illegible]	[illegible]
comp29774_c0_seq8.p1	sp|B9EMY6|FEN1_SALSA_Flap_endonuclease_1_OS=Salmo_salar_GN=fen1_PE=2_SV=1	1.00E-90	[illegible]	[illegible]
comp29774_c0_seq8.p2	sp|Q43468|STIP_SOYBN_Heat_shock_protein_STI_OS=Glycine_max_GN=STI_PE=2_SV=1	5.00E-12	[illegible]	[illegible]
comp29774_c0_seq9.p1	sp|B9EMY6|FEN1_SALSA_Flap_endonuclease_1_OS=Salmo_salar_GN=fen1_PE=2_SV=1	1.00E-90	[illegible]	[illegible]
comp29774_c0_seq9.p2	sp|Q43468|STIP_SOYBN_Heat_shock_protein_STI_OS=Glycine_max_GN=STI_PE=2_SV=1	1.00E-11	[illegible]	[illegible]
comp29775_c0_seq2.p1	sp|A0L4B2|HFLX_MAGSM_GTPase_HflX_OS=Magnetococcus_sp._(strain_MC-1)_GN=hflX_PE=3_SV=1	3.00E-56	[illegible]	[illegible]
comp29775_c0_seq2.p2	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	9.00E-23	[illegible]	[illegible]
comp29775_c0_seq4.p1	sp|A0L4B2|HFLX_MAGSM_GTPase_HflX_OS=Magnetococcus_sp._(strain_MC-1)_GN=hflX_PE=3_SV=1	3.00E-56	[illegible]	[illegible]
comp29775_c0_seq4.p2	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	9.00E-23	[illegible]	[illegible]
comp29776_c0_seq1.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-16	[illegible]	[illegible]
comp29776_c0_seq2.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-23	[illegible]	[illegible]
comp29777_c0_seq2.p1				
comp29778_c0_seq3.p1				
comp29778_c0_seq6.p1				
comp29779_c0_seq1.p1				
comp29779_c0_seq1.p2				
comp29781_c0_seq1.p1	sp|Q14676|MDC1_HUMAN_Mediator_of_DNA_damage_checkpoint_protein_1_OS=Homo_sapiens_GN=MDC1_PE=1_SV=3	4.00E-15	[illegible]	[illegible]
comp29781_c0_seq2.p1				
comp29783_c0_seq2.p1	sp|P23231|TOM70_NEUCR_Mitochondrial_import_receptor_subunit_tom-70_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=tom-70_PE=2_SV=2	3.00E-31	[illegible]	[illegible]
comp29783_c0_seq2.p4				
comp29783_c0_seq5.p1	sp|P44659|Y358_HAEIN_Uncharacterized_protein_HI_0358_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=HI_0358_PE=3_SV=1	3.00E-16	[illegible]	[illegible]
comp29784_c0_seq4.p1	sp|Q6DBP3|PT505_ARATH_Probable_sugar_phosphate/phosphate_translocator_At5g05820_OS=Arabidopsis_thaliana_GN=At5g05820_PE=2_SV=1	1.00E-25	[illegible]	[illegible]
comp29785_c0_seq3.p1	sp|A7HPT7|ARGB_PARL1_Acetylglutamate_kinase_OS=Parvibaculum_lavamentivorans_(strain_DS-1_/_DSM_13023_/_NCIMB_13966)_GN=argB_PE=3_SV=1	7.00E-92	[illegible]	[illegible]
comp29785_c0_seq3.p3				
comp29786_c0_seq2.p1				
comp29786_c0_seq3.p1				
comp29786_c0_seq5.p1				
comp29786_c0_seq5.p3	sp|Q54TC5|MAFL2_DICDI_Maf-like_protein_DDB_G0281937_OS=Dictyostelium_discoideum_GN=DDB_G0281937_PE=3_SV=1	1.00E-34	[illegible]	[illegible]
comp29787_c0_seq1.p2				
comp29787_c0_seq2.p1				
comp29787_c0_seq3.p1				
comp29787_c0_seq6.p1	sp|Q9BWU0|NADAP_HUMAN_Kanadaptin_OS=Homo_sapiens_GN=SLC4A1AP_PE=1_SV=1	1.00E-24	[illegible]	[illegible]
comp29787_c0_seq6.p2				
comp29789_c0_seq1.p1				
comp29789_c0_seq1.p2				
comp29789_c0_seq2.p1				
comp29791_c0_seq2.p1	sp|Q9MBF8|DYH1B_CHLRE_Dynein-1-beta_heavy_chain,_flagellar_inner_arm_I1_complex_OS=Chlamydomonas_reinhardtii_GN=DHC10_PE=1_SV=1	2.00E-170	[illegible]	[illegible]
comp29791_c1_seq1.p1	sp|Q8IVF4|DYH10_HUMAN_Dynein_heavy_chain_10,_axonemal_OS=Homo_sapiens_GN=DNAH10_PE=1_SV=4	0	[illegible]	[illegible]
comp29791_c1_seq2.p1	sp|Q9MBF8|DYH1B_CHLRE_Dynein-1-beta_heavy_chain,_flagellar_inner_arm_I1_complex_OS=Chlamydomonas_reinhardtii_GN=DHC10_PE=1_SV=1	0	[illegible]	[illegible]
comp29792_c0_seq1.p2	sp|B2RXR6|ANR44_MOUSE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_B_OS=Mus_musculus_GN=Ankrd44_PE=2_SV=1	9.00E-29	[illegible]	[illegible]
comp29792_c0_seq2.p1	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	2.00E-46	[illegible]	[illegible]
comp29793_c0_seq2.p1				
comp29795_c0_seq2.p1				
comp29796_c0_seq1.p2	sp|P23484|FECI_ECOLI_Probable_RNA_polymerase_sigma_factor_fecI_OS=Escherichia_coli_(strain_K12)_GN=fecI_PE=1_SV=3	5.00E-65	[illegible]	[illegible]
comp29796_c1_seq3.p1	sp|P62594|BLAT_SALTI_Beta-lactamase_TEM_OS=Salmonella_typhi_GN=bla_PE=3_SV=1	0	[illegible]	[illegible]
comp29796_c1_seq3.p2	sp|P02981|TCR3_ECOLX_Tetracycline_resistance_protein,_class_C_OS=Escherichia_coli_GN=tetA_PE=1_SV=1	2.00E-59	[illegible]	[illegible]
comp29796_c1_seq4.p1	sp|P00582|DPO1_ECOLI_DNA_polymerase_I_OS=Escherichia_coli_(strain_K12)_GN=polA_PE=1_SV=1	0	[illegible]	[illegible]
comp29796_c1_seq4.p2	sp|P03023|LACI_ECOLI_Lactose_operon_repressor_OS=Escherichia_coli_(strain_K12)_GN=lacI_PE=1_SV=3	0	[illegible]	[illegible]
comp29796_c1_seq4.p4	sp|P02981|TCR3_ECOLX_Tetracycline_resistance_protein,_class_C_OS=Escherichia_coli_GN=tetA_PE=1_SV=1	2.00E-59	[illegible]	[illegible]
comp29797_c0_seq1.p1	sp|Q6DDZ9|K1609_XENLA_TLD_domain-containing_protein_KIAA1609_homolog_OS=Xenopus_laevis_PE=2_SV=1	3.00E-15		
comp29797_c0_seq4.p2				
comp29798_c0_seq1.p1	sp|P55034|PSMD4_ARATH_26S_proteasome_non-ATPase_regulatory_subunit_4_OS=Arabidopsis_thaliana_GN=MBP1_PE=1_SV=1	2.00E-80	[illegible]	[illegible]
comp29798_c0_seq1.p2	sp|Q5QQ53|XYLT_DROPS_Xylosyltransferase_oxt_OS=Drosophila_pseudoobscura_pseudoobscura_GN=oxt_PE=2_SV=1	1.00E-12	[illegible]	[illegible]
comp29798_c0_seq1.p3				
comp29799_c0_seq3.p1	sp|Q59990|CP120_SYNY3_Putative_cytochrome_P450_120_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=cyp120_PE=1_SV=1	2.00E-22	[illegible]	[illegible]
comp29800_c0_seq2.p1				
comp29800_c0_seq5.p2				
comp29800_c0_seq5.p3				
comp29800_c0_seq6.p1				
comp29800_c0_seq7.p1				
comp29803_c0_seq1.p2	sp|P40692|MLH1_HUMAN_DNA_mismatch_repair_protein_Mlh1_OS=Homo_sapiens_GN=MLH1_PE=1_SV=1	1.00E-44	[illegible]	[illegible]
comp29803_c0_seq2.p1	sp|Q9JK91|MLH1_MOUSE_DNA_mismatch_repair_protein_Mlh1_OS=Mus_musculus_GN=Mlh1_PE=2_SV=2	4.00E-118	[illegible]	[illegible]
comp29804_c0_seq2.p1	sp|Q9MA15|Y1960_ARATH_Uncharacterized_aarF_domain-containing_protein_kinase_At1g79600,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g79600_PE=1_SV=1	5.00E-44	[illegible]	[illegible]
comp29804_c0_seq2.p2	sp|Q55680|Y005_SYNY3_Uncharacterized_protein_sll0005_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll0005_PE=3_SV=1	7.00E-39	[illegible]	[illegible]
comp29805_c0_seq1.p1				
comp29806_c0_seq3.p1				
comp29807_c0_seq1.p1	sp|Q67R57|COAE_SYMTH_Dephospho-CoA_kinase_OS=Symbiobacterium_thermophilum_GN=coaE_PE=3_SV=1	5.00E-23	[illegible]	[illegible]
comp29807_c0_seq3.p1	sp|Q74FU2|COAE_GEOSL_Dephospho-CoA_kinase_OS=Geobacter_sulfurreducens_(strain_ATCC_51573_/_DSM_12127_/_PCA)_GN=coaE_PE=3_SV=1	1.00E-37	[illegible]	[illegible]
comp29808_c0_seq1.p1	sp|Q6PGY6|UFL1_DANRE_E3_UFM1-protein_ligase_1_OS=Danio_rerio_GN=ufl1_PE=2_SV=1	3.00E-13	[illegible]	[illegible]
comp29810_c0_seq1.p1	sp|Q69QZ0|P2C27_ORYSJ_Probable_protein_phosphatase_2C_27_OS=Oryza_sativa_subsp._japonica_GN=Os02g0799000_PE=2_SV=1	2.00E-20	[illegible]	[illegible]
comp29811_c0_seq2.p1	sp|Q8T2I8|SEPA_DICDI_Serine/threonine-protein_kinase_sepA_OS=Dictyostelium_discoideum_GN=sepA_PE=2_SV=1	3.00E-86	[illegible]	[illegible]
comp29811_c0_seq2.p2	sp|Q8T2I8|SEPA_DICDI_Serine/threonine-protein_kinase_sepA_OS=Dictyostelium_discoideum_GN=sepA_PE=2_SV=1	4.00E-55	[illegible]	[illegible]
comp29811_c0_seq3.p1	sp|Q8T2I8|SEPA_DICDI_Serine/threonine-protein_kinase_sepA_OS=Dictyostelium_discoideum_GN=sepA_PE=2_SV=1	1.00E-84	[illegible]	[illegible]
comp29812_c0_seq1.p1	sp|P36062|AVT3_YEAST_Vacuolar_amino_acid_transporter_3_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=AVT3_PE=1_SV=1	4.00E-39	[illegible]	[illegible]
comp29812_c0_seq4.p1	sp|Q10074|YAN9_SCHPO_Putative_amino_acid_permease_C3H1.09c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC3H1.09c_PE=1_SV=1	1.00E-29	[illegible]	[illegible]
comp29812_c0_seq5.p2	sp|Q10074|YAN9_SCHPO_Putative_amino_acid_permease_C3H1.09c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC3H1.09c_PE=1_SV=1	1.00E-11	[illegible]	[illegible]
comp29812_c0_seq5.p3	sp|P36062|AVT3_YEAST_Vacuolar_amino_acid_transporter_3_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=AVT3_PE=1_SV=1	2.00E-22	[illegible]	[illegible]
comp29812_c0_seq7.p2	sp|Q10074|YAN9_SCHPO_Putative_amino_acid_permease_C3H1.09c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC3H1.09c_PE=1_SV=1	1.00E-11	[illegible]	[illegible]
comp29812_c0_seq7.p3	sp|Q495N2|S36A3_HUMAN_Proton-coupled_amino_acid_transporter_3_OS=Homo_sapiens_GN=SLC36A3_PE=1_SV=2	6.00E-16	[illegible]	[illegible]
comp29813_c0_seq1.p1				
comp29814_c0_seq4.p1	sp|Q27497|GLC7A_CAEEL_Serine/threonine-protein_phosphatase_PP1-alpha_OS=Caenorhabditis_elegans_GN=gsp-1_PE=2_SV=2	1.00E-167	[illegible]	[illegible]
comp29814_c0_seq4.p3				
comp29815_c0_seq1.p1	sp|Q5ZJC7|NOC4L_CHICK_Nucleolar_complex_protein_4_homolog_OS=Gallus_gallus_GN=NOC4L_PE=2_SV=1	1.00E-53	[illegible]	[illegible]
comp29815_c0_seq1.p2				
comp29818_c0_seq1.p1				
comp29818_c0_seq2.p1				
comp29818_c0_seq3.p1				
comp29818_c0_seq4.p1				
comp29819_c0_seq1.p3				
comp29819_c0_seq4.p1	sp|Q6T486|RBRA_DICDI_Probable_E3_ubiquitin-protein_ligase_rbrA_OS=Dictyostelium_discoideum_GN=rbrA_PE=3_SV=1	9.00E-111	[illegible]	[illegible]
comp29819_c0_seq4.p2				
comp29819_c0_seq5.p1	sp|Q9P3U4|YKX2_SCHPO_Uncharacterized_RING_finger_protein_C328.02_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC328.02_PE=2_SV=1	9.00E-68	[illegible]	[illegible]
comp29820_c0_seq1.p2	sp|P31692|ADT_PARKE_ADP,ATP_carrier_protein_OS=Parachlorella_kessleri_PE=3_SV=1	4.00E-108	[illegible]	[illegible]
comp29821_c0_seq1.p2	sp|Q54I56|SMC6_DICDI_Structural_maintenance_of_chromosomes_protein_6_OS=Dictyostelium_discoideum_GN=smc6_PE=3_SV=1	3.00E-24	[illegible]	[illegible]
comp29821_c0_seq2.p1	sp|Q96SB8|SMC6_HUMAN_Structural_maintenance_of_chromosomes_protein_6_OS=Homo_sapiens_GN=SMC6_PE=1_SV=2	1.00E-87	[illegible]	[illegible]
comp29822_c0_seq3.p1				
comp29823_c0_seq1.p1	sp|Q6ZUT9|DEN5B_HUMAN_DENN_domain-containing_protein_5B_OS=Homo_sapiens_GN=DENND5B_PE=1_SV=2	2.00E-13	[illegible]	[illegible]
comp29824_c0_seq1.p1				
comp29824_c0_seq3.p2				
comp29824_c0_seq4.p1				
comp29824_c0_seq5.p1				
comp29824_c0_seq6.p1				
comp29825_c0_seq2.p1				
comp29825_c0_seq2.p2	sp|Q39709|FCP_ISOGA_Fucoxanthin-chlorophyll_a-c_binding_protein,_chloroplastic_OS=Isochrysis_galbana_GN=FCP_PE=1_SV=1	1.00E-28	[illegible]	[illegible]
comp29826_c0_seq1.p1				
comp29826_c0_seq2.p1				
comp29827_c0_seq2.p1	sp|Q94AC1|STR6_ARATH_Rhodanese-like_domain-containing_protein_6_OS=Arabidopsis_thaliana_GN=STR6_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp29827_c0_seq5.p1	sp|Q94AC1|STR6_ARATH_Rhodanese-like_domain-containing_protein_6_OS=Arabidopsis_thaliana_GN=STR6_PE=2_SV=1	8.00E-30	[illegible]	[illegible]
comp29828_c0_seq1.p1	sp|Q5RAK7|SPCS_PONAB_O-phosphoseryl-tRNA(Sec)_selenium_transferase_OS=Pongo_abelii_GN=SEPSECS_PE=2_SV=1	9.00E-154	[illegible]	[illegible]
comp29828_c0_seq2.p1	sp|Q803A7|SPCS_DANRE_O-phosphoseryl-tRNA(Sec)_selenium_transferase_OS=Danio_rerio_GN=sepsecs_PE=2_SV=1	4.00E-110	[illegible]	[illegible]
comp29828_c0_seq2.p2	sp|Q5RAK7|SPCS_PONAB_O-phosphoseryl-tRNA(Sec)_selenium_transferase_OS=Pongo_abelii_GN=SEPSECS_PE=2_SV=1	8.00E-23	[illegible]	[illegible]
comp29830_c0_seq2.p1				
comp29831_c0_seq1.p1	sp|Q99575|POP1_HUMAN_Ribonucleases_P/MRP_protein_subunit_POP1_OS=Homo_sapiens_GN=POP1_PE=1_SV=2	1.00E-18	[illegible]	[illegible]
comp29833_c0_seq2.p1	sp|O95259|KCNH1_HUMAN_Potassium_voltage-gated_channel_subfamily_H_member_1_OS=Homo_sapiens_GN=KCNH1_PE=1_SV=1	6.00E-32	[illegible]	[illegible]
comp29834_c0_seq1.p1				
comp29835_c0_seq3.p1	sp|Q5R9R1|EDRF1_PONAB_Erythroid_differentiation-related_factor_1_OS=Pongo_abelii_GN=EDRF1_PE=2_SV=1	3.00E-15	[illegible]	[illegible]
comp29835_c0_seq5.p1	sp|Q5R9R1|EDRF1_PONAB_Erythroid_differentiation-related_factor_1_OS=Pongo_abelii_GN=EDRF1_PE=2_SV=1	5.00E-15	[illegible]	[illegible]
comp29836_c0_seq1.p1				
comp29836_c0_seq2.p1				
comp29837_c0_seq3.p1	sp|P35749|MYH11_HUMAN_Myosin-11_OS=Homo_sapiens_GN=MYH11_PE=1_SV=3	1.00E-13	[illegible]	[illegible]
comp29838_c1_seq1.p1	sp|Q6AWX0|XYLL2_ARATH_D-xylose-proton_symporter-like_2_OS=Arabidopsis_thaliana_GN=At5g17010_PE=1_SV=1	1.00E-11	[illegible]	[illegible]
comp29838_c1_seq2.p1	sp|Q0WWW9|XYLL3_ARATH_D-xylose-proton_symporter-like_3,_chloroplastic_OS=Arabidopsis_thaliana_GN=At5g59250_PE=1_SV=2	6.00E-23	[illegible]	[illegible]
comp29839_c0_seq2.p1				
comp29840_c0_seq3.p1	sp|Q8RWB8|UPL6_ARATH_E3_ubiquitin-protein_ligase_UPL6_OS=Arabidopsis_thaliana_GN=UPL6_PE=2_SV=1	1.00E-120	[illegible]	[illegible]
comp29840_c0_seq3.p2				
comp29841_c0_seq12.p1	sp|Q8VHE0|SEC63_MOUSE_Translocation_protein_SEC63_homolog_OS=Mus_musculus_GN=Sec63_PE=1_SV=4	3.00E-18	[illegible]	[illegible]
comp29841_c0_seq14.p1				
comp29842_c0_seq1.p1				
comp29843_c0_seq1.p1	sp|Q54TR2|Y1931_DICDI_Putative_leucine-rich_repeat-containing_protein_DDB_G0281931_OS=Dictyostelium_discoideum_GN=DDB_G0281931_PE=4_SV=1	7.00E-12	[illegible]	[illegible]
comp29844_c0_seq1.p1	sp|O50314|BCHH_CHLP8_Magnesium-chelatase_subunit_H_OS=Chlorobaculum_parvum_(strain_NCIB_8327)_GN=bchH_PE=3_SV=2	0	[illegible]	[illegible]
comp29846_c0_seq1.p1	sp|Q8RNT4|LOX_PSEAI_Oleic_acid_lipoxygenase_OS=Pseudomonas_aeruginosa_GN=lox_PE=1_SV=2	9.00E-16	[illegible]	[illegible]
comp29846_c0_seq6.p1				
comp29847_c0_seq1.p1	sp|O67638|Y1758_AQUAE_Uncharacterized_RNA_pseudouridine_synthase_aq_1758_OS=Aquifex_aeolicus_(strain_VF5)_GN=aq_1758_PE=3_SV=1	4.00E-32	[illegible]	[illegible]
comp29847_c0_seq4.p1	sp|Q45826|Y901_CHLAA_Uncharacterized_RNA_pseudouridine_synthase_Caur_0901_OS=Chloroflexus_aurantiacus_(strain_ATCC_29366_/_DSM_635_/_J-10-fl)_GN=Caur_0901_PE=3_SV=2	2.00E-58	[illegible]	[illegible]
comp29848_c0_seq1.p1				
comp29848_c0_seq4.p1				
comp29848_c0_seq5.p1				
comp29848_c0_seq6.p1				
comp29849_c0_seq2.p1	sp|Q9Y4I1|MYO5A_HUMAN_Unconventional_myosin-Va_OS=Homo_sapiens_GN=MYO5A_PE=1_SV=2	6.00E-155	[illegible]	[illegible]
comp29851_c0_seq2.p1				
comp29852_c0_seq1.p1				
comp29853_c0_seq4.p1				
comp29854_c0_seq1.p1	sp|P32483|PABS_STRGR_Para-aminobenzoate_synthase_OS=Streptomyces_griseus_GN=pab_PE=3_SV=1	4.00E-71	[illegible]	[illegible]
comp29855_c0_seq11.p1	sp|Q28EW0|TM87A_XENTR_Transmembrane_protein_87A_OS=Xenopus_tropicalis_GN=tmem87a_PE=2_SV=1	8.00E-16	[illegible]	[illegible]
comp29855_c0_seq11.p2				
comp29856_c0_seq1.p1				
comp29857_c0_seq1.p1				
comp29857_c0_seq1.p6				
comp29857_c0_seq2.p1				
comp29859_c0_seq1.p1				
comp29859_c1_seq2.p1	sp|Q5ZI89|TPC11_CHICK_Trafficking_protein_particle_complex_subunit_11_OS=Gallus_gallus_GN=TRAPPC11_PE=2_SV=1	2.00E-11	[illegible]	[illegible]
comp29859_c1_seq3.p1				
comp29859_c1_seq4.p1				
comp29860_c0_seq2.p1				
comp29861_c0_seq4.p1				
comp29862_c0_seq2.p1				
comp29863_c0_seq1.p1	sp|Q1HG60|PIF1_RAT_ATP-dependent_DNA_helicase_PIF1_OS=Rattus_norvegicus_GN=Pif1_PE=2_SV=1	3.00E-88	[illegible]	[illegible]
comp29864_c0_seq1.p2				
comp29864_c0_seq2.p1				
comp29865_c0_seq1.p1	sp|O15865|CDPK2_PLAFK_Calcium-dependent_protein_kinase_2_OS=Plasmodium_falciparum_(isolate_K1_/_Thailand)_GN=CPK2_PE=1_SV=3	1.00E-73	[illegible]	[illegible]
comp29865_c0_seq2.p1	sp|O15865|CDPK2_PLAFK_Calcium-dependent_protein_kinase_2_OS=Plasmodium_falciparum_(isolate_K1_/_Thailand)_GN=CPK2_PE=1_SV=3	2.00E-72	[illegible]	[illegible]
comp29866_c0_seq1.p1	sp|Q99LJ7|RCBT2_MOUSE_RCC1_and_BTB_domain-containing_protein_2_OS=Mus_musculus_GN=Rcbtb2_PE=2_SV=1	5.00E-64	[illegible]	[illegible]
comp29866_c0_seq1.p5				
comp29868_c0_seq4.p1				
comp29870_c0_seq1.p2				
comp29870_c0_seq2.p1				
comp29870_c0_seq2.p2				
comp29871_c0_seq3.p2				
comp29872_c0_seq1.p1	sp|P41154|HSF_XENLA_Heat_shock_factor_protein_OS=Xenopus_laevis_GN=hsf1_PE=2_SV=1	3.00E-13	[illegible]	[illegible]
comp29873_c0_seq3.p1				
comp29874_c0_seq1.p1	sp|Q96JC1|VPS39_HUMAN_Vam6/Vps39-like_protein_OS=Homo_sapiens_GN=VPS39_PE=1_SV=2	5.00E-20	[illegible]	[illegible]
comp29875_c0_seq2.p1				
comp29875_c0_seq3.p1				
comp29875_c0_seq4.p1				
comp29875_c0_seq4.p2				
comp29875_c0_seq7.p1				
comp29875_c0_seq8.p1				
comp29875_c0_seq9.p1				
comp29876_c0_seq1.p1				

comp29878_c0_seq1.p1	sp|B3M6I4|PLK4_DROAN_Serine/threonine-protein_kinase_PLK4_OS=Drosophila_ananassae_GN=SAK_PE=3_SV=1	2.00E-59
comp29878_c0_seq2.p1	sp|Q64702|PLK4_MOUSE_Serine/threonine-protein_kinase_PLK4_OS=Mus_musculus_GN=Plk4_PE=1_SV=2	3.00E-37
comp29879_c0_seq3.p1		
comp29879_c0_seq3.p3		
comp29880_c0_seq2.p1		
comp29880_c0_seq2.p2		
comp29880_c0_seq6.p1		
comp29882_c0_seq1.p1		
comp29884_c0_seq1.p1		
comp29884_c0_seq2.p1		
comp29884_c0_seq3.p1		
comp29884_c0_seq4.p1		
comp29886_c0_seq1.p2		
comp29886_c0_seq3.p1		
comp29887_c0_seq1.p1		
comp29887_c1_seq1.p1		
comp29888_c0_seq2.p1	sp|B2KI88|SETD3_RHIFE_Histone-lysine_N-methyltransferase_setd3_OS=Rhinolophus_ferrumequinum_GN=SETD3_PE=3_SV=1	6.00E-22
comp29890_c0_seq1.p1	sp|P50259|TBB_PORPU_Tubulin_beta_chain_OS=Porphyra_purpurea_GN=TUBB1_PE=3_SV=1	7.00E-15
comp29890_c0_seq4.p1	sp|P50259|TBB_PORPU_Tubulin_beta_chain_OS=Porphyra_purpurea_GN=TUBB1_PE=3_SV=1	7.00E-12
comp29890_c0_seq6.p1		
comp29890_c0_seq7.p2		
comp29891_c0_seq1.p1		
comp29891_c0_seq14.p1		
comp29891_c0_seq14.p2		
comp29891_c0_seq5.p1		
comp29891_c0_seq6.p1		
comp29891_c0_seq6.p2		
comp29891_c0_seq7.p1		
comp29891_c0_seq9.p1		
comp29892_c0_seq1.p1		
comp29892_c0_seq3.p1		
comp29892_c0_seq3.p2		
comp29893_c0_seq1.p1	sp|Q10MH8|RH24_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_24_OS=Oryza_sativa_subsp._japonica_GN=Os03g0308500_PE=2_SV=1	2.00E-156
comp29894_c0_seq1.p1	sp|Q54QG6|ALG6_DICDI_Probable_dolichyl_pyrophosphate_Man9GlcNAc2_alpha-1,3-glucosyltransferase_OS=Dictyostelium_discoideum_GN=alg6_PE=3_SV=1	1.00E-23
comp29894_c0_seq1.p2	sp|Q54QG6|ALG6_DICDI_Probable_dolichyl_pyrophosphate_Man9GlcNAc2_alpha-1,3-glucosyltransferase_OS=Dictyostelium_discoideum_GN=alg6_PE=3_SV=1	4.00E-48
comp29894_c0_seq2.p1	sp|Q54QG6|ALG6_DICDI_Probable_dolichyl_pyrophosphate_Man9GlcNAc2_alpha-1,3-glucosyltransferase_OS=Dictyostelium_discoideum_GN=alg6_PE=3_SV=1	2.00E-84
comp29896_c0_seq1.p1	sp|Q9QUL6|NSF_RAT_Vesicle-fusing_ATPase_OS=Rattus_norvegicus_GN=Nsf_PE=1_SV=1	9.00E-28
comp29896_c0_seq1.p2	sp|Q9P7Q4|SEC18_SCHPO_Vesicular-fusion_protein_sec18_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=sec18_PE=1_SV=1	1.00E-37
comp29896_c0_seq2.p1	sp|Q5R410|NSF_PONAB_Vesicle-fusing_ATPase_OS=Pongo_abelii_GN=NSF_PE=2_SV=1	1.00E-69
comp29896_c0_seq3.p1		
comp29896_c0_seq3.p2	sp|Q9P7Q4|SEC18_SCHPO_Vesicular-fusion_protein_sec18_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=sec18_PE=1_SV=1	1.00E-37
comp29896_c0_seq4.p1		
comp29896_c0_seq4.p2	sp|Q9P7Q4|SEC18_SCHPO_Vesicular-fusion_protein_sec18_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=sec18_PE=1_SV=1	1.00E-37
comp29897_c0_seq1.p1		
comp29898_c0_seq1.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	1.00E-22
comp29898_c0_seq5.p1		
comp29899_c0_seq1.p2		
comp29899_c0_seq2.p1		
comp29899_c0_seq3.p1		
comp29899_c0_seq3.p2		
comp29900_c0_seq1.p1		
comp29900_c0_seq2.p1		
comp29900_c1_seq1.p1	sp|Q8K4Y7|CANT1_RAT_Soluble_calcium-activated_nucleotidase_1_OS=Rattus_norvegicus_GN=Cant1_PE=1_SV=1	6.00E-73
comp29900_c1_seq2.p1	sp|P41095|RLA0_ORYSJ_60S_acidic_ribosomal_protein_P0_OS=Oryza_sativa_subsp._japonica_GN=Os08g0130500_PE=1_SV=3	2.00E-96
comp29900_c1_seq4.p1		
comp29901_c0_seq2.p1	sp|P97770|THUM3_MOUSE_THUMP_domain-containing_protein_3_OS=Mus_musculus_GN=Thumpd3_PE=2_SV=1	2.00E-26
comp29901_c0_seq2.p3	sp|Q9JLJ4|ELOV2_MOUSE_Elongation_of_very_long_chain_fatty_acids_protein_2_OS=Mus_musculus_GN=Elovl2_PE=2_SV=1	1.00E-43
comp29902_c0_seq3.p1		
comp29902_c0_seq3.p2	sp|Q2S591|Y495_SALRD_UPF0301_protein_SRU_0495_OS=Salinibacter_ruber_(strain_DSM_13855_/_M31)_GN=SRU_0495_PE=3_SV=1	9.00E-18
comp29905_c0_seq4.p1	sp|Q9FZD1|PPR58_ARATH_Pentatricopeptide_repeat-containing_protein_At1g26460,_mitochondrial_OS=Arabidopsis_thaliana_GN=At1g26460_PE=1_SV=1	8.00E-11
comp29905_c0_seq4.p2	sp|B2RXR6|ANR44_MOUSE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_B_OS=Mus_musculus_GN=Ankrd44_PE=2_SV=1	4.00E-63
comp29906_c0_seq1.p1		
comp29906_c0_seq5.p1		
comp29906_c0_seq6.p1		
comp29908_c0_seq2.p1	sp|B0TC10|PANB_HELMI_3-methyl-2-oxobutanoate_hydroxymethyltransferase_OS=Heliobacterium_modesticaldum_(strain_ATCC_51547_/_Ice1)_GN=panB_PE=3_SV=1	5.00E-79
comp29908_c0_seq3.p1	sp|A6LWN6|PANB_CLOB8_3-methyl-2-oxobutanoate_hydroxymethyltransferase_OS=Clostridium_beijerinckii_(strain_ATCC_51743_/_NCIMB_8052)_GN=panB_PE=3_SV=1	7.00E-35
comp29908_c0_seq3.p2	sp|Q2RM79|PANB_MOOTA_3-methyl-2-oxobutanoate_hydroxymethyltransferase_OS=Moorella_thermoacetica_(strain_ATCC_39073)_GN=panB_PE=3_SV=1	2.00E-16
comp29909_c0_seq2.p1		
comp29909_c0_seq3.p5		
comp29909_c0_seq4.p1		
comp29910_c0_seq1.p1		
comp29913_c0_seq1.p1		
comp29913_c0_seq1.p3	sp|P61759|PFD3_MOUSE_Prefoldin_subunit_3_OS=Mus_musculus_GN=Vbp1_PE=2_SV=2	7.00E-47
comp29914_c0_seq1.p1	sp|B3EHS7|Y777_CHLL2_UPF0301_protein_Clim_0777_OS=Chlorobium_limicola_(strain_DSM_245_/_NBRC_103803)_GN=Clim_0777_PE=3_SV=1	2.00E-19
comp29914_c0_seq2.p1		
comp29914_c0_seq3.p1	sp|B3EHS7|Y777_CHLL2_UPF0301_protein_Clim_0777_OS=Chlorobium_limicola_(strain_DSM_245_/_NBRC_103803)_GN=Clim_0777_PE=3_SV=1	4.00E-23
comp29914_c0_seq3.p2		
comp29915_c0_seq1.p1	sp|O35071|KIF1C_MOUSE_Kinesin-like_protein_KIF1C_OS=Mus_musculus_GN=Kif1c_PE=1_SV=2	2.00E-45
comp29915_c0_seq1.p2		
comp29915_c0_seq3.p3		
comp29916_c0_seq1.p1		
comp29917_c0_seq1.p1		
comp29917_c0_seq3.p1	sp|P35748|MYH11_RABIT_Myosin-11_OS=Oryctolagus_cuniculus_GN=MYH11_PE=2_SV=2	1.00E-11
comp29918_c0_seq1.p1		
comp29918_c0_seq4.p1		
comp29919_c0_seq1.p1	sp|Q55C16|UBA1_DICDI_Ubiquitin-like_modifier-activating_enzyme_1_OS=Dictyostelium_discoideum_GN=uba1_PE=3_SV=1	2.00E-100
comp29919_c0_seq2.p1	sp|Q55C16|UBA1_DICDI_Ubiquitin-like_modifier-activating_enzyme_1_OS=Dictyostelium_discoideum_GN=uba1_PE=3_SV=1	7.00E-27
comp29919_c0_seq3.p1		
comp29919_c0_seq4.p1	sp|Q55C16|UBA1_DICDI_Ubiquitin-like_modifier-activating_enzyme_1_OS=Dictyostelium_discoideum_GN=uba1_PE=3_SV=1	2.00E-51
comp29920_c0_seq4.p1		
comp29920_c0_seq4.p2	sp|P68827|NAGPA_BOVIN_N-acetylglucosamine-1-phosphodiester_alpha-N-acetylglucosaminidase_OS=Bos_taurus_GN=NAGPA_PE=1_SV=2	2.00E-19
comp29920_c0_seq4.p3	sp|P31108|SODF_LEGPH_Superoxide_dismutase_[Fe]_OS=Legionella_pneumophila_subsp._pneumophila_(strain_Philadelphia_1_/_ATCC_33152_/_DSM_7513)_GN=sodB_PE=3_SV=1	2.00E-90
comp29920_c0_seq5.p1		
comp29920_c0_seq5.p2	sp|P68827|NAGPA_BOVIN_N-acetylglucosamine-1-phosphodiester_alpha-N-acetylglucosaminidase_OS=Bos_taurus_GN=NAGPA_PE=1_SV=2	2.00E-19
comp29920_c0_seq5.p3	sp|P31108|SODF_LEGPH_Superoxide_dismutase_[Fe]_OS=Legionella_pneumophila_subsp._pneumophila_(strain_Philadelphia_1_/_ATCC_33152_/_DSM_7513)_GN=sodB_PE=3_SV=1	2.00E-90
comp29920_c2_seq1.p1		
comp29921_c0_seq1.p1		
comp29922_c0_seq1.p1	sp|Q38869|CDPK4_ARATH_Calcium-dependent_protein_kinase_4_OS=Arabidopsis_thaliana_GN=CPK4_PE=1_SV=1	1.00E-81
comp29922_c0_seq1.p2	sp|O15315|RA51B_HUMAN_DNA_repair_protein_RAD51_homolog_2_OS=Homo_sapiens_GN=RAD51B_PE=1_SV=2	9.00E-39
comp29923_c0_seq1.p1		
comp29923_c0_seq3.p1		
comp29923_c0_seq7.p1		
comp29923_c0_seq8.p1		
comp29923_c0_seq9.p3		
comp29924_c0_seq2.p1	sp|Q9D2R4|TMD11_MOUSE_Transmembrane_emp24_domain-containing_protein_11_OS=Mus_musculus_GN=Tmed11_PE=2_SV=1	1.00E-15
comp29924_c0_seq2.p2		
comp29924_c0_seq3.p1	sp|A0JNC4|ELOV7_BOVIN_Elongation_of_very_long_chain_fatty_acids_protein_7_OS=Bos_taurus_GN=ELOVL7_PE=2_SV=1	8.00E-17
comp29924_c0_seq3.p2	sp|Q9D2R4|TMD11_MOUSE_Transmembrane_emp24_domain-containing_protein_11_OS=Mus_musculus_GN=Tmed11_PE=2_SV=1	1.00E-15
comp29924_c1_seq1.p1	sp|Q55GK8|KIL1_DICDI_Membrane-associated_sulfotransferase_kil1_OS=Dictyostelium_discoideum_GN=kil1_PE=3_SV=1	6.00E-16
comp29924_c1_seq2.p1	sp|Q55GK8|KIL1_DICDI_Membrane-associated_sulfotransferase_kil1_OS=Dictyostelium_discoideum_GN=kil1_PE=3_SV=1	1.00E-12
comp29925_c0_seq1.p1		
comp29925_c0_seq2.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	2.00E-34
comp29925_c0_seq2.p2	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	3.00E-31
comp29925_c0_seq4.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	3.00E-31
comp29925_c0_seq4.p2	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	3.00E-23
comp29925_c0_seq5.p1		
comp29926_c0_seq5.p1	sp|B2RJG1|SYP_PORG3_Proline--tRNA_ligase_OS=Porphyromonas_gingivalis_(strain_ATCC_33277_/_DSM_20709_/_JCM_12257)_GN=proS_PE=3_SV=1	2.00E-173
comp29926_c0_seq5.p2		
comp29927_c1_seq3.p1	sp|Q9M291|SC24C_ARATH_Protein_transport_protein_Sec24-like_CEF_OS=Arabidopsis_thaliana_GN=CEF_PE=1_SV=3	1.00E-99
comp29928_c0_seq1.p1		
comp29928_c0_seq2.p1	sp|Q05086|UBE3A_HUMAN_Ubiquitin-protein_ligase_E3A_OS=Homo_sapiens_GN=UBE3A_PE=1_SV=4	5.00E-93
comp29928_c0_seq2.p2	sp|Q6GLI9|RPA49_XENLA_DNA-directed_RNA_polymerase_I_subunit_RPA49_OS=Xenopus_laevis_GN=polr1e_PE=2_SV=1	3.00E-12
comp29929_c0_seq1.p1	sp|Q6NXT6|TAPT1_HUMAN_Transmembrane_anterior_posterior_transformation_protein_1_homolog_OS=Homo_sapiens_GN=TAPT1_PE=1_SV=1	2.00E-67
comp29930_c0_seq5.p1		
comp29931_c0_seq2.p1		
comp29931_c0_seq2.p2	sp|Q1WSG3|PTH_LACS1_Peptidyl-tRNA_hydrolase_OS=Lactobacillus_salivarius_(strain_UCC118)_GN=pth_PE=3_SV=1	4.00E-27
comp29931_c0_seq3.p1		
comp29931_c0_seq4.p1		
comp29931_c0_seq4.p2	sp|Q1WSG3|PTH_LACS1_Peptidyl-tRNA_hydrolase_OS=Lactobacillus_salivarius_(strain_UCC118)_GN=pth_PE=3_SV=1	4.00E-27
comp29931_c0_seq5.p1	sp|Q6NTR1|MET13_XENLA_Methyltransferase-like_protein_13_OS=Xenopus_laevis_GN=mettl13_PE=2_SV=1	1.00E-10
comp29931_c0_seq5.p2		
comp29931_c0_seq5.p3		
comp29931_c0_seq8.p1	sp|Q0IDC6|PTH_SYNS3_Peptidyl-tRNA_hydrolase_OS=Synechococcus_sp._(strain_CC9311)_GN=pth_PE=3_SV=1	1.00E-45
comp29932_c0_seq1.p1		
comp29932_c0_seq1.p8		
comp29933_c0_seq1.p1		
comp29934_c1_seq1.p1		
comp29934_c1_seq2.p1		
comp29935_c0_seq3.p1	sp|O49160|EIF3C_ARATH_Eukaryotic_translation_initiation_factor_3_subunit_C_OS=Arabidopsis_thaliana_GN=TIF3C1_PE=1_SV=2	1.00E-134
comp29936_c0_seq1.p1	sp|A8JUV0|SBNO_DROME_Protein_strawberry_notch_OS=Drosophila_melanogaster_GN=sno_PE=1_SV=1	6.00E-70
comp29936_c0_seq1.p2	sp|Q5BJL5|SBNO1_RAT_Protein_strawberry_notch_homolog_1_OS=Rattus_norvegicus_GN=Sbno1_PE=2_SV=2	4.00E-87
comp29936_c0_seq2.p1	sp|A0JND4|SBNO2_BOVIN_Protein_strawberry_notch_homolog_2_OS=Bos_taurus_GN=SBNO2_PE=2_SV=1	2.00E-153
comp29937_c0_seq2.p1	sp|Q5FVL7|KTU_RAT_Protein_kintoun_OS=Rattus_norvegicus_GN=Dnaaf2_PE=2_SV=2	4.00E-25
comp29938_c0_seq2.p1		
comp29938_c0_seq3.p1		
comp29939_c0_seq2.p1	sp|Q5SPC5|OTOF_DANRE_Otoferlin_OS=Danio_rerio_GN=otof_PE=3_SV=1	2.00E-18
comp29940_c0_seq1.p1		
comp29941_c0_seq1.p1		
comp29943_c0_seq1.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	4.00E-18
comp29943_c0_seq13.p1	sp|Q54TK2|Y1931_DICDI_Putative_leucine-rich_repeat-containing_protein_DDB_G0281931_OS=Dictyostelium_discoideum_GN=DDB_G0281931_PE=4_SV=1	5.00E-13
comp29943_c0_seq13.p2	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	8.00E-17
comp29943_c0_seq16.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	8.00E-17
comp29943_c0_seq16.p3		
comp29943_c0_seq18.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	5.00E-16
comp29943_c0_seq2.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	2.00E-18
comp29943_c0_seq23.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	9.00E-19
comp29943_c0_seq24.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	3.00E-18
comp29943_c0_seq7.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	8.00E-17
comp29944_c0_seq1.p1		
comp29946_c0_seq1.p1		
comp29947_c0_seq1.p1		
comp29947_c1_seq1.p1		
comp29950_c1_seq1.p2		
comp29950_c1_seq4.p1		
comp29951_c0_seq1.p1		
comp29951_c0_seq3.p1		
comp29951_c0_seq3.p3		
comp29952_c0_seq4.p1		
comp29952_c0_seq4.p2		
comp29952_c0_seq4.p4		
comp29952_c0_seq8.p1	sp|Q29116|TENA_PIG_Tenascin_OS=Sus_scrofa_GN=TNC_PE=1_SV=1	5.00E-18
comp29953_c0_seq1.p1		
comp29953_c0_seq4.p1		
comp29953_c0_seq5.p1		
comp29953_c0_seq5.p2		
comp29953_c0_seq8.p1		
comp29953_c0_seq8.p2		
comp29954_c0_seq2.p1		
comp29954_c0_seq3.p1	sp|Q9VH90|TRBID_DROME_Ubiquitin_thioesterase_trabid_OS=Drosophila_melanogaster_GN=trbd_PE=1_SV=1	3.00E-16
comp29954_c0_seq4.p1	sp|Q9VH90|TRBID_DROME_Ubiquitin_thioesterase_trabid_OS=Drosophila_melanogaster_GN=trbd_PE=1_SV=1	1.00E-15
comp29954_c0_seq5.p1		
comp29954_c0_seq6.p1		
comp29955_c0_seq2.p1		
comp29956_c0_seq1.p1		
comp29956_c0_seq1.p2		
comp29957_c0_seq1.p1		
comp29957_c0_seq10.p1		
comp29957_c0_seq10.p2		
comp29957_c0_seq11.p1		
comp29957_c0_seq12.p1		
comp29957_c0_seq12.p2		
comp29957_c0_seq12.p5		
comp29957_c0_seq14.p1		
comp29957_c0_seq14.p4		
comp29957_c0_seq15.p1		
comp29957_c0_seq15.p4		
comp29957_c0_seq3.p1		
comp29957_c0_seq3.p2		
comp29957_c0_seq3.p5		
comp29957_c0_seq4.p1		
comp29957_c0_seq4.p2		
comp29958_c0_seq1.p1	sp|Q6NLC1|AB2D_ARATH_ABC_transporter_D_family_member_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=ABCD2_PE=1_SV=1	5.00E-30
comp29959_c0_seq2.p1		
comp29960_c0_seq2.p1		
comp29960_c0_seq4.p1		
comp29961_c0_seq3.p1		
comp29962_c0_seq6.p1	sp|P93655|LONM1_ARATH_Lon_protease_homolog_1,_mitochondrial_OS=Arabidopsis_thaliana_GN=LON1_PE=1_SV=2	0
comp29962_c0_seq6.p6	sp|Q58549|ADPP_METJA_ADP-ribose_pyrophosphatase_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=nudF_PE=1_SV=1	3.00E-17
comp29963_c0_seq2.p2	sp|Q14442|PIGH_HUMAN_Phosphatidylinositol_N-acetylglucosaminyltransferase_subunit_H_OS=Homo_sapiens_GN=PIGH_PE=1_SV=1	6.00E-16
comp29963_c0_seq3.p1	sp|Q14442|PIGH_HUMAN_Phosphatidylinositol_N-acetylglucosaminyltransferase_subunit_H_OS=Homo_sapiens_GN=PIGH_PE=1_SV=1	3.00E-15
comp29964_c0_seq1.p1		
comp29965_c0_seq2.p1	sp|Q2YDR3|IMPA3_DANRE_Inositol_monophosphatase_3_OS=Danio_rerio_GN=impad1_PE=2_SV=1	2.00E-34
comp29965_c0_seq3.p2		
comp29965_c0_seq4.p2		
comp29966_c0_seq3.p1		
comp29967_c0_seq4.p1	sp|Q8QHA5|DNA2L_XENLA_DNA2-like_helicase_OS=Xenopus_laevis_GN=dna2_PE=1_SV=1	1.00E-48
comp29967_c0_seq4.p3		
comp29967_c0_seq5.p1	sp|Q8QHA5|DNA2L_XENLA_DNA2-like_helicase_OS=Xenopus_laevis_GN=dna2_PE=1_SV=1	1.00E-98
comp29968_c0_seq1.p2		
comp29968_c0_seq3.p1		
comp29970_c0_seq1.p1	sp|P02640|VILI_CHICK_Villin-1_OS=Gallus_gallus_GN=VIL1_PE=1_SV=2	3.00E-167
comp29970_c0_seq2.p1	sp|P02640|VILI_CHICK_Villin-1_OS=Gallus_gallus_GN=VIL1_PE=1_SV=2	8.00E-173
comp29971_c0_seq1.p1	sp|Q9SS47|PUM4_ARATH_Pumilio_homolog_4_OS=Arabidopsis_thaliana_GN=APUM4_PE=1_SV=2	1.00E-110
comp29971_c0_seq1.p5		
comp29971_c0_seq1.p7		
comp29972_c0_seq4.p1	sp|Q15034|HERC3_HUMAN_Probable_E3_ubiquitin-protein_ligase_HERC3_OS=Homo_sapiens_GN=HERC3_PE=1_SV=1	5.00E-23
comp29973_c0_seq1.p1	sp|Q9UY49|IMDH_PYRAB_Inosine-5'-monophosphate_dehydrogenase_OS=Pyrococcus_abyssi_(strain_GE5_/_Orsay)_GN=guaB_PE=3_SV=1	1.00E-13
comp29974_c0_seq1.p1		
comp29974_c0_seq1.p6		
comp29975_c0_seq1.p1		
comp29975_c1_seq1.p2	sp|P23921|RIR1_HUMAN_Ribonucleoside-diphosphate_reductase_large_subunit_OS=Homo_sapiens_GN=RRM1_PE=1_SV=1	5.00E-117
comp29975_c2_seq1.p1	sp|P36602|RIR1_SCHPO_Ribonucleoside-diphosphate_reductase_large_chain_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=cdc22_PE=1_SV=2	0
comp29976_c0_seq1.p1		
comp29976_c0_seq2.p1		
comp29976_c0_seq4.p1		
comp29977_c0_seq1.p1	sp|Q9SYM1|MSL6_ARATH_Mechanosensitive_ion_channel_protein_6_OS=Arabidopsis_thaliana_GN=MSL6_PE=1_SV=1	3.00E-19
comp29977_c0_seq1.p2	sp|Q9ES53|UFD1_RAT_Ubiquitin_fusion_degradation_protein_1_homolog_OS=Rattus_norvegicus_GN=Ufd1l_PE=1_SV=1	1.00E-15
comp29978_c0_seq1.p1		
comp29978_c0_seq5.p1	sp|Q7Z9I4|YCP6_SCHPO_Uncharacterized_oxidoreductase_C663.06c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC663.06c_PE=2_SV=1	4.00E-23
comp29978_c0_seq5.p3		
comp29978_c0_seq6.p1		
comp29979_c0_seq2.p1		
comp29979_c0_seq2.p2	sp|Q58424|SERA_METJA_D-3-phosphoglycerate_dehydrogenase_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=serA_PE=3_SV=1	1.00E-12
comp29979_c0_seq4.p1	sp|Q58424|SERA_METJA_D-3-phosphoglycerate_dehydrogenase_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=serA_PE=3_SV=1	1.00E-30
comp29979_c0_seq6.p1	sp|O29445|SERA_ARCFU_D-3-phosphoglycerate_dehydrogenase_OS=Archaeoglobus_fulgidus_(strain_ATCC_49558_/_VC-16_/_DSM_4304_/_JCM_9628_/_NBRC_100126)_GN=serA_PE=3_SV=1	1.00E-44
comp29979_c0_seq7.p1	sp|Q9C4M5|GYAR_THELI_Glyoxylate_reductase_OS=Thermococcus_litoralis_GN=gyaR_PE=1_SV=1	5.00E-32
comp29982_c0_seq1.p1		
comp29982_c0_seq2.p1	sp|Q5HZK1|CEP44_MOUSE_Centrosomal_protein_of_44_kDa_OS=Mus_musculus_GN=Cep44_PE=2_SV=1	4.00E-12
comp29983_c0_seq2.p1		
comp29984_c0_seq1.p1	sp|P35182|PP2C1_YEAST_Protein_phosphatase_2C_homolog_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PTC1_PE=1_SV=1	5.00E-54
comp29984_c0_seq2.p1	sp|P35182|PP2C1_YEAST_Protein_phosphatase_2C_homolog_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PTC1_PE=1_SV=1	1.00E-47
comp29985_c0_seq1.p1		
comp29986_c0_seq1.p1	sp|Q8RXV3|P2C59_ARATH_Probable_protein_phosphatase_2C_59_OS=Arabidopsis_thaliana_GN=WIN2_PE=1_SV=1	1.00E-32
comp29988_c1_seq1.p1		
comp29989_c0_seq1.p1	sp|Q9P2S5|WRP73_HUMAN_WD_repeat-containing_protein_WRAP73_OS=Homo_sapiens_GN=WRAP73_PE=2_SV=1	3.00E-76
comp29989_c0_seq1.p3	sp|Q9JM98|WRP73_MOUSE_WD_repeat-containing_protein_WRAP73_OS=Mus_musculus_GN=Wrap73_PE=2_SV=2	6.00E-29
comp29989_c0_seq2.p1	sp|Q9JM98|WRP73_MOUSE_WD_repeat-containing_protein_WRAP73_OS=Mus_musculus_GN=Wrap73_PE=2_SV=2	2.00E-109
comp29990_c0_seq11.p2		
comp29990_c0_seq2.p1		
comp29990_c0_seq4.p2		
comp29990_c0_seq6.p1		
comp29990_c0_seq7.p1		
comp29991_c0_seq2.p1		
comp29991_c0_seq4.p1		
comp29991_c0_seq5.p1		
comp29991_c0_seq6.p1		
comp29993_c0_seq2.p1		
comp29994_c0_seq2.p1		
comp29994_c0_seq3.p1	sp|Q00771|KCC1_EMENI_Calcium/calmodulin-dependent_protein_kinase_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=cmkA_PE=2_SV=2	1.00E-30
comp29995_c0_seq1.p1		
comp29995_c0_seq1.p5		
comp29995_c0_seq11.p2		
comp29995_c0_seq2.p3	sp|Q6C603|RL7_YARLI_60S_ribosomal_protein_L7_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=RPL7_PE=3_SV=1	2.00E-22
comp29995_c0_seq4.p1	sp|Q5VYK3|ECM29_HUMAN_Proteasome-associated_protein_ECM29_homolog_OS=Homo_sapiens_GN=ECM29_PE=1_SV=2	1.00E-54
comp29995_c0_seq6.p1		
comp29996_c0_seq1.p1		
comp29996_c0_seq2.p1	sp|P15848|ARSB_HUMAN_Arylsulfatase_B_OS=Homo_sapiens_GN=ARSB_PE=1_SV=1	2.00E-79
comp29997_c0_seq3.p1	sp|P24920|TRPC_PHYPR_Tryptophan_biosynthesis_protein_TRP1_OS=Phytophthora_parasitica_GN=TRP1_PE=3_SV=1	4.00E-108
comp29998_c0_seq1.p1		
comp29999_c0_seq1.p1	sp|O73787|GCP3_XENLA_Gamma-tubulin_complex_component_3_homolog_OS=Xenopus_laevis_GN=tubgcp3_PE=1_SV=1	2.00E-13
comp29999_c0_seq2.p1	sp|O73787|GCP3_XENLA_Gamma-tubulin_complex_component_3_homolog_OS=Xenopus_laevis_GN=tubgcp3_PE=1_SV=1	1.00E-118
comp29999_c0_seq5.p1	sp|O73787|GCP3_XENLA_Gamma-tubulin_complex_component_3_homolog_OS=Xenopus_laevis_GN=tubgcp3_PE=1_SV=1	1.00E-118
comp30000_c0_seq2.p1		
comp30001_c0_seq2.p1	sp|Q869Q3|NAPA_DICDI_Nck-associated_protein_1_homolog_OS=Dictyostelium_discoideum_GN=napA_PE=1_SV=1	2.00E-67
comp30003_c0_seq2.p1		
comp30004_c0_seq1.p1	sp|Q641Z6|EHD1_RAT_EH_domain-containing_protein_1_OS=Rattus_norvegicus_GN=Ehd1_PE=1_SV=1	4.00E-110
comp30004_c0_seq1.p2	sp|Q8LFJ5|T112A_ARATH_TRM112-like_protein_At1g22270_OS=Arabidopsis_thaliana_GN=At1g22270_PE=2_SV=1	2.00E-25
comp30004_c0_seq2.p1	sp|Q641Z6|EHD1_RAT_EH_domain-containing_protein_1_OS=Rattus_norvegicus_GN=Ehd1_PE=1_SV=1	1.00E-102
comp30004_c0_seq3.p1	sp|Q8LFJ5|T112A_ARATH_TRM112-like_protein_At1g22270_OS=Arabidopsis_thaliana_GN=At1g22270_PE=2_SV=1	3.00E-28
comp30004_c0_seq4.p1	sp|Q8LFJ5|T112A_ARATH_TRM112-like_protein_At1g22270_OS=Arabidopsis_thaliana_GN=At1g22270_PE=2_SV=1	8.00E-23
comp30005_c0_seq1.p1		
comp30006_c0_seq1.p1		
comp30008_c0_seq1.p1	sp|Q6TMK4|POXA_DICDI_Peroxinectin_A_OS=Dictyostelium_discoideum_GN=poxA_PE=2_SV=1	4.00E-16
comp30009_c0_seq1.p1		
comp30010_c0_seq1.p1		
comp30011_c0_seq4.p1	sp|Q9STV4|CIPK8_ARATH_CBL-interacting_serine/threonine-protein_kinase_8_OS=Arabidopsis_thaliana_GN=CIPK8_PE=1_SV=1	4.00E-44
comp30011_c0_seq5.p2		
comp30012_c0_seq2.p1	sp|Q8K1H7|T11L2_MOUSE_T-complex_protein_11-like_protein_2_OS=Mus_musculus_GN=Tcp11l2_PE=2_SV=1	3.00E-12
comp30013_c1_seq1.p1		
comp30014_c0_seq1.p1	sp|P0CM22|ARO1_CRYNJ_Pentafunctional_AROM_polypeptide_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=CNB01990_PE=3_SV=1	2.00E-79
comp30014_c0_seq1.p2	sp|O74362|ESF2_SCHPO_Pre-rRNA-processing_protein_esf2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=esf2_PE=1_SV=1	2.00E-48
comp30015_c0_seq1.p1	sp|Q94AH8|TPS6_ARATH_Alpha,alpha-trehalose-phosphate_synthase_[UDP-forming]_6_OS=Arabidopsis_thaliana_GN=TPS6_PE=1_SV=2	8.00E-138
comp30016_c0_seq1.p1		
comp30016_c0_seq2.p1		
comp30016_c0_seq3.p1	sp|O65195|INO1_HORVU_Inositol-3-phosphate_synthase_OS=Hordeum_vulgare_PE=2_SV=1	1.00E-62
comp30016_c0_seq4.p1		
comp30018_c0_seq2.p1		
comp30019_c0_seq8.p2		
comp30020_c0_seq5.p1		
comp30021_c0_seq12.p2	sp|O13983|HRQ1_SCHPO_Putative_ATP-dependent_helicase_hrq1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=hrq1_PE=2_SV=4	4.00E-22
comp30021_c0_seq18.p3		
comp30021_c0_seq3.p1	sp|O13983|HRQ1_SCHPO_Putative_ATP-dependent_helicase_hrq1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=hrq1_PE=2_SV=4	1.00E-64
comp30021_c0_seq3.p9		
comp30021_c0_seq8.p1		
comp30022_c0_seq1.p1		
comp30022_c0_seq1.p2		
comp30022_c0_seq1.p4		
comp30022_c0_seq2.p1		
comp30022_c0_seq3.p1		
comp30022_c0_seq3.p2		
comp30023_c0_seq1.p1	sp|Q69QQ6|HSP82_ORYSJ_Heat_shock_protein_81-2_OS=Oryza_sativa_subsp._japonica_GN=HSP81-2_PE=2_SV=1	0
comp30024_c0_seq2.p1		
comp30024_c0_seq2.p2		
comp30024_c0_seq3.p1		
comp30025_c0_seq4.p1	sp|Q9FPR6|ARR17_ARATH_Two-component_response_regulator_ARR17_OS=Arabidopsis_thaliana_GN=ARR17_PE=2_SV=1	2.00E-11
comp30026_c0_seq1.p1		
comp30026_c0_seq2.p1	sp|P59326|YTHD1_MOUSE_YTH_domain_family_protein_1_OS=Mus_musculus_GN=Ythdf1_PE=2_SV=1	2.00E-21
comp30026_c0_seq4.p1		
comp30027_c0_seq1.p1		
comp30028_c0_seq2.p2		
comp30029_c0_seq1.p1		
comp30030_c0_seq1.p1	sp|O31634|YJCL_BACSU_Uncharacterized_membrane_protein_yjcL_OS=Bacillus_subtilis_GN=yjcL_PE=4_SV=1	1.00E-29
comp30030_c0_seq2.p1	sp|Q9LZ98|AB20I_ARATH_ABC_transporter_I_family_member_20_OS=Arabidopsis_thaliana_GN=ABCI20_PE=2_SV=1	1.00E-61
comp30030_c0_seq3.p1		
comp30031_c0_seq1.p1		
comp30031_c0_seq4.p1		

comp30031_c0_seq4.p2				
comp30032_c0_seq1.p1	sp|P54697|MYOJ_DICDI_Myosin-J_heavy_chain_OS=Dictyostelium_discoideum_GN=myoJ_PE=4_SV=2	2.00E-139	[illegible]	[illegible]
comp30032_c0_seq2.p1	sp|Q6LA54|YF48_SCHPO_Uncharacterized_WD_repeat-containing_protein_C3H5.08c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC3H5.08c_PE=1_SV=2	7.00E-13	[illegible]	[illegible]
comp30032_c0_seq2.p2				
comp30034_c0_seq2.p1				
comp30034_c0_seq5.p1				
comp30034_c0_seq7.p1				
comp30034_c0_seq8.p1				
comp30034_c0_seq9.p1				
comp30036_c0_seq1.p1	sp|Q07647|GTR3_RAT_Solute_carrier_family_2,_facilitated_glucose_transporter_member_3_OS=Rattus_norvegicus_GN=Slc2a3_PE=1_SV=1	4.00E-14	[illegible]	[illegible]
comp30036_c0_seq6.p1	sp|Q07647|GTR3_RAT_Solute_carrier_family_2,_facilitated_glucose_transporter_member_3_OS=Rattus_norvegicus_GN=Slc2a3_PE=1_SV=1	4.00E-14	[illegible]	[illegible]
comp30038_c0_seq1.p1				
comp30038_c0_seq2.p1				
comp30038_c0_seq5.p1				
comp30039_c0_seq1.p1				
comp30039_c0_seq2.p1				
comp30040_c0_seq1.p1				
comp30040_c0_seq2.p1				
comp30040_c0_seq2.p2	sp|Q86AW9|GUAD_DICDI_Guanine_deaminase_OS=Dictyostelium_discoideum_GN=guaD_PE=1_SV=1	3.00E-118	[illegible]	[illegible]
comp30041_c0_seq1.p1				
comp30042_c0_seq1.p1				
comp30042_c1_seq3.p4				
comp30042_c2_seq1.p2				
comp30043_c0_seq2.p1				
comp30043_c1_seq1.p1				
comp30043_c1_seq2.p1	sp|O13769|ULP2_SCHPO_Ubiquitin-like-specific_protease_2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ulp2_PE=1_SV=2	3.00E-19	[illegible]	[illegible]
comp30044_c0_seq3.p1	sp|Q42523|MCCA_ARATH_Methylcrotonoyl-CoA_carboxylase_subunit_alpha,_mitochondrial_OS=Arabidopsis_thaliana_GN=MCCA_PE=1_SV=2	0	[illegible]	[illegible]
comp30045_c0_seq3.p1				
comp30045_c0_seq3.p2				
comp30045_c0_seq3.p4				
comp30046_c0_seq1.p1				
comp30046_c1_seq1.p1	sp|Q05609|CTR1_ARATH_Serine/threonine-protein_kinase_CTR1_OS=Arabidopsis_thaliana_GN=CTR1_PE=1_SV=1	3.00E-28	[illegible]	[illegible]
comp30047_c0_seq1.p1	sp|Q08BW0|OTU5A_DANRE_OTU_domain-containing_protein_5-A_OS=Danio_rerio_GN=otud5a_PE=2_SV=1	7.00E-44	[illegible]	[illegible]
comp30048_c1_seq1.p1				
comp30048_c1_seq4.p1				
comp30048_c1_seq6.p1				
comp30048_c1_seq7.p1				
comp30049_c0_seq1.p1	sp|Q9S7U9|M2K2_ARATH_Mitogen-activated_protein_kinase_kinase_2_OS=Arabidopsis_thaliana_GN=MKK2_PE=1_SV=2	1.00E-46	[illegible]	[illegible]
comp30049_c0_seq2.p1	sp|Q9S7U9|M2K2_ARATH_Mitogen-activated_protein_kinase_kinase_2_OS=Arabidopsis_thaliana_GN=MKK2_PE=1_SV=2	1.00E-46	[illegible]	[illegible]
comp30050_c0_seq11.p1				
comp30050_c0_seq11.p3				
comp30050_c0_seq11.p6				
comp30050_c0_seq14.p1				
comp30050_c0_seq14.p2				
comp30050_c0_seq18.p1				
comp30050_c0_seq18.p2				
comp30050_c0_seq18.p4				
comp30050_c0_seq4.p1				
comp30050_c0_seq4.p3				
comp30050_c0_seq4.p6				
comp30050_c0_seq4.p7				
comp30051_c0_seq1.p1	sp|Q54JC0|CMBB_DICDI_Calmodulin-binding_protein_CmbB_OS=Dictyostelium_discoideum_GN=cmbB_PE=1_SV=1	1.00E-19	[illegible]	[illegible]
comp30052_c0_seq2.p1	sp|P46595|UBC4_SCHPO_Ubiquitin-conjugating_enzyme_E2_4_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ubc4_PE=2_SV=1	2.00E-90	[illegible]	[illegible]
comp30055_c0_seq2.p1	sp|Q3TIU4|PDE12_MOUSE_2',5'-phosphodiesterase_12_OS=Mus_musculus_GN=Pde12_PE=2_SV=2	3.00E-28	[illegible]	[illegible]
comp30055_c0_seq3.p1	sp|Q3TIU4|PDE12_MOUSE_2',5'-phosphodiesterase_12_OS=Mus_musculus_GN=Pde12_PE=2_SV=2	5.00E-31	[illegible]	[illegible]
comp30055_c0_seq4.p1				
comp30056_c0_seq1.p1	sp|Q9U7D0|H4_MASBA_Histone_H4_OS=Mastigamoeba_balamuthi_PE=3_SV=3	2.00E-50	[illegible]	[illegible]
comp30056_c0_seq2.p1	sp|Q9U7D0|H4_MASBA_Histone_H4_OS=Mastigamoeba_balamuthi_PE=3_SV=3	1.00E-50	[illegible]	[illegible]
comp30056_c0_seq3.p1	sp|Q9U7D0|H4_MASBA_Histone_H4_OS=Mastigamoeba_balamuthi_PE=3_SV=3	7.00E-51	[illegible]	[illegible]
comp30057_c0_seq1.p1				
comp30057_c0_seq2.p1				
comp30057_c0_seq3.p1				
comp30057_c0_seq4.p1				
comp30057_c0_seq4.p2	sp|P10768|ESTD_HUMAN_S-formylglutathione_hydrolase_OS=Homo_sapiens_GN=ESD_PE=1_SV=2	3.00E-102	[illegible]	[illegible]
comp30058_c0_seq2.p1	sp|A1A5G2|UBP47_XENTR_Ubiquitin_carboxyl-terminal_hydrolase_47_OS=Xenopus_tropicalis_GN=usp47_PE=2_SV=1	4.00E-70	[illegible]	[illegible]
comp30059_c0_seq1.p1				
comp30060_c0_seq2.p1	sp|Q9LSM5|SGT1_ARATH_Protein_SGT1_homolog_At5g65490_OS=Arabidopsis_thaliana_GN=At5g65490_PE=2_SV=1	2.00E-55	GO:0005515,GO:0008150	[illegible]
comp30060_c0_seq2.p2				
comp30060_c0_seq3.p1				
comp30060_c0_seq5.p1	sp|Q9LSM5|SGT1_ARATH_Protein_SGT1_homolog_At5g65490_OS=Arabidopsis_thaliana_GN=At5g65490_PE=2_SV=1	3.00E-55	GO:0005515,GO:0008150	[illegible]
comp30060_c0_seq5.p2				
comp30061_c0_seq2.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	3.00E-26		
comp30061_c0_seq4.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	4.00E-26		
comp30062_c0_seq1.p1				
comp30063_c0_seq1.p1	sp|Q9LDI3|CIPKO_ARATH_CBL-interacting_serine/threonine-protein_kinase_24_OS=Arabidopsis_thaliana_GN=CIPK24_PE=1_SV=1	5.00E-117	[illegible]	[illegible]
comp30063_c0_seq2.p1				
comp30063_c1_seq1.p1	sp|Q8BYI6|PCAT2_MOUSE_Lysophosphatidylcholine_acyltransferase_2_OS=Mus_musculus_GN=Lpcat2_PE=1_SV=1	2.00E-53	[illegible]	[illegible]
comp30064_c0_seq3.p1				
comp30064_c0_seq3.p2	sp|Q8XJR3|DPO3_CLOPE_DNA_polymerase_III_polC-type_OS=Clostridium_perfringens_GN=polC_PE=3_SV=1	2.00E-12	[illegible]	[illegible]
comp30065_c2_seq1.p1				
comp30065_c2_seq2.p1				
comp30066_c0_seq3.p1				
comp30068_c0_seq2.p1				
comp30068_c0_seq4.p1	sp|Q49VP4|GTAB2_STAS1_UTP--glucose-1-phosphate_uridylyltransferase_2_OS=Staphylococcus_saprophyticus_subsp._saprophyticus_(strain_ATCC_15305_/_DSM_20229)_GN=gtaB2_PE=3_SV=1	1.00E-14	[illegible]	[illegible]
comp30068_c0_seq7.p1	sp|Q49VP4|GTAB2_STAS1_UTP--glucose-1-phosphate_uridylyltransferase_2_OS=Staphylococcus_saprophyticus_subsp._saprophyticus_(strain_ATCC_15305_/_DSM_20229)_GN=gtaB2_PE=3_SV=1	1.00E-14	[illegible]	[illegible]
comp30069_c0_seq1.p1				
comp30069_c0_seq2.p1				
comp30069_c0_seq3.p1	sp|Q91Z92|B3GT6_MOUSE_Beta-1,3-galactosyltransferase_6_OS=Mus_musculus_GN=B3galt6_PE=2_SV=1	3.00E-14	[illegible]	[illegible]
comp30070_c0_seq2.p1				
comp30071_c0_seq2.p1	sp|C0LGN2|Y3148_ARATH_Probable_leucine-rich_repeat_receptor-like_serine/threonine-protein_kinase_At3g14840_OS=Arabidopsis_thaliana_GN=LRR-RLK_PE=1_SV=1	2.00E-15	[illegible]	[illegible]
comp30073_c0_seq2.p1				
comp30073_c0_seq3.p1				
comp30074_c0_seq1.p1				
comp30074_c0_seq4.p1	sp|P0CO44|BBP_CRYNJ_Branchpoint-bridging_protein_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=BBP_PE=3_SV=1	1.00E-45	[illegible]	[illegible]
comp30074_c0_seq5.p1	sp|O43390|HNRPR_HUMAN_Heterogeneous_nuclear_ribonucleoprotein_R_OS=Homo_sapiens_GN=HNRNPR_PE=1_SV=1	1.00E-19	[illegible]	[illegible]
comp30074_c0_seq6.p1	sp|P0CO44|BBP_CRYNJ_Branchpoint-bridging_protein_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=BBP_PE=3_SV=1	1.00E-45	[illegible]	[illegible]
comp30077_c1_seq4.p1				
comp30080_c0_seq1.p1	sp|Q9FNS4|MBB1_CHLRE_PsbB_mRNA_maturation_factor_Mbb1,_chloroplastic_OS=Chlamydomonas_reinhardtii_GN=MBB1_PE=2_SV=1	6.00E-42	[illegible]	[illegible]
comp30081_c0_seq1.p1				
comp30081_c0_seq3.p1				
comp30081_c0_seq3.p2				
comp30085_c0_seq1.p1	sp|Q54TM7|DRKD_DICDI_Probable_serine/threonine-protein_kinase_drkD_OS=Dictyostelium_discoideum_GN=drkD_PE=2_SV=1	2.00E-32	[illegible]	[illegible]
comp30086_c0_seq1.p1				
comp30086_c0_seq3.p1	sp|O54956|DPOE2_MOUSE_DNA_polymerase_epsilon_subunit_2_OS=Mus_musculus_GN=Pole2_PE=2_SV=2	5.00E-102	[illegible]	[illegible]
comp30086_c0_seq5.p1	sp|O54956|DPOE2_MOUSE_DNA_polymerase_epsilon_subunit_2_OS=Mus_musculus_GN=Pole2_PE=2_SV=2	2.00E-87	[illegible]	[illegible]
comp30086_c1_seq1.p3				
comp30087_c0_seq1.p1				
comp30088_c0_seq2.p1				
comp30088_c0_seq4.p1	sp|Q5R1T0|CAF1A_CHICK_Chromatin_assembly_factor_1_subunit_A_OS=Gallus_gallus_GN=CHAF1A_PE=1_SV=1	6.00E-15	[illegible]	[illegible]
comp30089_c0_seq4.p1				
comp30089_c0_seq7.p1				
comp30091_c0_seq2.p1				
comp30091_c0_seq3.p1				
comp30092_c0_seq1.p1	sp|Q9LU89|2A5N_ARATH_Serine/threonine_protein_phosphatase_2A_59_kDa_regulatory_subunit_B'_eta_isoform_OS=Arabidopsis_thaliana_GN=B'ETA_PE=2_SV=1	6.00E-119	[illegible]	[illegible]
comp30093_c0_seq2.p1	sp|O24600|RPOT3_ARATH_DNA-directed_RNA_polymerase_3,_chloroplastic_OS=Arabidopsis_thaliana_GN=RPOT3_PE=2_SV=1	0	[illegible]	[illegible]
comp30093_c0_seq2.p2	sp|A0JM23|NPHP3_XENTR_Nephrocystin-3_OS=Xenopus_tropicalis_GN=nphp3_PE=2_SV=2	4.00E-11	[illegible]	[illegible]
comp30093_c0_seq2.p3				
comp30094_c0_seq4.p1				
comp30094_c0_seq8.p1				
comp30095_c0_seq1.p1	sp|Q94AH6|CUL1_ARATH_Cullin-1_OS=Arabidopsis_thaliana_GN=CUL1_PE=1_SV=1	0	[illegible]	[illegible]
comp30096_c0_seq1.p1				
comp30096_c0_seq2.p1				
comp30097_c0_seq1.p1	sp|Q9FMU5|UTP18_ARATH_U3_small_nucleolar_RNA-associated_protein_18_homolog_OS=Arabidopsis_thaliana_GN=At5g14050_PE=1_SV=1	1.00E-85	[illegible]	[illegible]
comp30098_c0_seq2.p1				
comp30098_c0_seq3.p2				
comp30098_c1_seq1.p1	sp|O23685|AP1S2_ARATH_AP-1_complex_subunit_sigma-2_OS=Arabidopsis_thaliana_GN=AAP19-2_PE=2_SV=1	7.00E-67	[illegible]	[illegible]
comp30098_c1_seq2.p1	sp|O23685|AP1S2_ARATH_AP-1_complex_subunit_sigma-2_OS=Arabidopsis_thaliana_GN=AAP19-2_PE=2_SV=1	4.00E-62	[illegible]	[illegible]
comp30098_c2_seq1.p1				
comp30098_c2_seq2.p1				
comp30098_c2_seq4.p1				
comp30098_c2_seq7.p1				
comp30099_c0_seq2.p2				
comp30099_c0_seq2.p3				
comp30099_c0_seq3.p1				
comp30100_c0_seq4.p1	sp|Q7SXW3|LRC40_DANRE_Leucine-rich_repeat-containing_protein_40_OS=Danio_rerio_GN=lrrc40_PE=2_SV=1	6.00E-54	GO:0005575,GO:0008150	[illegible]
comp30101_c0_seq3.p1	sp|Q05865|FOLC_BACSU_Folylpolyglutamate_synthase_OS=Bacillus_subtilis_GN=folC_PE=3_SV=2	4.00E-35	[illegible]	[illegible]
comp30101_c0_seq8.p1	sp|Q05865|FOLC_BACSU_Folylpolyglutamate_synthase_OS=Bacillus_subtilis_GN=folC_PE=3_SV=2	9.00E-32	[illegible]	[illegible]
comp30101_c1_seq2.p1				
comp30101_c1_seq3.p1				
comp30103_c0_seq2.p1				
comp30105_c0_seq2.p1				
comp30106_c0_seq1.p1				
comp30106_c0_seq1.p2				
comp30106_c0_seq2.p1				
comp30106_c0_seq2.p2				
comp30107_c0_seq1.p1	sp|Q54TH6|Y9863_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0281745_OS=Dictyostelium_discoideum_GN=DDB_G0281745_PE=3_SV=1	4.00E-37	[illegible]	[illegible]
comp30107_c0_seq2.p1				
comp30107_c0_seq5.p1	sp|Q54TH6|Y9863_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0281745_OS=Dictyostelium_discoideum_GN=DDB_G0281745_PE=3_SV=1	1.00E-38	[illegible]	[illegible]
comp30107_c0_seq5.p5				
comp30107_c0_seq6.p2				
comp30107_c0_seq8.p2				
comp30109_c0_seq2.p1				
comp30109_c0_seq2.p5				
comp30110_c0_seq1.p1	sp|P38758|TDA3_YEAST_Putative_oxidoreductase_TDA3_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TDA3_PE=1_SV=2	4.00E-13	[illegible]	[illegible]
comp30110_c1_seq12.p1	sp|Q7T0Y4|CC164_XENLA_Coiled-coil_domain-containing_protein_164_OS=Xenopus_laevis_GN=ccdc164_PE=2_SV=1	5.00E-68	[illegible]	[illegible]
comp30110_c1_seq16.p3				
comp30110_c1_seq17.p1				
comp30110_c1_seq18.p1	sp|Q7T0Y4|CC164_XENLA_Coiled-coil_domain-containing_protein_164_OS=Xenopus_laevis_GN=ccdc164_PE=2_SV=1	8.00E-12	[illegible]	[illegible]
comp30110_c1_seq2.p4				
comp30110_c1_seq21.p1	sp|Q96MC2|CC164_HUMAN_Coiled-coil_domain-containing_protein_164_OS=Homo_sapiens_GN=CCDC164_PE=2_SV=2	3.00E-13	[illegible]	[illegible]
comp30110_c1_seq29.p1				
comp30110_c1_seq30.p1	sp|Q7T0Y4|CC164_XENLA_Coiled-coil_domain-containing_protein_164_OS=Xenopus_laevis_GN=ccdc164_PE=2_SV=1	3.00E-86	[illegible]	[illegible]
comp30110_c1_seq5.p1				
comp30110_c1_seq7.p1	sp|Q7T0Y4|CC164_XENLA_Coiled-coil_domain-containing_protein_164_OS=Xenopus_laevis_GN=ccdc164_PE=2_SV=1	5.00E-73	[illegible]	[illegible]
comp30111_c0_seq2.p1				
comp30111_c0_seq2.p2				
comp30111_c1_seq1.p1				
comp30112_c0_seq1.p1	sp|Q8RXY0|Y3333_ARATH_Probable_inactive_protein_kinase_At3g63330_OS=Arabidopsis_thaliana_GN=At3g63330_PE=2_SV=1	2.00E-33	[illegible]	[illegible]
comp30112_c0_seq11.p1	sp|Q8RXY0|Y3333_ARATH_Probable_inactive_protein_kinase_At3g63330_OS=Arabidopsis_thaliana_GN=At3g63330_PE=2_SV=1	2.00E-33	[illegible]	[illegible]
comp30112_c0_seq11.p3				
comp30112_c0_seq13.p1	sp|Q8RXY0|Y3333_ARATH_Probable_inactive_protein_kinase_At3g63330_OS=Arabidopsis_thaliana_GN=At3g63330_PE=2_SV=1	1.00E-36	[illegible]	[illegible]
comp30112_c0_seq3.p1				
comp30113_c0_seq1.p1				
comp30113_c0_seq2.p1				
comp30113_c0_seq2.p4				
comp30113_c0_seq3.p1				
comp30114_c0_seq1.p1	sp|Q9JKU3|IF172_RAT_Intraflagellar_transport_protein_172_homolog_OS=Rattus_norvegicus_GN=Ift172_PE=1_SV=1	5.00E-88	[illegible]	[illegible]
comp30114_c0_seq1.p2	sp|Q5DM57|IF172_CHLRE_Intraflagellar_transport_protein_172_OS=Chlamydomonas_reinhardtii_GN=IFT172_PE=1_SV=1	2.00E-30	[illegible]	[illegible]
comp30114_c0_seq5.p1	sp|Q5RHH4|IF172_DANRE_Intraflagellar_transport_protein_172_homolog_OS=Danio_rerio_GN=ift172_PE=2_SV=1	6.00E-60	[illegible]	[illegible]
comp30114_c0_seq6.p1	sp|Q6VH22|IF172_MOUSE_Intraflagellar_transport_protein_172_homolog_OS=Mus_musculus_GN=Ift172_PE=1_SV=1	2.00E-80	[illegible]	[illegible]
comp30115_c0_seq1.p1	sp|Q9ST43|PH1_ARATH_Pleckstrin_homology_domain-containing_protein_1_OS=Arabidopsis_thaliana_GN=PH1_PE=2_SV=2	2.00E-23	[illegible]	[illegible]
comp30116_c1_seq1.p1				
comp30116_c1_seq2.p1	sp|Q9U9R7|SNAG_DICDI_Gamma-soluble_NSF_attachment_protein_OS=Dictyostelium_discoideum_GN=snpC_PE=1_SV=1	5.00E-19	[illegible]	[illegible]
comp30117_c0_seq3.p1				
comp30117_c0_seq4.p1				
comp30119_c0_seq1.p1				
comp30119_c0_seq2.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	3.00E-16	[illegible]	[illegible]
comp30119_c0_seq3.p2				
comp30123_c0_seq3.p1	sp|O34849|YERD_BACSU_Uncharacterized_membrane_protein_yerD_OS=Bacillus_subtilis_GN=yerD_PE=4_SV=1	3.00E-96	[illegible]	[illegible]
comp30124_c0_seq2.p1	sp|Q08J23|NSUN2_HUMAN_tRNA_(cytosine(34)-C(5))-methyltransferase_OS=Homo_sapiens_GN=NSUN2_PE=1_SV=2	8.00E-76	[illegible]	[illegible]
comp30128_c0_seq3.p1				
comp30129_c0_seq2.p1				
comp30130_c0_seq1.p1				
comp30131_c1_seq5.p1	sp|Q8VZG8|Y4885_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At4g08850_OS=Arabidopsis_thaliana_GN=At4g08850_PE=1_SV=3	3.00E-15	[illegible]	[illegible]
comp30132_c0_seq2.p2				
comp30132_c0_seq5.p3				
comp30133_c0_seq4.p1				
comp30133_c0_seq7.p1				
comp30133_c0_seq7.p2				
comp30133_c0_seq8.p1				
comp30134_c0_seq1.p1				
comp30134_c0_seq6.p1				
comp30136_c0_seq1.p1	sp|Q9UNX4|WDR3_HUMAN_WD_repeat-containing_protein_3_OS=Homo_sapiens_GN=WDR3_PE=1_SV=1	1.00E-25	[illegible]	[illegible]
comp30136_c0_seq3.p1	sp|Q8BHB4|WDR3_MOUSE_WD_repeat-containing_protein_3_OS=Mus_musculus_GN=Wdr3_PE=2_SV=1	6.00E-127	[illegible]	[illegible]
comp30137_c0_seq1.p1				
comp30140_c0_seq1.p1	sp|Q9RB65|PMP10_CHLPN_Probable_outer_membrane_protein_pmp10_OS=Chlamydia_pneumoniae_GN=pmp10_PE=3_SV=2	6.00E-15	[illegible]	[illegible]
comp30140_c0_seq2.p1	sp|Q9RB65|PMP10_CHLPN_Probable_outer_membrane_protein_pmp10_OS=Chlamydia_pneumoniae_GN=pmp10_PE=3_SV=2	7.00E-14	[illegible]	[illegible]
comp30142_c0_seq1.p1	sp|Q9LXD7|MYST2_ARATH_MYST-like_histone_acetyltransferase_2_OS=Arabidopsis_thaliana_GN=HAG5_PE=2_SV=1	2.00E-102	[illegible]	[illegible]
comp30142_c0_seq2.p1	sp|Q9LXD7|MYST2_ARATH_MYST-like_histone_acetyltransferase_2_OS=Arabidopsis_thaliana_GN=HAG5_PE=2_SV=1	4.00E-89	[illegible]	[illegible]
comp30142_c0_seq3.p1	sp|Q9LXD7|MYST2_ARATH_MYST-like_histone_acetyltransferase_2_OS=Arabidopsis_thaliana_GN=HAG5_PE=2_SV=1	9.00E-89	[illegible]	[illegible]
comp30142_c0_seq4.p1	sp|Q9LXD7|MYST2_ARATH_MYST-like_histone_acetyltransferase_2_OS=Arabidopsis_thaliana_GN=HAG5_PE=2_SV=1	5.00E-91	[illegible]	[illegible]
comp30142_c0_seq5.p1	sp|Q9LXD7|MYST2_ARATH_MYST-like_histone_acetyltransferase_2_OS=Arabidopsis_thaliana_GN=HAG5_PE=2_SV=1	1.00E-102	[illegible]	[illegible]
comp30142_c0_seq6.p1	sp|Q9LXD7|MYST2_ARATH_MYST-like_histone_acetyltransferase_2_OS=Arabidopsis_thaliana_GN=HAG5_PE=2_SV=1	9.00E-105	[illegible]	[illegible]
comp30145_c0_seq2.p1	sp|Q8TDN6|BRX1_HUMAN_Ribosome_biogenesis_protein_BRX1_homolog_OS=Homo_sapiens_GN=BRIX1_PE=1_SV=2	2.00E-74	[illegible]	[illegible]
comp30145_c0_seq2.p2				
comp30145_c0_seq3.p1				
comp30145_c0_seq7.p1	sp|Q9FLM3|ZDH23_ARATH_Probable_S-acyltransferase_At5g41060_OS=Arabidopsis_thaliana_GN=At5g41060_PE=2_SV=1	7.00E-30	[illegible]	[illegible]
comp30146_c0_seq1.p1				
comp30146_c0_seq3.p1				
comp30147_c0_seq1.p1				
comp30147_c0_seq3.p1				
comp30148_c0_seq2.p1	sp|P39153|YWLC_BACSU_Probable_tRNA_threonylcarbamoyladenosine_biosynthesis_protein_YwlC_OS=Bacillus_subtilis_GN=ywlC_PE=3_SV=1	6.00E-17	[illegible]	[illegible]
comp30148_c0_seq7.p1	sp|Q7Q5D4|S35B3_ANOGA_Adenosine_3'-phospho_5'-phosphosulfate_transporter_2_OS=Anopheles_gambiae_GN=Papst2_PE=3_SV=4	3.00E-56	[illegible]	[illegible]
comp30148_c0_seq7.p2	sp|P39153|YWLC_BACSU_Probable_tRNA_threonylcarbamoyladenosine_biosynthesis_protein_YwlC_OS=Bacillus_subtilis_GN=ywlC_PE=3_SV=1	4.00E-29	[illegible]	[illegible]
comp30149_c0_seq2.p1	sp|Q8RXF1|SF3A1_ARATH_Probable_splicing_factor_3A_subunit_1_OS=Arabidopsis_thaliana_GN=At1g14650_PE=1_SV=2	7.00E-47	[illegible]	[illegible]
comp30149_c0_seq2.p6				
comp30150_c0_seq2.p1				
comp30151_c0_seq2.p1				
comp30151_c0_seq2.p3	sp|Q84WM0|RL292_ARATH_60S_ribosomal_protein_L29-2_OS=Arabidopsis_thaliana_GN=RPL29B_PE=2_SV=2	7.00E-14	[illegible]	[illegible]
comp30151_c0_seq4.p1				
comp30151_c0_seq5.p1	sp|Q84WM0|RL292_ARATH_60S_ribosomal_protein_L29-2_OS=Arabidopsis_thaliana_GN=RPL29B_PE=2_SV=2	7.00E-14	[illegible]	[illegible]
comp30152_c0_seq1.p1	sp|A0JM51|CELF5_XENTR_CUGBP_Elav-like_family_member_5_OS=Xenopus_tropicalis_GN=celf5_PE=2_SV=1	3.00E-67	[illegible]	[illegible]
comp30152_c0_seq2.p3	sp|Q4R535|CELF4_MACFA_CUGBP_Elav-like_family_member_4_OS=Macaca_fascicularis_GN=CELF4_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp30153_c0_seq1.p1	sp|Q657S5|PHO11_ORYSJ_Phosphate_transporter_PHO1-1_OS=Oryza_sativa_subsp._japonica_GN=PHO1-1_PE=2_SV=2	2.00E-17	[illegible]	[illegible]
comp30154_c0_seq2.p1	sp|O05389|YRBE_BACSU_Uncharacterized_oxidoreductase_yrbE_OS=Bacillus_subtilis_GN=yrbE_PE=3_SV=2	3.00E-76	[illegible]	[illegible]
comp30154_c0_seq3.p1	sp|O05389|YRBE_BACSU_Uncharacterized_oxidoreductase_yrbE_OS=Bacillus_subtilis_GN=yrbE_PE=3_SV=2	3.00E-76	[illegible]	[illegible]
comp30154_c0_seq3.p2				
comp30154_c0_seq4.p1	sp|O05389|YRBE_BACSU_Uncharacterized_oxidoreductase_yrbE_OS=Bacillus_subtilis_GN=yrbE_PE=3_SV=2	3.00E-76	[illegible]	[illegible]
comp30155_c0_seq3.p1				
comp30155_c0_seq4.p1	sp|Q84KJ5|CRYD_ARATH_Cryptochrome_DASH,_chloroplastic/mitochondrial_OS=Arabidopsis_thaliana_GN=CRYD_PE=1_SV=2	8.00E-132	[illegible]	[illegible]
comp30156_c0_seq3.p1	sp|Q9SL76|P2C19_ARATH_Protein_phosphatase_2C_and_cyclic_nucleotide-binding/kinase_domain-containing_protein_OS=Arabidopsis_thaliana_GN=At2g20050_PE=1_SV=2	1.00E-36	[illegible]	[illegible]
comp30157_c0_seq1.p1				
comp30159_c0_seq2.p1				
comp30160_c0_seq3.p1				
comp30162_c0_seq1.p1	sp|Q641I1|F135B_XENLA_Protein_FAM135B_OS=Xenopus_laevis_GN=fam135b_PE=2_SV=1	2.00E-14		
comp30163_c0_seq1.p1				
comp30163_c0_seq1.p2	sp|O65084|PSB3_PICMA_Proteasome_subunit_beta_type-3_OS=Picea_mariana_GN=PBC1_PE=2_SV=1	1.00E-81	[illegible]	[illegible]
comp30163_c0_seq1.p3				
comp30163_c0_seq2.p1				
comp30163_c0_seq2.p2	sp|O65084|PSB3_PICMA_Proteasome_subunit_beta_type-3_OS=Picea_mariana_GN=PBC1_PE=2_SV=1	1.00E-81	[illegible]	[illegible]
comp30163_c0_seq2.p3				
comp30163_c0_seq2.p4				
comp30163_c0_seq4.p1	sp|O65084|PSB3_PICMA_Proteasome_subunit_beta_type-3_OS=Picea_mariana_GN=PBC1_PE=2_SV=1	2.00E-57	[illegible]	[illegible]
comp30164_c0_seq1.p1				
comp30164_c0_seq2.p1				
comp30165_c0_seq2.p1				
comp30165_c0_seq2.p2	sp|O94673|YG75_SCHPO_Uncharacterized_membrane_protein_C776.05_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC776.05_PE=2_SV=1	3.00E-42	[illegible]	[illegible]
comp30167_c0_seq2.p1	sp|Q94C40|CIPKH_ARATH_CBL-interacting_serine/threonine-protein_kinase_17_OS=Arabidopsis_thaliana_GN=CIPK17_PE=1_SV=1	3.00E-32	[illegible]	[illegible]
comp30167_c0_seq2.p2				
comp30172_c0_seq1.p1				
comp30173_c0_seq1.p1	sp|Q54VR8|ELMOB_DICDI_ELMO_domain-containing_protein_B_OS=Dictyostelium_discoideum_GN=elmoB_PE=4_SV=1	1.00E-33	[illegible]	[illegible]
comp30173_c0_seq2.p1	sp|P11118|CALM_EUGGR_Calmodulin_OS=Euglena_gracilis_PE=1_SV=2	8.00E-32	GO:0005509,GO:0046872	[illegible]
comp30173_c1_seq1.p1				
comp30173_c1_seq2.p1				
comp30174_c0_seq1.p1				
comp30174_c0_seq2.p1				
comp30175_c0_seq2.p1	sp|Q84N64|ARC5_ARATH_Dynamin-like_protein_ARC5_OS=Arabidopsis_thaliana_GN=ARC5_PE=1_SV=2	7.00E-164	[illegible]	[illegible]
comp30175_c0_seq2.p4				
comp30176_c0_seq1.p1				
comp30177_c0_seq3.p1	sp|Q63699|CDK2_RAT_Cyclin-dependent_kinase_2_OS=Rattus_norvegicus_GN=Cdk2_PE=1_SV=1	8.00E-118	[illegible]	[illegible]
comp30177_c0_seq6.p1	sp|P04551|CDK1_SCHPO_Cyclin-dependent_kinase_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=cdc2_PE=1_SV=1	7.00E-75	[illegible]	[illegible]
comp30178_c0_seq10.p1	sp|P32644|ECM32_YEAST_Putative_ATP-dependent_RNA_helicase_ECM32_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=ECM32_PE=1_SV=1	3.00E-15	[illegible]	[illegible]
comp30178_c0_seq10.p3				
comp30178_c0_seq2.p1	sp|Q9P2E3|ZNFX1_HUMAN_NFX1-type_zinc_finger-containing_protein_1_OS=Homo_sapiens_GN=ZNFX1_PE=1_SV=2	3.00E-19	[illegible]	[illegible]
comp30178_c0_seq3.p1	sp|Q8R151|ZNFX1_MOUSE_NFX1-type_zinc_finger-containing_protein_1_OS=Mus_musculus_GN=Znfx1_PE=2_SV=3	7.00E-31	[illegible]	[illegible]
comp30178_c0_seq4.p1				
comp30178_c0_seq6.p1	sp|Q8R151|ZNFX1_MOUSE_NFX1-type_zinc_finger-containing_protein_1_OS=Mus_musculus_GN=Znfx1_PE=2_SV=3	7.00E-35	[illegible]	[illegible]
comp30180_c0_seq1.p1				
comp30180_c0_seq2.p1				
comp30181_c0_seq1.p1				
comp30182_c0_seq3.p1	sp|O14232|YDVG_SCHPO_Uncharacterized_helicase_C6F12.16c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC6F12.16c_PE=2_SV=1	0	[illegible]	[illegible]
comp30182_c0_seq3.p2	sp|Q6DFS0|TMX2_XENTR_Thioredoxin-related_transmembrane_protein_2_OS=Xenopus_tropicalis_GN=tmx2_PE=2_SV=1	2.00E-21	[illegible]	[illegible]
comp30182_c0_seq6.p1				
comp30183_c0_seq2.p1	sp|Q9HCF6|TRPM3_HUMAN_Transient_receptor_potential_cation_channel_subfamily_M_member_3_OS=Homo_sapiens_GN=TRPM3_PE=2_SV=4	5.00E-14	[illegible]	[illegible]
comp30184_c0_seq6.p1				
comp30185_c0_seq3.p1	sp|Q8T277|PRKAG_DICDI_5'-AMP-activated_protein_kinase_subunit_gamma_OS=Dictyostelium_discoideum_GN=prkag_PE=3_SV=3	4.00E-49	[illegible]	[illegible]
comp30186_c0_seq3.p1	sp|Q75HV0|CCP31_ORYSJ_Cyclin-P3-1_OS=Oryza_sativa_subsp._japonica_GN=CYCP3-1_PE=3_SV=1	1.00E-11	[illegible]	[illegible]
comp30186_c0_seq6.p1	sp|Q75HV0|CCP31_ORYSJ_Cyclin-P3-1_OS=Oryza_sativa_subsp._japonica_GN=CYCP3-1_PE=3_SV=1	2.00E-14	[illegible]	[illegible]
comp30187_c0_seq2.p1	sp|P0AE55|BCP_SHIFL_Putative_peroxiredoxin_bcp_OS=Shigella_flexneri_GN=bcp_PE=3_SV=1	9.00E-24	[illegible]	[illegible]
comp30187_c0_seq5.p1	sp|Q75J93|CPAS1_DICDI_Circularly_permutated_Ras_protein_1_OS=Dictyostelium_discoideum_GN=cpras1_PE=3_SV=1	4.00E-44	[illegible]	[illegible]
comp30188_c0_seq1.p1				
comp30188_c0_seq10.p2				
comp30188_c0_seq8.p1				
comp30188_c0_seq8.p6				
comp30189_c0_seq1.p1	sp|A0JM23|NPHP3_XENTR_Nephrocystin-3_OS=Xenopus_tropicalis_GN=nphp3_PE=2_SV=2	1.00E-46	[illegible]	[illegible]
comp30190_c0_seq2.p1	sp|D1C8C0|FTSH4_SPHTD_ATP-dependent_zinc_metalloprotease_FtsH_4_OS=Sphaerobacter_thermophilus_(strain_DSM_20745_/_S_6022)_GN=ftsh4_PE=3_SV=1	8.00E-71	[illegible]	[illegible]
comp30191_c0_seq3.p1				
comp30191_c0_seq3.p2				
comp30192_c0_seq3.p1	sp|Q53P54|PHT46_ORYSJ_Probable_anion_transporter_6_OS=Oryza_sativa_subsp._japonica_GN=PHT4;6_PE=2_SV=1	2.00E-36	[illegible]	[illegible]
comp30192_c0_seq3.p3				
comp30192_c0_seq5.p1	sp|Q53P54|PHT46_ORYSJ_Probable_anion_transporter_6_OS=Oryza_sativa_subsp._japonica_GN=PHT4;6_PE=2_SV=1	9.00E-38	[illegible]	[illegible]
comp30192_c0_seq5.p3				
comp30192_c0_seq5.p4				
comp30193_c0_seq1.p1				
comp30194_c0_seq4.p1	sp|P25323|MYLKA_DICDI_Myosin_light_chain_kinase_A_OS=Dictyostelium_discoideum_GN=mlkA_PE=1_SV=2	1.00E-17	[illegible]	[illegible]
comp30194_c0_seq6.p1	sp|Q38870|CDPK2_ARATH_Calcium-dependent_protein_kinase_2_OS=Arabidopsis_thaliana_GN=CPK2_PE=1_SV=1	2.00E-64	[illegible]	[illegible]
comp30194_c0_seq7.p1	sp|Q9S9V0|CDPKV_ARATH_Calcium-dependent_protein_kinase_31_OS=Arabidopsis_thaliana_GN=CPK31_PE=2_SV=2	2.00E-55	[illegible]	[illegible]
comp30196_c0_seq1.p1				
comp30196_c0_seq2.p1	sp|Q17348|SMD3_CAEEL_Small_nuclear_ribonucleoprotein_Sm_D3_OS=Caenorhabditis_elegans_GN=snr-1_PE=2_SV=2	2.00E-23	[illegible]	[illegible]
comp30196_c0_seq4.p1				
comp30196_c0_seq5.p1				
comp30196_c0_seq6.p1	sp|Q17348|SMD3_CAEEL_Small_nuclear_ribonucleoprotein_Sm_D3_OS=Caenorhabditis_elegans_GN=snr-1_PE=2_SV=2	7.00E-23	[illegible]	[illegible]
comp30197_c0_seq1.p1				
comp30198_c0_seq2.p1				
comp30198_c0_seq3.p1	sp|Q6PGP7|TTC37_HUMAN_Tetratricopeptide_repeat_protein_37_OS=Homo_sapiens_GN=TTC37_PE=1_SV=1	1.00E-19	[illegible]	[illegible]
comp30199_c0_seq1.p1	sp|Q0P4U8|SMAL1_XENTR_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A-like_protein_1_OS=Xenopus_tropicalis_GN=smarcal1_PE=2_SV=1	5.00E-74	[illegible]	[illegible]
comp30199_c0_seq2.p1	sp|B2ZFP3|SMAL1_DANRE_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A-like_protein_1_OS=Danio_rerio_GN=smarcal1_PE=2_SV=1	7.00E-30	[illegible]	[illegible]
comp30200_c0_seq1.p1				
comp30200_c0_seq3.p1				
comp30201_c0_seq1.p1				
comp30201_c0_seq5.p1	sp|Q7XJS0|ASHR1_ARATH_Histone-lysine_N-methyltransferase_ASHR1_OS=Arabidopsis_thaliana_GN=ASHR1_PE=2_SV=2	4.00E-15	[illegible]	[illegible]
comp30203_c0_seq2.p1				
comp30203_c0_seq4.p1				
comp30203_c0_seq5.p1				
comp30205_c0_seq1.p1				
comp30205_c0_seq3.p1				
comp30206_c0_seq2.p1	sp|Q80TN5|ZDH17_MOUSE_Palmitoyltransferase_ZDHHC17_OS=Mus_musculus_GN=Zdhhc17_PE=1_SV=2	2.00E-62	[illegible]	[illegible]
comp30207_c0_seq2.p1	sp|Q01490|PPIB_ORPSP_Peptidyl-prolyl_cis-trans_isomerase_B_OS=Orpinomyces_sp._(strain_PC-2)_GN=CYPB_PE=1_SV=1	1.00E-35	[illegible]	[illegible]
comp30207_c0_seq3.p1	sp|Q9TW32|PPIB_DICDI_Peptidyl-prolyl_cis-trans_isomerase_B_OS=Dictyostelium_discoideum_GN=cypB_PE=1_SV=1	3.00E-22	[illegible]	[illegible]
comp30207_c0_seq5.p1	sp|Q01490|PPIB_ORPSP_Peptidyl-prolyl_cis-trans_isomerase_B_OS=Orpinomyces_sp._(strain_PC-2)_GN=CYPB_PE=1_SV=1	1.00E-35	[illegible]	[illegible]
comp30209_c0_seq2.p1				
comp30209_c0_seq3.p1				
comp30210_c0_seq1.p1				
comp30211_c0_seq1.p2				
comp30211_c0_seq2.p2				
comp30212_c0_seq1.p1	sp|Q9TSV6|VATG2_PIG_V-type_proton_ATPase_subunit_G_2_OS=Sus_scrofa_GN=ATP6V1G2_PE=3_SV=1	1.00E-14	[illegible]	[illegible]
comp30214_c0_seq4.p1				
comp30214_c1_seq2.p1				
comp30214_c1_seq3.p2				
comp30214_c2_seq1.p1				
comp30215_c0_seq1.p2				
comp30215_c0_seq2.p1				

comp30216_c0_seq1.p1	sp|Q9BY12|SCAPE_HUMAN_S_phase_cyclin_A-associated_protein_in_the_endoplasmic_reticulum_OS=Homo_sapiens_GN=SCAPER_PE=1_SV=1	3.00E-13	[illegible]	[illegible]
comp30217_c0_seq1.p1	sp|P94026|RBCMT_TOBAC_Ribulose-1,5_bisphosphate_carboxylase/oxygenase_large_subunit_N-methyltransferase,_chloroplastic_OS=Nicotiana_tabacum_GN=RBCMT_PE=2_SV=1	8.00E-41	[illegible]	[illegible]
comp30217_c0_seq2.p1	sp|Q43088|RBCMT_PEA_Ribulose-1,5_bisphosphate_carboxylase/oxygenase_large_subunit_N-methyltransferase,_chloroplastic_OS=Pisum_sativum_GN=RBCMT_PE=1_SV=1	6.00E-13	[illegible]	[illegible]
comp30217_c0_seq2.p2	sp|P94026|RBCMT_TOBAC_Ribulose-1,5_bisphosphate_carboxylase/oxygenase_large_subunit_N-methyltransferase,_chloroplastic_OS=Nicotiana_tabacum_GN=RBCMT_PE=2_SV=1	6.00E-20	[illegible]	[illegible]
comp30217_c0_seq4.p1	sp|P94026|RBCMT_TOBAC_Ribulose-1,5_bisphosphate_carboxylase/oxygenase_large_subunit_N-methyltransferase,_chloroplastic_OS=Nicotiana_tabacum_GN=RBCMT_PE=2_SV=1	8.00E-14	[illegible]	[illegible]
comp30217_c0_seq4.p2	sp|P94026|RBCMT_TOBAC_Ribulose-1,5_bisphosphate_carboxylase/oxygenase_large_subunit_N-methyltransferase,_chloroplastic_OS=Nicotiana_tabacum_GN=RBCMT_PE=2_SV=1	6.00E-20	[illegible]	[illegible]
comp30218_c0_seq1.p1	sp|Q7RTR2|NLRC3_HUMAN_Protein_NLRC3_OS=Homo_sapiens_GN=NLRC3_PE=2_SV=2	3.00E-43	[illegible]	[illegible]
comp30220_c0_seq1.p1	sp|Q60HE6|MRE11_MACFA_Double-strand_break_repair_protein_MRE11A_OS=Macaca_fascicularis_GN=MRE11A_PE=2_SV=1	2.00E-51	[illegible]	[illegible]
comp30220_c0_seq3.p1	sp|Q61216|MRE11_MOUSE_Double-strand_break_repair_protein_MRE11A_OS=Mus_musculus_GN=Mre11a_PE=2_SV=1	5.00E-132	[illegible]	[illegible]
comp30220_c0_seq4.p1	sp|Q9XGM2|MRE11_ARATH_Double-strand_break_repair_protein_MRE11_OS=Arabidopsis_thaliana_GN=MRE11_PE=2_SV=1	3.00E-45	[illegible]	[illegible]
comp30221_c0_seq1.p1				
comp30221_c0_seq2.p1				
comp30222_c0_seq1.p1	sp|Q54GD3|NPL4_DICDI_Nuclear_protein_localization_protein_4_homolog_OS=Dictyostelium_discoideum_GN=nploc4_PE=3_SV=1	1.00E-17	GO:0003674,GO:0005783,GO:0030433,GO:0042175,GO:0043161	[illegible]
comp30222_c0_seq1.p7				
comp30223_c0_seq1.p1				
comp30223_c0_seq2.p1				
comp30224_c0_seq1.p1				
comp30224_c0_seq2.p1				
comp30224_c0_seq3.p1				
comp30226_c0_seq1.p1				
comp30226_c0_seq4.p1				
comp30227_c1_seq1.p1				
comp30227_c2_seq2.p1				
comp30227_c2_seq4.p1				
comp30228_c0_seq1.p1				
comp30228_c0_seq3.p1				
comp30229_c0_seq1.p1	sp|Q9FVX1|GRXC3_ARATH_Glutaredoxin-C3_OS=Arabidopsis_thaliana_GN=GRXC3_PE=2_SV=1	6.00E-15	[illegible]	[illegible]
comp30229_c0_seq2.p2	sp|Q9FVX1|GRXC3_ARATH_Glutaredoxin-C3_OS=Arabidopsis_thaliana_GN=GRXC3_PE=2_SV=1	3.00E-15	[illegible]	[illegible]
comp30231_c0_seq1.p1	sp|Q9UU99|YJX4_SCHPO_CRAL-TRIO_domain-containing_protein_C23B6.04c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC23B6.04c_PE=1_SV=1	4.00E-17	[illegible]	[illegible]
comp30231_c0_seq2.p1				
comp30231_c0_seq2.p2				
comp30233_c0_seq3.p1	sp|Q8R2R6|MTG1_MOUSE_Mitochondrial_GTPase_1_OS=Mus_musculus_GN=Mtg1_PE=2_SV=2	6.00E-36	[illegible]	[illegible]
comp30234_c0_seq1.p1	sp|Q27256|WHITE_ANOGA_Protein_white_OS=Anopheles_gambiae_GN=w_PE=2_SV=1	5.00E-75	[illegible]	[illegible]
comp30235_c0_seq2.p1	sp|Q9BTV6|WDR85_HUMAN_WD_repeat-containing_protein_85_OS=Homo_sapiens_GN=WDR85_PE=2_SV=2	1.00E-35	GO:0017183,GO:0017183	[illegible]
comp30236_c0_seq1.p1				
comp30236_c0_seq3.p1	sp|Q10181|YAW6_SCHPO_Uncharacterized_protein_C3F10.06c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC3F10.06c_PE=2_SV=1	4.00E-12	GO:0005634,GO:0005737,GO:0005829,GO:0016763,GO:0019988,GO:0043399	[illegible]
comp30236_c0_seq5.p1	sp|Q10181|YAW6_SCHPO_Uncharacterized_protein_C3F10.06c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC3F10.06c_PE=2_SV=1	1.00E-39	GO:0005634,GO:0005737,GO:0005829,GO:0016763,GO:0019988,GO:0043399	[illegible]
comp30236_c0_seq8.p1				
comp30237_c0_seq1.p1	sp|Q5XIL3|RPC3_RAT_DNA-directed_RNA_polymerase_III_subunit_RPC3_OS=Rattus_norvegicus_GN=Polr3c_PE=2_SV=1	3.00E-20	[illegible]	[illegible]
comp30237_c0_seq2.p1				
comp30237_c0_seq3.p1	sp|Q5XIL3|RPC3_RAT_DNA-directed_RNA_polymerase_III_subunit_RPC3_OS=Rattus_norvegicus_GN=Polr3c_PE=2_SV=1	8.00E-25	[illegible]	[illegible]
comp30239_c0_seq1.p1	sp|Q55GU0|Y9955_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0267514_OS=Dictyostelium_discoideum_GN=DDB_G0267514_PE=3_SV=1	6.00E-33	[illegible]	[illegible]
comp30239_c1_seq1.p1	sp|Q9ZU38|RPIA_ARATH_Probable_ribose-5-phosphate_isomerase_OS=Arabidopsis_thaliana_GN=At2g01290_PE=2_SV=1	6.00E-58	[illegible]	[illegible]
comp30240_c0_seq2.p1				
comp30240_c0_seq3.p1				
comp30240_c1_seq1.p1				
comp30241_c0_seq4.p1	sp|P54926|IMP1_SOLLC_Inositol_monophosphatase_1_OS=Solanum_lycopersicum_GN=IMP1_PE=2_SV=1	3.00E-27	[illegible]	[illegible]
comp30241_c0_seq9.p1	sp|Q9M8S8|VTC4_ARATH_Inositol-phosphate_phosphatase_OS=Arabidopsis_thaliana_GN=VTC4_PE=1_SV=1	1.00E-50	[illegible]	[illegible]
comp30242_c1_seq5.p1	sp|O27296|QUED_METTH_Putative_6-carboxy-5,6,7,8-tetrahydropterin_synthase_OS=Methanothermobacter_thermautotrophicus_(strain_ATCC_29096_/_DSM_1053_/_JCM_10044_/_NBRC_100330_/_Delta_H)_GN=queD_PE=3_SV=1	5.00E-14	GO:0008152,GO:0016829,GO:0046872	[illegible]
comp30243_c0_seq1.p1				
comp30243_c0_seq2.p1				
comp30244_c0_seq2.p1	sp|Q97ZC4|NADA_SULSO_Quinolinate_synthase_A_OS=Sulfolobus_solfataricus_(strain_ATCC_35092_/_DSM_1617_/_JCM_11322_/_P2)_GN=nadA_PE=3_SV=1	2.00E-11	[illegible]	[illegible]
comp30244_c0_seq3.p1				
comp30244_c0_seq4.p1				
comp30244_c3_seq4.p1	sp|Q92359|YDHE_SCHPO_Pumilio_domain-containing_protein_C6G9.14_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC6G9.14_PE=2_SV=1	9.00E-74	GO:0000288,GO:0003723,GO:0003729,GO:0005737,GO:0005829	[illegible]
comp30245_c0_seq2.p1				
comp30245_c0_seq2.p2	sp|P51135|UCRI5_TOBAC_Cytochrome_b-c1_complex_subunit_Rieske-5,_mitochondrial_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-69	[illegible]	[illegible]
comp30246_c0_seq2.p1	sp|Q9WTK3|GPAA1_MOUSE_Glycosylphosphatidylinositol_anchor_attachment_1_protein_OS=Mus_musculus_GN=Gpaa1_PE=1_SV=3	3.00E-18	[illegible]	[illegible]
comp30248_c0_seq2.p1	sp|Q8BIW9|CTF18_MOUSE_Chromosome_transmission_fidelity_protein_18_homolog_OS=Mus_musculus_GN=Chtf18_PE=2_SV=2	2.00E-86	[illegible]	[illegible]
comp30249_c0_seq1.p1				
comp30249_c0_seq2.p1	sp|Q7D8I1|PKS18_MYCTU_Alpha-pyrone_synthesis_polyketide_synthase-like_Pks18_OS=Mycobacterium_tuberculosis_GN=pks18_PE=1_SV=1	6.00E-40		
comp30249_c0_seq2.p5	sp|Q9SLX9|VPS_PSINU_Phloroisovalerophenone_synthase_OS=Psilotum_nudum_GN=VPS_PE=2_SV=1	2.00E-14	[illegible]	[illegible]
comp30249_c0_seq3.p1				
comp30249_c0_seq4.p1				
comp30250_c0_seq2.p1	sp|P62630|EF1A1_RAT_Elongation_factor_1-alpha_1_OS=Rattus_norvegicus_GN=Eef1a1_PE=1_SV=1	0	[illegible]	[illegible]
comp30250_c0_seq3.p1	sp|P62630|EF1A1_RAT_Elongation_factor_1-alpha_1_OS=Rattus_norvegicus_GN=Eef1a1_PE=1_SV=1	0	[illegible]	[illegible]
comp30252_c0_seq3.p1				
comp30253_c0_seq2.p1				
comp30254_c0_seq11.p1				
comp30254_c0_seq11.p3				
comp30254_c0_seq12.p1				
comp30254_c0_seq12.p2				
comp30254_c0_seq13.p1				
comp30254_c0_seq13.p2				
comp30254_c0_seq14.p1				
comp30254_c0_seq19.p1				
comp30254_c0_seq19.p3				
comp30254_c0_seq22.p1				
comp30254_c0_seq24.p1				
comp30254_c0_seq24.p2				
comp30254_c0_seq25.p1				
comp30254_c0_seq5.p1				
comp30254_c0_seq6.p1				
comp30254_c0_seq6.p3				
comp30254_c0_seq7.p1				
comp30254_c0_seq9.p1				
comp30256_c0_seq4.p1				
comp30256_c0_seq6.p1				
comp30257_c0_seq1.p1				
comp30257_c0_seq4.p1				
comp30257_c0_seq4.p3				
comp30257_c1_seq1.p1				
comp30257_c1_seq1.p2	sp|Q68W89|RL24_RICTY_50S_ribosomal_protein_L24_OS=Rickettsia_typhi_(strain_ATCC_VR-144_/_Wilmington)_GN=rplX_PE=3_SV=1	2.00E-23	[illegible]	[illegible]
comp30257_c2_seq1.p1	sp|Q9FG93|MNS4_ARATH_Probable_alpha-mannosidase_I_MNS4_OS=Arabidopsis_thaliana_GN=MNS4_PE=2_SV=1	4.00E-82	[illegible]	[illegible]
comp30259_c0_seq1.p1				
comp30259_c0_seq2.p1				
comp30259_c0_seq4.p1				
comp30259_c0_seq4.p2				
comp30260_c0_seq1.p1				
comp30260_c0_seq1.p6				
comp30261_c0_seq1.p1				
comp30261_c0_seq1.p2				
comp30261_c0_seq11.p1				
comp30261_c0_seq11.p2				
comp30261_c0_seq12.p1				
comp30261_c0_seq12.p2				
comp30261_c0_seq12.p3				
comp30261_c0_seq3.p1				
comp30261_c0_seq3.p2				
comp30261_c0_seq4.p1				
comp30261_c0_seq4.p2				
comp30261_c0_seq7.p1				
comp30261_c0_seq8.p1				
comp30261_c0_seq9.p1				
comp30262_c0_seq2.p2				
comp30264_c0_seq1.p1	sp|Q812A3|ANR23_MOUSE_Ankyrin_repeat_domain-containing_protein_23_OS=Mus_musculus_GN=Ankrd23_PE=2_SV=1	3.00E-28	[illegible]	[illegible]
comp30264_c0_seq1.p3				
comp30264_c0_seq3.p1	sp|Q8LEK4|TRL21_ARATH_Thioredoxin-like_2-1,_chloroplastic_OS=Arabidopsis_thaliana_GN=At4g26160_PE=2_SV=2	3.00E-14	[illegible]	[illegible]
comp30265_c0_seq11.p1	sp|Q8BKC5|IPO5_MOUSE_Importin-5_OS=Mus_musculus_GN=Ipo5_PE=1_SV=3	4.00E-74	[illegible]	[illegible]
comp30265_c0_seq11.p3				
comp30265_c0_seq3.p1	sp|Q8BKC5|IPO5_MOUSE_Importin-5_OS=Mus_musculus_GN=Ipo5_PE=1_SV=3	1.00E-39	[illegible]	[illegible]
comp30265_c0_seq3.p2				
comp30265_c0_seq4.p1				
comp30265_c0_seq7.p1				
comp30266_c0_seq3.p1				
comp30266_c0_seq3.p2				
comp30267_c0_seq2.p1	sp|Q9EPE9|AT131_MOUSE_Probable_cation-transporting_ATPase_13A1_OS=Mus_musculus_GN=Atp13a1_PE=1_SV=2	2.00E-19	[illegible]	[illegible]
comp30267_c0_seq3.p1	sp|P90747|YE56_CAEEL_Probable_cation-transporting_ATPase_C10C6.6_OS=Caenorhabditis_elegans_GN=C10C6.6_PE=2_SV=3	1.00E-39	[illegible]	[illegible]
comp30267_c0_seq5.p1	sp|Q9LT02|ATY1_ARATH_Probable_cation-transporting_ATPase_OS=Arabidopsis_thaliana_GN=At5g23630_PE=2_SV=1	1.00E-49	[illegible]	[illegible]
comp30268_c0_seq1.p1				
comp30268_c0_seq1.p2	sp|A0RR75|RIBA_CAMFF_GTP_cyclohydrolase-2_OS=Campylobacter_fetus_subsp._fetus_(strain_82-40)_GN=ribA_PE=3_SV=1	1.00E-54	[illegible]	[illegible]
comp30269_c0_seq1.p1				
comp30269_c0_seq3.p1				
comp30270_c0_seq2.p1				
comp30270_c0_seq3.p1				
comp30271_c0_seq1.p1	sp|Q6DW75|DGDG2_SOYBN_Digalactosyldiacylglycerol_synthase_2,_chloroplastic_OS=Glycine_max_GN=DGD2_PE=2_SV=1	3.00E-17	[illegible]	[illegible]
comp30271_c1_seq1.p1				
comp30271_c1_seq2.p1	sp|Q6DW73|DGDG2_LOTJA_Digalactosyldiacylglycerol_synthase_2,_chloroplastic_OS=Lotus_japonicus_GN=DGD2_PE=2_SV=1	7.00E-78	[illegible]	[illegible]
comp30271_c1_seq4.p1				
comp30271_c1_seq5.p1				
comp30272_c0_seq1.p1				
comp30273_c0_seq1.p1	sp|Q90YB1|DNLI4_CHICK_DNA_ligase_4_OS=Gallus_gallus_GN=LIG4_PE=2_SV=2	6.00E-31	[illegible]	[illegible]
comp30273_c0_seq4.p1	sp|Q90YB1|DNLI4_CHICK_DNA_ligase_4_OS=Gallus_gallus_GN=LIG4_PE=2_SV=2	1.00E-58	[illegible]	[illegible]
comp30273_c0_seq5.p1				
comp30274_c0_seq2.p1				
comp30274_c0_seq2.p2				
comp30274_c0_seq5.p1				
comp30274_c0_seq5.p2				
comp30275_c0_seq1.p1				
comp30275_c1_seq1.p1	sp|Q54GV8|Y8625_DICDI_Uncharacterized_transmembrane_protein_DDB_G0289901_OS=Dictyostelium_discoideum_GN=DDB_G0289901_PE=4_SV=1	9.00E-14	GO:0003674,GO:0005575,GO:0008150,GO:0016020,GO:0016020,GO:0016021	[illegible]
comp30276_c0_seq4.p1	sp|Q74GW7|TTCA_GEOSL_tRNA_2-thiocytidine_biosynthesis_protein_TtcA_OS=Geobacter_sulfurreducens_(strain_ATCC_51573_/_DSM_12127_/_PCA)_GN=ttcA_PE=3_SV=1	9.00E-44	[illegible]	[illegible]
comp30278_c0_seq10.p1				
comp30278_c0_seq10.p2				
comp30278_c0_seq2.p1				
comp30278_c0_seq2.p2				
comp30278_c0_seq3.p1	sp|Q5QN75|M2K1_ORYSJ_Mitogen-activated_protein_kinase_kinase_1_OS=Oryza_sativa_subsp._japonica_GN=MEK1_PE=1_SV=1	2.00E-29	[illegible]	[illegible]
comp30278_c0_seq8.p1	sp|Q8CGU4|AGAP2_RAT_Arf-GAP_with_GTPase,_ANK_repeat_and_PH_domain-containing_protein_2_OS=Rattus_norvegicus_GN=Agap2_PE=1_SV=1	3.00E-26	[illegible]	[illegible]
comp30279_c0_seq3.p1				
comp30279_c0_seq4.p1	sp|Q8TX03|PAN_METKA_Proteasome-activating_nucleotidase_OS=Methanopyrus_kandleri_(strain_AV19_/_DSM_6324_/_JCM_9639_/_NBRC_100938)_GN=pan_PE=3_SV=1	7.00E-33	[illegible]	[illegible]
comp30280_c0_seq1.p1	sp|Q9V242|CSD_PYRAB_Probable_cysteine_desulfurase_OS=Pyrococcus_abyssi_(strain_GE5_/_Orsay)_GN=csd_PE=3_SV=1	5.00E-41	GO:0003824,GO:0008152,GO:0016740,GO:0030170,GO:0031071	[illegible]
comp30280_c0_seq1.p2				
comp30280_c0_seq1.p3	sp|O96552|CHMP1_DICDI_Charged_multivesicular_body_protein_1_OS=Dictyostelium_discoideum_GN=chmp1_PE=3_SV=1	4.00E-60	[illegible]	[illegible]
comp30283_c0_seq3.p1				
comp30283_c0_seq4.p1	sp|Q76NT0|MRM1_DICDI_Mitochondrial_rRNA_methyltransferase_OS=Dictyostelium_discoideum_GN=mrm1_PE=3_SV=1	5.00E-37	[illegible]	[illegible]
comp30283_c0_seq4.p2				
comp30283_c0_seq4.p3	sp|Q86CR6|ATG12_DICDI_Ubiquitin-like_protein_atg12_OS=Dictyostelium_discoideum_GN=atg12_PE=3_SV=1	2.00E-15	[illegible]	[illegible]
comp30284_c0_seq2.p1				
comp30284_c0_seq2.p4				
comp30284_c0_seq3.p1				
comp30284_c0_seq6.p1				
comp30284_c0_seq9.p1	sp|Q75IP6|KU80_ORYSJ_ATP-dependent_DNA_helicase_2_subunit_KU80_OS=Oryza_sativa_subsp._japonica_GN=KU80_PE=1_SV=1	3.00E-55	[illegible]	[illegible]
comp30285_c0_seq1.p1	sp|Q6CGG3|FKBP2_YARLI_FK506-binding_protein_2_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=FPR2_PE=3_SV=1	6.00E-20	[illegible]	[illegible]
comp30285_c0_seq3.p1				
comp30286_c0_seq3.p1				
comp30286_c0_seq8.p1				
comp30288_c0_seq2.p1				
comp30289_c0_seq2.p1				
comp30289_c0_seq2.p2				
comp30291_c1_seq1.p1				
comp30291_c2_seq1.p1				
comp30291_c2_seq2.p1				
comp30291_c3_seq1.p1	sp|Q3SWY8|ZUFSP_BOVIN_Zinc_finger_with_UFM1-specific_peptidase_domain_protein_OS=Bos_taurus_GN=ZUFSP_PE=2_SV=1	1.00E-13	GO:0046872,GO:0046872	[illegible]
comp30291_c3_seq1.p2				
comp30292_c1_seq1.p1	sp|Q03516|RSN1_YEAST_Uncharacterized_protein_RSN1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=RSN1_PE=1_SV=1	3.00E-25	[illegible]	[illegible]
comp30292_c1_seq1.p2				
comp30293_c0_seq1.p1				
comp30294_c0_seq2.p1				
comp30294_c0_seq3.p1				
comp30295_c0_seq1.p1				
comp30296_c0_seq4.p1	sp|Q9SD88|ASTER_ARATH_Protein_Asterix_OS=Arabidopsis_thaliana_GN=At5g07960_PE=2_SV=1	2.00E-12	GO:0006661,GO:0008150,GO:0016020,GO:0016020,GO:0016021	[illegible]
comp30297_c1_seq1.p1	sp|Q5QQ53|XYLT_DROPS_Xylosyltransferase_oxt_OS=Drosophila_pseudoobscura_pseudoobscura_GN=oxt_PE=2_SV=1	1.00E-17	[illegible]	[illegible]
comp30297_c1_seq3.p1				
comp30298_c0_seq11.p1				
comp30298_c0_seq2.p1	sp|P40556|YIA6_YEAST_Mitochondrial_nicotinamide_adenine_dinucleotide_transporter_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YIA6_PE=1_SV=1	9.00E-49	[illegible]	[illegible]
comp30298_c0_seq5.p1				
comp30298_c0_seq5.p2				
comp30298_c0_seq7.p1				
comp30298_c0_seq7.p2				
comp30298_c0_seq9.p1				
comp30299_c0_seq1.p1	sp|C0LGQ5|GSO1_ARATH_LRR_receptor-like_serine/threonine-protein_kinase_GSO1_OS=Arabidopsis_thaliana_GN=GSO1_PE=2_SV=1	5.00E-33	[illegible]	[illegible]
comp30300_c0_seq2.p1	sp|Q54IP0|DNJC7_DICDI_DnaJ_homolog_subfamily_C_member_7_homolog_OS=Dictyostelium_discoideum_GN=dnajc7_PE=1_SV=1	1.00E-74	GO:0045335	[illegible]
comp30301_c0_seq2.p1				
comp30301_c0_seq4.p1	sp|B9RAJ0|DNPEP_RICCO_Probable_aspartyl_aminopeptidase_OS=Ricinus_communis_GN=RCOM_1506700_PE=2_SV=2	6.00E-151	[illegible]	[illegible]
comp30302_c0_seq1.p1				
comp30302_c0_seq2.p1				
comp30303_c0_seq1.p1				
comp30303_c0_seq10.p1				
comp30303_c0_seq2.p1				
comp30303_c0_seq5.p1				
comp30303_c0_seq5.p2				
comp30303_c0_seq7.p1				
comp30304_c0_seq3.p1				
comp30304_c0_seq3.p2				
comp30304_c0_seq5.p1				
comp30305_c0_seq3.p1	sp|Q6NS38|ALKB2_HUMAN_Alpha-ketoglutarate-dependent_dioxygenase_alkB_homolog_2_OS=Homo_sapiens_GN=ALKBH2_PE=1_SV=1	1.00E-20	[illegible]	[illegible]
comp30305_c0_seq4.p1	sp|Q6NS38|ALKB2_HUMAN_Alpha-ketoglutarate-dependent_dioxygenase_alkB_homolog_2_OS=Homo_sapiens_GN=ALKBH2_PE=1_SV=1	5.00E-15	[illegible]	[illegible]
comp30306_c0_seq1.p3				
comp30306_c0_seq2.p3				
comp30307_c0_seq1.p1				
comp30307_c0_seq3.p1				
comp30309_c0_seq1.p1				
comp30311_c0_seq3.p1				
comp30311_c0_seq4.p1				
comp30312_c0_seq1.p1				
comp30312_c0_seq3.p1				
comp30313_c1_seq1.p1	sp|Q9JLG8|CAN15_MOUSE_Calpain-15_OS=Mus_musculus_GN=Solh_PE=1_SV=1	1.00E-13	[illegible]	[illegible]
comp30313_c1_seq5.p1	sp|Q9JLG8|CAN15_MOUSE_Calpain-15_OS=Mus_musculus_GN=Solh_PE=1_SV=1	6.00E-14	[illegible]	[illegible]
comp30314_c0_seq1.p1				
comp30315_c1_seq1.p2				
comp30315_c1_seq1.p3	sp|P0CS14|DDI1_CRYNJ_DNA_damage-inducible_protein_1_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=DDI1_PE=3_SV=1	2.00E-16	GO:0004190,GO:0005737,GO:0005737,GO:0006508,GO:0006810,GO:0015031	[illegible]
comp30315_c1_seq2.p1				
comp30316_c0_seq4.p1				
comp30316_c0_seq4.p4	sp|O26715|OGT_METTH_Methylated-DNA--protein-cysteine_methyltransferase_OS=Methanothermobacter_thermautotrophicus_(strain_ATCC_29096_/_DSM_1053_/_JCM_10044_/_NBRC_100330_/_Delta_H)_GN=ogt_PE=3_SV=1	1.00E-15	[illegible]	[illegible]
comp30317_c0_seq2.p1				
comp30318_c0_seq2.p1	sp|O00566|MPP10_HUMAN_U3_small_nucleolar_ribonucleoprotein_protein_MPP10_OS=Homo_sapiens_GN=MPHOSPH10_PE=1_SV=2	1.00E-35	[illegible]	[illegible]
comp30318_c0_seq2.p2	sp|Q0ANR7|RS5_MARMM_30S_ribosomal_protein_S5_OS=Maricaulis_maris_(strain_MCS10)_GN=rpsE_PE=3_SV=1	5.00E-25	[illegible]	[illegible]
comp30320_c0_seq4.p1				
comp30321_c0_seq2.p1	sp|Q62940|NEDD4_RAT_E3_ubiquitin-protein_ligase_NEDD4_OS=Rattus_norvegicus_GN=Nedd4_PE=1_SV=1	6.00E-19	[illegible]	[illegible]
comp30321_c0_seq3.p1	sp|Q62940|NEDD4_RAT_E3_ubiquitin-protein_ligase_NEDD4_OS=Rattus_norvegicus_GN=Nedd4_PE=1_SV=1	2.00E-19	[illegible]	[illegible]
comp30322_c0_seq5.p1	sp|Q8C0S1|DI3L1_MOUSE_DIS3-like_exonuclease_1_OS=Mus_musculus_GN=Dis3l_PE=2_SV=2	2.00E-88	[illegible]	[illegible]
comp30322_c0_seq6.p1				
comp30322_c0_seq8.p1				
comp30324_c0_seq1.p1	sp|P41891|GAR2_SCHPO_Protein_gar2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=gar2_PE=1_SV=2	5.00E-15	[illegible]	[illegible]
comp30324_c0_seq5.p1				
comp30326_c1_seq2.p1	sp|Q9NVI1|FANCI_HUMAN_Fanconi_anemia_group_I_protein_OS=Homo_sapiens_GN=FANCI_PE=1_SV=4	3.00E-20	[illegible]	[illegible]
comp30328_c0_seq1.p1				
comp30330_c0_seq1.p1				
comp30330_c0_seq3.p1				
comp30330_c0_seq4.p1				
comp30331_c0_seq1.p1				
comp30332_c0_seq1.p1	sp|Q1MTP1|THP3_SCHPO_THP3_homolog_C2A9.11c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC2A9.11c_PE=3_SV=1	1.00E-61	[illegible]	[illegible]
comp30332_c0_seq2.p1	sp|Q1MTP1|THP3_SCHPO_THP3_homolog_C2A9.11c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC2A9.11c_PE=3_SV=1	2.00E-52	[illegible]	[illegible]
comp30334_c1_seq1.p1				
comp30335_c0_seq2.p1	sp|P34101|FHKC_DICDI_Probable_serine/threonine-protein_kinase_fhkC_OS=Dictyostelium_discoideum_GN=fhkC_PE=3_SV=2	7.00E-44	[illegible]	[illegible]
comp30336_c0_seq1.p1				
comp30336_c0_seq7.p1				
comp30336_c0_seq8.p1				
comp30336_c0_seq9.p1				
comp30336_c0_seq9.p3				
comp30338_c0_seq2.p1	sp|Q8VBT9|ASPC1_MOUSE_Tether_containing_UBX_domain_for_GLUT4_OS=Mus_musculus_GN=Aspscr1_PE=1_SV=1	5.00E-13	[illegible]	[illegible]
comp30340_c0_seq1.p1				
comp30340_c0_seq4.p1				
comp30341_c0_seq1.p2	sp|Q7SXR3|MAEA_DANRE_Macrophage_erythroblast_attacher_OS=Danio_rerio_GN=maea_PE=2_SV=2	9.00E-26	[illegible]	[illegible]
comp30341_c0_seq1.p3				
comp30341_c2_seq1.p1	sp|Q55GE2|ODC_DICDI_Probable_mitochondrial_2-oxodicarboxylate_carrier_OS=Dictyostelium_discoideum_GN=mcfT_PE=3_SV=1	7.00E-68	[illegible]	[illegible]
comp30342_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	1.00E-11		
comp30343_c0_seq16.p1	sp|Q8Z8H8|COBD_SALTI_Threonine-phosphate_decarboxylase_OS=Salmonella_typhi_GN=cobD_PE=3_SV=1	3.00E-13	[illegible]	[illegible]
comp30343_c0_seq16.p2				
comp30344_c0_seq3.p1	sp|Q10MN8|C3H21_ORYSJ_Putative_zinc_finger_CCCH_domain-containing_protein_21_OS=Oryza_sativa_subsp._japonica_GN=Os03g0301500_PE=4_SV=1	9.00E-12	GO:0003677,GO:0046872,GO:0046872	[illegible]
comp30345_c1_seq1.p1				
comp30345_c1_seq2.p1				
comp30347_c0_seq1.p1	sp|Q8NX11|RECG_STAAW_ATP-dependent_DNA_helicase_recG_OS=Staphylococcus_aureus_(strain_MW2)_GN=recG_PE=3_SV=1	4.00E-83	[illegible]	[illegible]
comp30347_c0_seq1.p2				
comp30347_c0_seq3.p1				
comp30349_c0_seq1.p1				
comp30349_c0_seq4.p1				
comp30349_c0_seq5.p1	sp|P38531|HSF3_CHICK_Heat_shock_factor_protein_3_OS=Gallus_gallus_GN=HSF3_PE=2_SV=1	4.00E-26	[illegible]	[illegible]
comp30349_c0_seq7.p1	sp|P38531|HSF3_CHICK_Heat_shock_factor_protein_3_OS=Gallus_gallus_GN=HSF3_PE=2_SV=1	5.00E-25	[illegible]	[illegible]
comp30349_c1_seq1.p1				
comp30349_c1_seq2.p1				
comp30349_c1_seq2.p2				
comp30349_c1_seq4.p1				
comp30350_c0_seq1.p1				
comp30350_c0_seq2.p1				
comp30350_c0_seq4.p1				
comp30351_c3_seq1.p1	sp|Q7G8Y3|ISW2_ORYSJ_Probable_chromatin-remodeling_complex_ATPase_chain_OS=Oryza_sativa_subsp._japonica_GN=Os01g0367900_PE=2_SV=2	0	[illegible]	[illegible]
comp30353_c0_seq1.p3				
comp30353_c0_seq2.p1	sp|Q9D3U0|PUS10_MOUSE_Putative_tRNA_pseudouridine_synthase_Pus10_OS=Mus_musculus_GN=Pus10_PE=1_SV=1	1.00E-46	[illegible]	[illegible]
comp30353_c0_seq3.p1				
comp30354_c0_seq1.p1	sp|Q9BTW9|TBCD_HUMAN_Tubulin-specific_chaperone_D_OS=Homo_sapiens_GN=TBCD_PE=1_SV=2	3.00E-172	[illegible]	[illegible]
comp30354_c0_seq2.p1	sp|Q9BTW9|TBCD_HUMAN_Tubulin-specific_chaperone_D_OS=Homo_sapiens_GN=TBCD_PE=1_SV=2	0	[illegible]	[illegible]
comp30357_c0_seq3.p2				
comp30357_c0_seq4.p1				
comp30357_c0_seq6.p1	sp|Q11011|PSA_MOUSE_Puromycin-sensitive_aminopeptidase_OS=Mus_musculus_GN=Npepps_PE=1_SV=2	2.00E-30	[illegible]	[illegible]
comp30358_c0_seq2.p1				
comp30358_c0_seq2.p2	sp|Q14684|RRP1B_HUMAN_Ribosomal_RNA_processing_protein_1_homolog_B_OS=Homo_sapiens_GN=RRP1B_PE=1_SV=3	8.00E-22	[illegible]	[illegible]
comp30358_c0_seq3.p1	sp|Q14684|RRP1B_HUMAN_Ribosomal_RNA_processing_protein_1_homolog_B_OS=Homo_sapiens_GN=RRP1B_PE=1_SV=3	2.00E-20	[illegible]	[illegible]
comp30359_c1_seq1.p1				
comp30359_c1_seq1.p2				
comp30359_c1_seq2.p1				
comp30359_c1_seq2.p2				
comp30359_c1_seq4.p1				
comp30360_c0_seq3.p1				
comp30362_c0_seq2.p1	sp|Q9P4U6|TCSB_EMENI_Two-component_system_protein_B_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=tcsB_PE=1_SV=2	1.00E-21	[illegible]	[illegible]
comp30364_c0_seq1.p1				
comp30365_c0_seq2.p1	sp|P14735|IDE_HUMAN_Insulin-degrading_enzyme_OS=Homo_sapiens_GN=IDE_PE=1_SV=4	6.00E-27	[illegible]	[illegible]
comp30365_c0_seq2.p4				
comp30365_c0_seq3.p1	sp|O22941|PXM16_ARATH_Zinc-metallopeptidase,_peroxisomal_OS=Arabidopsis_thaliana_GN=PXM16_PE=2_SV=1	1.00E-29	[illegible]	[illegible]
comp30365_c0_seq6.p1	sp|Q06010|STE23_YEAST_A-factor-processing_enzyme_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=STE23_PE=1_SV=2	3.00E-38	[illegible]	[illegible]
comp30366_c0_seq1.p1	sp|P31512|FMO4_HUMAN_Dimethylaniline_monooxygenase_[N-oxide-forming]_4_OS=Homo_sapiens_GN=FMO4_PE=2_SV=3	9.00E-42	[illegible]	[illegible]
comp30366_c0_seq1.p2	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	3.00E-25		
comp30366_c0_seq12.p1	sp|P32417|FMO3_RABIT_Dimethylaniline_monooxygenase_[N-oxide-forming]_3_OS=Oryctolagus_cuniculus_GN=FMO3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp30366_c0_seq12.p2	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	3.00E-25		
comp30366_c0_seq14.p1	sp|P32417|FMO3_RABIT_Dimethylaniline_monooxygenase_[N-oxide-forming]_3_OS=Oryctolagus_cuniculus_GN=FMO3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp30366_c0_seq14.p2				
comp30366_c0_seq19.p1	sp|P32417|FMO3_RABIT_Dimethylaniline_monooxygenase_[N-oxide-forming]_3_OS=Oryctolagus_cuniculus_GN=FMO3_PE=1_SV=3	2.00E-35	[illegible]	[illegible]
comp30366_c0_seq19.p2	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	3.00E-25		
comp30366_c0_seq27.p1	sp|P32417|FMO3_RABIT_Dimethylaniline_monooxygenase_[N-oxide-forming]_3_OS=Oryctolagus_cuniculus_GN=FMO3_PE=1_SV=3	2.00E-35	[illegible]	[illegible]
comp30366_c0_seq27.p2				
comp30366_c0_seq5.p1	sp|P31512|FMO4_HUMAN_Dimethylaniline_monooxygenase_[N-oxide-forming]_4_OS=Homo_sapiens_GN=FMO4_PE=2_SV=3	9.00E-42	[illegible]	[illegible]
comp30366_c0_seq5.p2				
comp30368_c0_seq2.p2	sp|Q9P6N9|PER1_SCHPO_Protein_PER1_homolog_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC823.07_PE=2_SV=1	2.00E-15	[illegible]	[illegible]
comp30368_c0_seq5.p1	sp|A2A559|PGAP3_MOUSE_Post-GPI_attachment_to_proteins_factor_3_OS=Mus_musculus_GN=Pgap3_PE=2_SV=1	6.00E-46	[illegible]	[illegible]
comp30368_c0_seq6.p1				
comp30370_c0_seq4.p1	sp|Q8NHQ9|DDX55_HUMAN_ATP-dependent_RNA_helicase_DDX55_OS=Homo_sapiens_GN=DDX55_PE=1_SV=3	4.00E-154	[illegible]	[illegible]
comp30370_c0_seq4.p2				
comp30370_c0_seq6.p1	sp|Q5ZLN8|DDX55_CHICK_ATP-dependent_RNA_helicase_DDX55_OS=Gallus_gallus_GN=DDX55_PE=2_SV=1	3.00E-149	[illegible]	[illegible]
comp30371_c0_seq3.p1				
comp30372_c0_seq2.p1				
comp30372_c0_seq2.p5				
comp30372_c0_seq4.p1				
comp30372_c1_seq2.p1	sp|Q76C99|RF1_ORYSI_Protein_Rf1,_mitochondrial_OS=Oryza_sativa_subsp._indica_GN=Rf1_PE=2_SV=1	5.00E-36	GO:0005739,GO:0005739	[illegible]
comp30374_c0_seq2.p1				
comp30375_c0_seq1.p1	sp|P09189|HSP7C_PETHY_Heat_shock_cognate_70_kDa_protein_OS=Petunia_hybrida_GN=HSP70_PE=2_SV=1	0	GO:0000166,GO:0005524	[illegible]
comp30376_c0_seq2.p1				
comp30377_c0_seq8.p1	sp|Q54YP4|VPS11_DICDI_Vacuolar_protein_sorting-associated_protein_11_homolog_OS=Dictyostelium_discoideum_GN=vps11_PE=3_SV=1	5.00E-114	[illegible]	[illegible]
comp30377_c0_seq8.p3				
comp30377_c0_seq8.p5				
comp30377_c0_seq9.p1	sp|Q54YP4|VPS11_DICDI_Vacuolar_protein_sorting-associated_protein_11_homolog_OS=Dictyostelium_discoideum_GN=vps11_PE=3_SV=1	5.00E-114	[illegible]	[illegible]
comp30377_c0_seq9.p3				
comp30377_c0_seq9.p5				
comp30378_c0_seq5.p1	sp|Q07307|UAPA_EMENI_Uric_acid-xanthine_permease_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=uapA_PE=1_SV=3	2.00E-129	[illegible]	[illegible]
comp30378_c0_seq6.p1	sp|P48777|UAPC_EMENI_Purine_permease_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=uapC_PE=2_SV=2	5.00E-34	[illegible]	[illegible]

comp30378_c0_seq7.p1	sp|Q07307|UAPA_EMENI_Uric_acid-xanthine_permease_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=uapA_PE=1_SV=3	8.00E-118	[illegible]	[illegible]
comp30378_c0_seq7.p4				
comp30379_c0_seq2.p1	sp|A6TD42|CYSC_KLEP7_Adenylyl-sulfate_kinase_OS=Klebsiella_pneumoniae_subsp._pneumoniae_(strain_ATCC_700721_/_MGH_78578)_GN=cysC_PE=3_SV=1	5.00E-39	[illegible]	[illegible]
comp30379_c0_seq4.p1	sp|Q99390|YPT2_ECOLX_Uncharacterized_31.7_kDa_protein_in_traX-finO_intergenic_region_OS=Escherichia_coli_PE=3_SV=1	9.00E-15		
comp30379_c0_seq4.p2	sp|Q9KCT0|CYSC1_BACHD_Probable_adenylyl-sulfate_kinase_OS=Bacillus_halodurans_(strain_ATCC_BAA-125_/_DSM_18197_/_FERM_7344_/_JCM_9153_/_C-125)_GN=BH1489_PE=3_SV=1	3.00E-76	[illegible]	[illegible]
comp30380_c0_seq1.p1				
comp30381_c0_seq1.p1	sp|Q9WVR1|INP5E_RAT_72_kDa_inositol_polyphosphate_5-phosphatase_OS=Rattus_norvegicus_GN=Inpp5e_PE=2_SV=2	2.00E-26	[illegible]	[illegible]
comp30382_c0_seq3.p1	sp|Q9HX48|RLUE_PSEAE_Ribosomal_large_subunit_pseudouridine_synthase_E_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=rluE_PE=3_SV=1	2.00E-19	[illegible]	[illegible]
comp30382_c0_seq3.p2	sp|Q7NNK8|THIE_GLOVI_Thiamine-phosphate_synthase_OS=Gloeobacter_violaceus_(strain_PCC_7421)_GN=thiE_PE=3_SV=2	6.00E-20	[illegible]	[illegible]
comp30382_c0_seq4.p1	sp|Q7NNK8|THIE_GLOVI_Thiamine-phosphate_synthase_OS=Gloeobacter_violaceus_(strain_PCC_7421)_GN=thiE_PE=3_SV=2	6.00E-20	[illegible]	[illegible]
comp30382_c0_seq4.p2	sp|Q9HX48|RLUE_PSEAE_Ribosomal_large_subunit_pseudouridine_synthase_E_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=rluE_PE=3_SV=1	1.00E-17	[illegible]	[illegible]
comp30382_c0_seq5.p1	sp|Q9HX48|RLUE_PSEAE_Ribosomal_large_subunit_pseudouridine_synthase_E_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=rluE_PE=3_SV=1	9.00E-18	[illegible]	[illegible]
comp30383_c0_seq1.p1				
comp30384_c0_seq3.p1				
comp30385_c0_seq1.p1	sp|Q9K0B0|RLUD_NEIMB_Ribosomal_large_subunit_pseudouridine_synthase_D_OS=Neisseria_meningitidis_serogroup_B_(strain_MC58)_GN=rluD_PE=3_SV=1	2.00E-30	[illegible]	[illegible]
comp30385_c0_seq5.p1	sp|Q32TG3|EFHC2_CHICK_EF-hand_domain-containing_family_member_C2_OS=Gallus_gallus_GN=EFHC2_PE=2_SV=1	1.00E-56	GO:0005509	[illegible]
comp30385_c0_seq5.p2	sp|Q9K0B0|RLUD_NEIMB_Ribosomal_large_subunit_pseudouridine_synthase_D_OS=Neisseria_meningitidis_serogroup_B_(strain_MC58)_GN=rluD_PE=3_SV=1	2.00E-30	[illegible]	[illegible]
comp30385_c0_seq6.p1	sp|Q32TG3|EFHC2_CHICK_EF-hand_domain-containing_family_member_C2_OS=Gallus_gallus_GN=EFHC2_PE=2_SV=1	2.00E-59	GO:0005509	[illegible]
comp30385_c0_seq6.p2	sp|Q9K0B0|RLUD_NEIMB_Ribosomal_large_subunit_pseudouridine_synthase_D_OS=Neisseria_meningitidis_serogroup_B_(strain_MC58)_GN=rluD_PE=3_SV=1	2.00E-30	[illegible]	[illegible]
comp30386_c1_seq6.p1				
comp30387_c0_seq1.p1				
comp30387_c0_seq1.p2				
comp30388_c0_seq1.p1				
comp30388_c0_seq6.p1				
comp30388_c0_seq6.p3				
comp30389_c1_seq1.p1				
comp30389_c2_seq1.p1				
comp30389_c2_seq2.p1				
comp30390_c0_seq1.p1	sp|O46606|DDHD1_BOVIN_Phospholipase_DDHD1_OS=Bos_taurus_GN=DDHD1_PE=1_SV=1	9.00E-22	[illegible]	[illegible]
comp30390_c0_seq2.p1				
comp30391_c0_seq1.p1				
comp30391_c0_seq2.p1				
comp30391_c0_seq3.p1				
comp30391_c0_seq3.p2	sp|A1VAE6|LEUD_DESVV_3-isopropylmalate_dehydratase_small_subunit_OS=Desulfovibrio_vulgaris_subsp._vulgaris_(strain_DP4)_GN=leuD_PE=3_SV=1	8.00E-24	[illegible]	[illegible]
comp30391_c0_seq4.p1	sp|A1VAE6|LEUD_DESVV_3-isopropylmalate_dehydratase_small_subunit_OS=Desulfovibrio_vulgaris_subsp._vulgaris_(strain_DP4)_GN=leuD_PE=3_SV=1	8.00E-24	[illegible]	[illegible]
comp30391_c0_seq4.p2				
comp30391_c0_seq5.p1				
comp30392_c0_seq1.p1				
comp30392_c0_seq1.p2				
comp30394_c0_seq1.p1	sp|A0JM23|NPHP3_XENTR_Nephrocystin-3_OS=Xenopus_tropicalis_GN=nphp3_PE=2_SV=2	8.00E-32	[illegible]	[illegible]
comp30394_c0_seq2.p1	sp|Q7TNH6|NPHP3_MOUSE_Nephrocystin-3_OS=Mus_musculus_GN=Nphp3_PE=1_SV=2	5.00E-39	[illegible]	[illegible]
comp30395_c0_seq2.p1	sp|Q6EPQ3|SPXM1_ORYSJ_SPX_domain-containing_membrane_protein_Os02g45520_OS=Oryza_sativa_subsp._japonica_GN=Os02g0678200_PE=2_SV=1	8.00E-14	[illegible]	[illegible]
comp30395_c1_seq2.p1				
comp30396_c0_seq1.p1	sp|O13282|TAF5_SCHPO_Transcription_initiation_factor_TFIID_subunit_5_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=taf5_PE=1_SV=1	3.00E-64	[illegible]	[illegible]
comp30397_c0_seq2.p1	sp|Q94CD5|ATG7_ARATH_Ubiquitin-like_modifier-activating_enzyme_atg7_OS=Arabidopsis_thaliana_GN=ATG7_PE=1_SV=1	1.00E-145	[illegible]	[illegible]
comp30397_c0_seq2.p2				
comp30397_c0_seq8.p1	sp|Q94CD5|ATG7_ARATH_Ubiquitin-like_modifier-activating_enzyme_atg7_OS=Arabidopsis_thaliana_GN=ATG7_PE=1_SV=1	6.00E-143	[illegible]	[illegible]
comp30397_c0_seq8.p2				
comp30398_c0_seq1.p1	sp|Q6LL68|BGAL_PHOPR_Beta-galactosidase_OS=Photobacterium_profundum_GN=lacZ_PE=3_SV=1	1.00E-105	[illegible]	[illegible]
comp30399_c0_seq2.p1	sp|Q96S06|LMF1_HUMAN_Lipase_maturation_factor_1_OS=Homo_sapiens_GN=LMF1_PE=1_SV=1	8.00E-77	[illegible]	[illegible]
comp30400_c0_seq2.p1	sp|Q9H477|RBSK_HUMAN_Ribokinase_OS=Homo_sapiens_GN=RBKS_PE=1_SV=1	3.00E-57	[illegible]	[illegible]
comp30400_c0_seq2.p2				
comp30400_c0_seq4.p1	sp|Q9H477|RBSK_HUMAN_Ribokinase_OS=Homo_sapiens_GN=RBKS_PE=1_SV=1	4.00E-65	[illegible]	[illegible]
comp30400_c0_seq4.p2				
comp30401_c0_seq2.p1				
comp30401_c0_seq3.p1				
comp30402_c0_seq2.p1	sp|Q9H611|PIF1_HUMAN_ATP-dependent_DNA_helicase_PIF1_OS=Homo_sapiens_GN=PIF1_PE=1_SV=2	1.00E-102	[illegible]	[illegible]
comp30403_c0_seq3.p1	sp|P52009|CYP1_CAEEL_Peptidyl-prolyl_cis-trans_isomerase_1_OS=Caenorhabditis_elegans_GN=cyn-1_PE=2_SV=1	8.00E-64	[illegible]	[illegible]
comp30403_c0_seq3.p3				
comp30404_c0_seq2.p1	sp|Q69VD9|P2C57_ORYSJ_Probable_protein_phosphatase_2C_57_OS=Oryza_sativa_subsp._japonica_GN=Os06g0597200_PE=2_SV=1	2.00E-15	[illegible]	[illegible]
comp30404_c0_seq4.p1	sp|O75688|PPM1B_HUMAN_Protein_phosphatase_1B_OS=Homo_sapiens_GN=PPM1B_PE=1_SV=1	3.00E-16	[illegible]	[illegible]
comp30405_c0_seq3.p1				
comp30406_c0_seq1.p1				
comp30408_c0_seq4.p1				
comp30408_c0_seq4.p2				
comp30409_c0_seq1.p1				
comp30409_c0_seq2.p1				
comp30410_c0_seq2.p1				
comp30411_c0_seq5.p1				
comp30412_c0_seq2.p1	sp|O94487|PPK35_SCHPO_Serine/threonine-protein_kinase_ppk35_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ppk35_PE=1_SV=1	2.00E-26	[illegible]	[illegible]
comp30412_c0_seq2.p2				
comp30412_c0_seq4.p1	sp|Q28651|2A5G_RABIT_Serine/threonine-protein_phosphatase_2A_56_kDa_regulatory_subunit_gamma_isoform_OS=Oryctolagus_cuniculus_GN=PPP2R5C_PE=2_SV=1	3.00E-11	[illegible]	[illegible]
comp30412_c1_seq2.p1				
comp30412_c1_seq4.p1				
comp30413_c0_seq1.p1				
comp30413_c0_seq2.p1				
comp30413_c0_seq3.p2				
comp30414_c0_seq1.p1	sp|O75417|DPOLQ_HUMAN_DNA_polymerase_theta_OS=Homo_sapiens_GN=POLQ_PE=1_SV=2	4.00E-68	[illegible]	[illegible]
comp30414_c1_seq2.p1	sp|Q6PBM8|RBM18_DANRE_Probable_RNA-binding_protein_18_OS=Danio_rerio_GN=rbm18_PE=2_SV=1	5.00E-13	[illegible]	[illegible]
comp30414_c1_seq2.p2				
comp30414_c1_seq2.p5				
comp30416_c0_seq1.p1				
comp30416_c0_seq2.p1				
comp30416_c0_seq4.p1				
comp30416_c0_seq6.p2				
comp30416_c1_seq2.p1				
comp30418_c0_seq1.p1				
comp30419_c0_seq1.p1	sp|B9G2A8|BIG_ORYSJ_Auxin_transport_protein_BIG_OS=Oryza_sativa_subsp._japonica_GN=Os09g0247700_PE=2_SV=1	3.00E-32	[illegible]	[illegible]
comp30419_c0_seq2.p1	sp|B9G2A8|BIG_ORYSJ_Auxin_transport_protein_BIG_OS=Oryza_sativa_subsp._japonica_GN=Os09g0247700_PE=2_SV=1	3.00E-25	[illegible]	[illegible]
comp30422_c0_seq1.p1	sp|Q5NBJ3|GYRB_ORYSJ_DNA_gyrase_subunit_B,_chloroplastic/mitochondrial_OS=Oryza_sativa_subsp._japonica_GN=GYRB_PE=2_SV=1	0	[illegible]	[illegible]
comp30422_c0_seq1.p2				
comp30422_c0_seq1.p6				
comp30422_c0_seq3.p1				
comp30423_c0_seq6.p1	sp|Q5RC98|S38AA_PONAB_Putative_sodium-coupled_neutral_amino_acid_transporter_10_OS=Pongo_abelii_GN=SLC38A10_PE=2_SV=1	4.00E-12	[illegible]	[illegible]
comp30423_c0_seq7.p1	sp|Q5E9S9|S38A5_BOVIN_Sodium-coupled_neutral_amino_acid_transporter_5_OS=Bos_taurus_GN=SLC38A5_PE=2_SV=1	3.00E-29	[illegible]	[illegible]
comp30423_c0_seq9.p1				
comp30425_c0_seq2.p1				
comp30426_c0_seq1.p1	sp|Q2UAP8|TIM22_ASPOR_Mitochondrial_import_inner_membrane_translocase_subunit_tim22_OS=Aspergillus_oryzae_(strain_ATCC_42149_/_RIB_40)_GN=tim22_PE=3_SV=1	2.00E-21	[illegible]	[illegible]
comp30426_c0_seq1.p3				
comp30426_c0_seq1.p4	sp|Q22708|SYM2_CAEEL_RNA-binding_protein_sym-2_OS=Caenorhabditis_elegans_GN=sym-2_PE=2_SV=3	2.00E-17	[illegible]	[illegible]
comp30428_c0_seq1.p1				
comp30428_c1_seq1.p1				
comp30429_c0_seq3.p1	sp|Q5UP39|YR873_MIMIV_Putative_ankyrin_repeat_protein_R873_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R873_PE=4_SV=1	3.00E-18		
comp30430_c0_seq2.p1	sp|Q13637|RAB32_HUMAN_Ras-related_protein_Rab-32_OS=Homo_sapiens_GN=RAB32_PE=1_SV=3	2.00E-65	[illegible]	[illegible]
comp30431_c0_seq1.p1				
comp30431_c0_seq2.p1				
comp30431_c0_seq3.p1				
comp30433_c0_seq1.p1	sp|C1F407|HFLX_ACIC5_GTPase_HflX_OS=Acidobacterium_capsulatum_(strain_ATCC_51196_/_DSM_11244_/_JCM_7670)_GN=hflX_PE=3_SV=1	3.00E-60	[illegible]	[illegible]
comp30433_c0_seq4.p1	sp|C1F407|HFLX_ACIC5_GTPase_HflX_OS=Acidobacterium_capsulatum_(strain_ATCC_51196_/_DSM_11244_/_JCM_7670)_GN=hflX_PE=3_SV=1	1.00E-84	[illegible]	[illegible]
comp30433_c0_seq4.p5				
comp30434_c0_seq1.p1				
comp30434_c1_seq2.p1	sp|Q02614|S30BP_MOUSE_SAP30-binding_protein_OS=Mus_musculus_GN=Sap30bp_PE=2_SV=2	3.00E-11	[illegible]	[illegible]
comp30434_c1_seq3.p1				
comp30435_c0_seq4.p1				
comp30436_c0_seq1.p1				
comp30436_c0_seq2.p2				
comp30436_c0_seq2.p3				
comp30436_c0_seq3.p1				
comp30437_c0_seq2.p1	sp|Q9TZM3|LRK1_CAEEL_Leucine-rich_repeat_serine/threonine-protein_kinase_1_OS=Caenorhabditis_elegans_GN=lrk-1_PE=1_SV=6	4.00E-11	[illegible]	[illegible]
comp30438_c0_seq4.p1	sp|P49079|AKH1_MAIZE_Bifunctional_aspartokinase/homoserine_dehydrogenase_1,_chloroplastic_OS=Zea_mays_GN=AKHSDH1_PE=2_SV=1	4.00E-152	[illegible]	[illegible]
comp30439_c0_seq3.p1				
comp30441_c0_seq5.p1	sp|Q54F07|METK_DICDI_S-adenosylmethionine_synthase_OS=Dictyostelium_discoideum_GN=metK_PE=1_SV=1	0	[illegible]	[illegible]
comp30441_c0_seq5.p3				
comp30442_c0_seq1.p1				
comp30442_c0_seq4.p1	sp|O08901|BUB1_MOUSE_Mitotic_checkpoint_serine/threonine-protein_kinase_BUB1_OS=Mus_musculus_GN=Bub1_PE=2_SV=1	9.00E-16	[illegible]	[illegible]
comp30443_c0_seq3.p1				
comp30443_c0_seq4.p1				
comp30444_c0_seq1.p1	sp|Q80SY5|PR38B_MOUSE_Pre-mRNA-splicing_factor_38B_OS=Mus_musculus_GN=Prpf38b_PE=1_SV=1	8.00E-43	[illegible]	[illegible]
comp30444_c0_seq2.p1	sp|Q6AXY7|PR38B_RAT_Pre-mRNA-splicing_factor_38B_OS=Rattus_norvegicus_GN=Prpf38b_PE=2_SV=1	2.00E-28	[illegible]	[illegible]
comp30445_c0_seq3.p1				
comp30445_c0_seq4.p1				
comp30446_c0_seq1.p1				
comp30446_c0_seq1.p10				
comp30446_c0_seq1.p2				
comp30447_c0_seq2.p1	sp|Q9X248|FABG_THEMA_3-oxoacyl-[acyl-carrier-protein]_reductase_FabG_OS=Thermotoga_maritima_GN=fabG_PE=3_SV=1	3.00E-18	[illegible]	[illegible]
comp30448_c0_seq5.p1	sp|O00462|MANBA_HUMAN_Beta-mannosidase_OS=Homo_sapiens_GN=MANBA_PE=1_SV=3	4.00E-26	[illegible]	[illegible]
comp30448_c0_seq5.p4				
comp30448_c0_seq6.p1	sp|O00462|MANBA_HUMAN_Beta-mannosidase_OS=Homo_sapiens_GN=MANBA_PE=1_SV=3	5.00E-25	[illegible]	[illegible]
comp30448_c0_seq7.p1	sp|Q8K2I4|MANBA_MOUSE_Beta-mannosidase_OS=Mus_musculus_GN=Manba_PE=2_SV=1	4.00E-22	[illegible]	[illegible]
comp30448_c0_seq8.p1	sp|O00462|MANBA_HUMAN_Beta-mannosidase_OS=Homo_sapiens_GN=MANBA_PE=1_SV=3	3.00E-23	[illegible]	[illegible]
comp30448_c0_seq8.p4				
comp30449_c0_seq3.p1				
comp30449_c0_seq4.p1	sp|A0PJX2|CT118_HUMAN_Uncharacterized_protein_C20orf118_OS=Homo_sapiens_GN=C20orf118_PE=2_SV=1	1.00E-26		
comp30449_c0_seq6.p1	sp|A0PJX2|CT118_HUMAN_Uncharacterized_protein_C20orf118_OS=Homo_sapiens_GN=C20orf118_PE=2_SV=1	1.00E-26		
comp30450_c0_seq1.p3				
comp30450_c0_seq2.p1				
comp30450_c0_seq2.p3				
comp30450_c0_seq4.p1				
comp30451_c0_seq3.p2				
comp30451_c0_seq5.p1	sp|Q9LXI7|PPA20_ARATH_Probable_purple_acid_phosphatase_20_OS=Arabidopsis_thaliana_GN=PAP20_PE=2_SV=1	5.00E-42	[illegible]	[illegible]
comp30452_c0_seq3.p1	sp|Q9SL76|P2C19_ARATH_Protein_phosphatase_2C_and_cyclic_nucleotide-binding/kinase_domain-containing_protein_OS=Arabidopsis_thaliana_GN=At2g20050_PE=1_SV=2	2.00E-166	[illegible]	[illegible]
comp30454_c0_seq1.p1				
comp30454_c0_seq2.p1	sp|Q8CIB9|ESCO2_MOUSE_N-acetyltransferase_ESCO2_OS=Mus_musculus_GN=Esco2_PE=2_SV=3	4.00E-16	[illegible]	[illegible]
comp30455_c0_seq1.p1	sp|Q9LJL3|PREP1_ARATH_Presequence_protease_1,_chloroplastic/mitochondrial_OS=Arabidopsis_thaliana_GN=PREP1_PE=1_SV=2	2.00E-67	[illegible]	[illegible]
comp30455_c1_seq1.p1	sp|Q8VY06|PREP2_ARATH_Presequence_protease_2,_chloroplastic/mitochondrial_OS=Arabidopsis_thaliana_GN=PREP2_PE=1_SV=1	6.00E-58	[illegible]	[illegible]
comp30455_c1_seq3.p1	sp|Q9LJL3|PREP1_ARATH_Presequence_protease_1,_chloroplastic/mitochondrial_OS=Arabidopsis_thaliana_GN=PREP1_PE=1_SV=2	4.00E-59	[illegible]	[illegible]
comp30455_c1_seq4.p1	sp|Q9LJL3|PREP1_ARATH_Presequence_protease_1,_chloroplastic/mitochondrial_OS=Arabidopsis_thaliana_GN=PREP1_PE=1_SV=2	0	[illegible]	[illegible]
comp30457_c1_seq3.p1	sp|P25341|KIN82_YEAST_Serine/threonine-protein_kinase_KIN82_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=KIN82_PE=1_SV=3	2.00E-24	[illegible]	[illegible]
comp30457_c1_seq3.p2	sp|O42626|NRC2_NEUCR_Serine/threonine-protein_kinase_nrc-2_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=nrc-2_PE=3_SV=1	4.00E-27	[illegible]	[illegible]
comp30458_c0_seq1.p1				
comp30458_c0_seq1.p4				
comp30459_c0_seq12.p1				
comp30459_c0_seq13.p1				
comp30459_c0_seq26.p1	sp|Q1LWH4|FAN1_DANRE_Fanconi-associated_nuclease_1_OS=Danio_rerio_GN=fan1_PE=2_SV=2	1.00E-14	[illegible]	[illegible]
comp30459_c0_seq32.p1				
comp30459_c0_seq46.p1				
comp30459_c0_seq47.p1	sp|Q1LWH4|FAN1_DANRE_Fanconi-associated_nuclease_1_OS=Danio_rerio_GN=fan1_PE=2_SV=2	6.00E-15	[illegible]	[illegible]
comp30459_c0_seq47.p3				
comp30459_c0_seq48.p1	sp|Q1LWH4|FAN1_DANRE_Fanconi-associated_nuclease_1_OS=Danio_rerio_GN=fan1_PE=2_SV=2	6.00E-15	[illegible]	[illegible]
comp30459_c0_seq48.p2				
comp30459_c0_seq55.p2				
comp30459_c0_seq55.p3				
comp30459_c0_seq7.p1				
comp3046_c0_seq1.p1	sp|P15112|EF2_DICDI_Elongation_factor_2_OS=Dictyostelium_discoideum_GN=efbA_PE=1_SV=2	4.00E-51	[illegible]	[illegible]
comp30460_c0_seq1.p1				
comp30460_c0_seq2.p1				
comp30460_c1_seq1.p1	sp|B7KLL5|GATA_CYAP7_Glutamyl-tRNA(Gln)_amidotransferase_subunit_A_OS=Cyanothece_sp._(strain_PCC_7424)_GN=gatA_PE=3_SV=1	9.00E-140	[illegible]	[illegible]
comp30461_c0_seq1.p1	sp|O57589|SURF2_TAKRU_Surfeit_locus_protein_2_OS=Takifugu_rubripes_GN=surf2_PE=3_SV=1	2.00E-12		
comp30463_c0_seq1.p2				
comp30463_c0_seq1.p4				
comp30463_c0_seq10.p2				
comp30463_c0_seq10.p3				
comp30463_c0_seq2.p1				
comp30463_c0_seq2.p2				
comp30463_c0_seq7.p3				
comp30465_c0_seq1.p1				
comp30465_c0_seq2.p1				
comp30466_c0_seq1.p1				
comp30467_c0_seq2.p1	sp|Q9Z2A8|MBTP1_CRIGR_Membrane-bound_transcription_factor_site-1_protease_OS=Cricetulus_griseus_GN=MBTPS1_PE=1_SV=1	0	[illegible]	[illegible]
comp30467_c0_seq5.p1	sp|Q9Z2A8|MBTP1_CRIGR_Membrane-bound_transcription_factor_site-1_protease_OS=Cricetulus_griseus_GN=MBTPS1_PE=1_SV=1	0	[illegible]	[illegible]
comp30468_c0_seq1.p1				
comp30469_c0_seq1.p1				
comp30469_c0_seq4.p1				
comp30469_c0_seq4.p2				
comp30470_c0_seq1.p1				
comp30470_c0_seq2.p1				
comp30470_c0_seq4.p1				
comp30472_c0_seq5.p1	sp|P54677|PI4K_DICDI_Phosphatidylinositol_4-kinase_OS=Dictyostelium_discoideum_GN=pikD_PE=3_SV=3	6.00E-56	[illegible]	[illegible]
comp30472_c0_seq5.p11				
comp30473_c0_seq1.p1				
comp30474_c0_seq3.p1				
comp30474_c0_seq6.p1				
comp30474_c0_seq7.p1				
comp30474_c0_seq8.p1				
comp30475_c0_seq1.p1				
comp30476_c0_seq3.p1	sp|Q54VD8|RIO1_DICDI_Serine/threonine-protein_kinase_rio1_OS=Dictyostelium_discoideum_GN=rio1_PE=3_SV=1	2.00E-106	[illegible]	[illegible]
comp30476_c0_seq3.p4				
comp30476_c0_seq3.p7	sp|O96952|THIO_GEOCY_Thioredoxin_OS=Geodia_cydonium_GN=THIO_PE=3_SV=1	5.00E-19	[illegible]	[illegible]
comp30477_c0_seq4.p1				
comp30477_c0_seq6.p1	sp|Q8W4G3|MATE4_ARATH_MATE_efflux_family_protein_4,_chloroplastic_OS=Arabidopsis_thaliana_GN=DTX46_PE=2_SV=1	4.00E-43	[illegible]	[illegible]
comp30478_c0_seq1.p1				
comp30478_c1_seq1.p1				
comp30478_c1_seq5.p1				
comp30478_c3_seq1.p5				
comp30478_c4_seq1.p1	sp|P34101|FHKC_DICDI_Probable_serine/threonine-protein_kinase_fhkC_OS=Dictyostelium_discoideum_GN=fhkC_PE=3_SV=2	2.00E-42	[illegible]	[illegible]
comp30479_c0_seq1.p1	sp|Q9Z3R3|ACSA1_RHIME_Acetoacetyl-coenzyme_A_synthetase_OS=Rhizobium_meliloti_(strain_1021)_GN=acsA1_PE=3_SV=2	8.00E-160	[illegible]	[illegible]
comp30479_c0_seq2.p1	sp|Q9Z3R3|ACSA1_RHIME_Acetoacetyl-coenzyme_A_synthetase_OS=Rhizobium_meliloti_(strain_1021)_GN=acsA1_PE=3_SV=2	3.00E-140	[illegible]	[illegible]
comp30479_c0_seq3.p1	sp|Q9Z3R3|ACSA1_RHIME_Acetoacetyl-coenzyme_A_synthetase_OS=Rhizobium_meliloti_(strain_1021)_GN=acsA1_PE=3_SV=2	2.00E-114	[illegible]	[illegible]
comp30479_c0_seq4.p1	sp|Q9Z3R3|ACSA1_RHIME_Acetoacetyl-coenzyme_A_synthetase_OS=Rhizobium_meliloti_(strain_1021)_GN=acsA1_PE=3_SV=2	3.00E-95	[illegible]	[illegible]
comp30480_c0_seq6.p1	sp|P0CS53|TRM82_CRYNB_tRNA_(guanine-N(7)-)-methyltransferase_subunit_TRM82_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_B-3501A)_GN=TRM82_PE=3_SV=1	2.00E-11	[illegible]	[illegible]
comp30480_c0_seq7.p2	sp|P0CS52|TRM82_CRYNJ_tRNA_(guanine-N(7)-)-methyltransferase_subunit_TRM82_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=TRM82_PE=3_SV=1	4.00E-11	[illegible]	[illegible]
comp30481_c0_seq1.p1				
comp30481_c0_seq3.p1	sp|Q54MQ7|DHYS_DICDI_Probable_deoxyhypusine_synthase_OS=Dictyostelium_discoideum_GN=dhps_PE=3_SV=1	5.00E-153	[illegible]	[illegible]
comp30481_c0_seq3.p2				
comp30482_c0_seq1.p1	sp|Q8BZI6|CV013_MOUSE_Uncharacterized_protein_C22orf13_homolog_OS=Mus_musculus_PE=2_SV=2	3.00E-23	[illegible]	[illegible]
comp30482_c0_seq1.p2				
comp30484_c0_seq1.p1				
comp30484_c0_seq2.p1	sp|Q5XHH7|SYVNB_XENLA_E3_ubiquitin-protein_ligase_synoviolin_B_OS=Xenopus_laevis_GN=syvn1-b_PE=2_SV=1	9.00E-60	[illegible]	[illegible]
comp30484_c0_seq2.p3				
comp30484_c0_seq3.p1	sp|Q5XHH7|SYVNB_XENLA_E3_ubiquitin-protein_ligase_synoviolin_B_OS=Xenopus_laevis_GN=syvn1-b_PE=2_SV=1	9.00E-60	[illegible]	[illegible]
comp30484_c0_seq3.p3				
comp30484_c0_seq5.p1	sp|Q5XHH7|SYVNB_XENLA_E3_ubiquitin-protein_ligase_synoviolin_B_OS=Xenopus_laevis_GN=syvn1-b_PE=2_SV=1	9.00E-60	[illegible]	[illegible]
comp30484_c0_seq5.p3				
comp30485_c0_seq2.p1				
comp30485_c0_seq5.p1	sp|Q498F0|WDR44_XENLA_WD_repeat-containing_protein_44_OS=Xenopus_laevis_GN=wdr44_PE=2_SV=1	6.00E-48	[illegible]	[illegible]
comp30486_c0_seq6.p1				
comp30488_c0_seq1.p1	sp|Q5MB13|ABCG2_MACMU_ATP-binding_cassette_sub-family_G_member_2_OS=Macaca_mulatta_GN=ABCG2_PE=2_SV=1	2.00E-36	[illegible]	[illegible]
comp30488_c0_seq1.p2	sp|Q9FNB5|AB6G_ARATH_ABC_transporter_G_family_member_6_OS=Arabidopsis_thaliana_GN=ABCG6_PE=2_SV=1	3.00E-42	[illegible]	[illegible]
comp30489_c0_seq2.p1	sp|Q2TBP8|MET17_BOVIN_Methyltransferase-like_protein_17,_mitochondrial_OS=Bos_taurus_GN=METTL17_PE=2_SV=1	1.00E-12	[illegible]	[illegible]
comp30490_c0_seq1.p1				
comp30490_c0_seq2.p1				
comp30491_c0_seq4.p2	sp|Q4R4S4|ARL8B_MACFA_ADP-ribosylation_factor-like_protein_8B_OS=Macaca_fascicularis_GN=ARL8B_PE=2_SV=1	5.00E-39	[illegible]	[illegible]
comp30491_c0_seq7.p1				
comp30491_c0_seq7.p4	sp|Q4R4S4|ARL8B_MACFA_ADP-ribosylation_factor-like_protein_8B_OS=Macaca_fascicularis_GN=ARL8B_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp30491_c0_seq9.p2				
comp30491_c0_seq9.p4				
comp30491_c0_seq9.p5	sp|Q4R4S4|ARL8B_MACFA_ADP-ribosylation_factor-like_protein_8B_OS=Macaca_fascicularis_GN=ARL8B_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp30491_c0_seq9.p8				
comp30494_c1_seq1.p1				
comp30494_c2_seq1.p1	sp|Q02357|ANK1_MOUSE_Ankyrin-1_OS=Mus_musculus_GN=Ank1_PE=1_SV=2	6.00E-40	[illegible]	[illegible]
comp30494_c2_seq1.p2				
comp30494_c2_seq1.p3				
comp30494_c2_seq3.p1				
comp30495_c0_seq1.p1				
comp30495_c0_seq3.p1				
comp30496_c0_seq1.p1				
comp30499_c0_seq2.p1				
comp30499_c0_seq3.p1				
comp30500_c0_seq12.p1				
comp30500_c0_seq13.p1	sp|Q949R4|DIOXL_ARATH_4,5-DOPA_dioxygenase_extradiol-like_protein_OS=Arabidopsis_thaliana_GN=At4g15093_PE=2_SV=1	1.00E-46	[illegible]	[illegible]
comp30500_c0_seq15.p1	sp|O42877|FCF2_SCHPO_rRNA-processing_protein_fcf2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=fcf2_PE=2_SV=1	5.00E-26	[illegible]	[illegible]
comp30500_c0_seq15.p2	sp|Q0WUU6|PLT4_ARATH_Probable_polyol_transporter_4_OS=Arabidopsis_thaliana_GN=PLT4_PE=2_SV=1	7.00E-107	[illegible]	[illegible]
comp30501_c0_seq1.p1	sp|Q9ZPV5|NOC2L_ARATH_Nucleolar_complex_protein_2_homolog_OS=Arabidopsis_thaliana_GN=At2g18220_PE=2_SV=2	3.00E-48	[illegible]	[illegible]
comp30501_c0_seq3.p1				
comp30501_c0_seq4.p1				
comp30502_c0_seq2.p1	sp|O83823|Y851_TREPA_Uncharacterized_protein_TP_0851_OS=Treponema_pallidum_(strain_Nichols)_GN=TP_0851_PE=4_SV=1	1.00E-27		
comp30502_c0_seq2.p2				
comp30502_c0_seq4.p1				
comp30502_c0_seq4.p2				
comp30502_c0_seq4.p3	sp|O83823|Y851_TREPA_Uncharacterized_protein_TP_0851_OS=Treponema_pallidum_(strain_Nichols)_GN=TP_0851_PE=4_SV=1	5.00E-16		
comp30502_c0_seq8.p1				
comp30502_c0_seq8.p2				
comp30502_c0_seq9.p1	sp|O83823|Y851_TREPA_Uncharacterized_protein_TP_0851_OS=Treponema_pallidum_(strain_Nichols)_GN=TP_0851_PE=4_SV=1	1.00E-10		
comp30502_c0_seq9.p2				
comp30503_c2_seq2.p1	sp|Q8LB17|Y3846_ARATH_Uncharacterized_protein_At3g58460_OS=Arabidopsis_thaliana_GN=At3g58460_PE=1_SV=2	2.00E-12	[illegible]	[illegible]
comp30505_c0_seq2.p1				
comp30506_c0_seq1.p1	sp|Q9P6C8|ADH1_NEUCR_Alcohol_dehydrogenase_1_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=adh-1_PE=3_SV=1	3.00E-73	[illegible]	[illegible]
comp30507_c0_seq2.p1				
comp30508_c0_seq2.p2				
comp30509_c0_seq1.p1	sp|Q96CP6|GRM1A_HUMAN_GRAM_domain-containing_protein_1A_OS=Homo_sapiens_GN=GRAMD1A_PE=1_SV=2	3.00E-19	[illegible]	[illegible]
comp30509_c0_seq2.p1	sp|O42643|PRP22_SCHPO_Pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_prp22_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=prp22_PE=2_SV=1	2.00E-151	[illegible]	[illegible]
comp30509_c0_seq4.p1	sp|Q09530|MOG5_CAEEL_Probable_pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_mog-5_OS=Caenorhabditis_elegans_GN=mog-5_PE=1_SV=1	1.00E-91	[illegible]	[illegible]
comp30509_c0_seq4.p2	sp|O42643|PRP22_SCHPO_Pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_prp22_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=prp22_PE=2_SV=1	3.00E-53	[illegible]	[illegible]
comp30511_c0_seq1.p1				
comp30512_c0_seq1.p1				
comp30513_c0_seq1.p2				
comp30513_c0_seq2.p1				
comp30513_c0_seq3.p2				
comp30514_c0_seq1.p1	sp|Q60L58|SIRT1_CAEBR_NAD-dependent_deacetylase_SIR2_homolog_OS=Caenorhabditis_briggsae_GN=sir-2.1_PE=3_SV=1	6.00E-65	[illegible]	[illegible]
comp30514_c0_seq1.p2				
comp30514_c0_seq4.p1	sp|Q60L58|SIRT1_CAEBR_NAD-dependent_deacetylase_SIR2_homolog_OS=Caenorhabditis_briggsae_GN=sir-2.1_PE=3_SV=1	4.00E-56	[illegible]	[illegible]
comp30515_c0_seq1.p1	sp|P51784|UBP11_HUMAN_Ubiquitin_carboxyl-terminal_hydrolase_11_OS=Homo_sapiens_GN=USP11_PE=1_SV=3	6.00E-79	[illegible]	[illegible]
comp30516_c0_seq11.p2				
comp30516_c0_seq13.p1				
comp30516_c0_seq13.p2	sp|P05132|KAPCA_MOUSE_cAMP-dependent_protein_kinase_catalytic_subunit_alpha_OS=Mus_musculus_GN=Prkaca_PE=1_SV=3	2.00E-47	[illegible]	[illegible]
comp30516_c0_seq13.p4	sp|Q74CR0|GPMA_GEOSL_2,3-bisphosphoglycerate-dependent_phosphoglycerate_mutase_OS=Geobacter_sulfurreducens_(strain_ATCC_51573_/_DSM_12127_/_PCA)_GN=gpmA_PE=3_SV=1	1.00E-41	[illegible]	[illegible]
comp30516_c0_seq15.p1	sp|P05132|KAPCA_MOUSE_cAMP-dependent_protein_kinase_catalytic_subunit_alpha_OS=Mus_musculus_GN=Prkaca_PE=1_SV=3	4.00E-47	[illegible]	[illegible]
comp30516_c0_seq15.p3	sp|Q39V40|GPMA_GEOMG_2,3-bisphosphoglycerate-dependent_phosphoglycerate_mutase_OS=Geobacter_metallireducens_(strain_GS-15_/_ATCC_53774_/_DSM_7210)_GN=gpmA_PE=3_SV=1	1.00E-32	[illegible]	[illegible]
comp30516_c0_seq21.p1	sp|Q39V40|GPMA_GEOMG_2,3-bisphosphoglycerate-dependent_phosphoglycerate_mutase_OS=Geobacter_metallireducens_(strain_GS-15_/_ATCC_53774_/_DSM_7210)_GN=gpmA_PE=3_SV=1	1.00E-32	[illegible]	[illegible]
comp30516_c0_seq21.p3				
comp30516_c0_seq22.p1				
comp30516_c0_seq4.p1	sp|P05132|KAPCA_MOUSE_cAMP-dependent_protein_kinase_catalytic_subunit_alpha_OS=Mus_musculus_GN=Prkaca_PE=1_SV=3	4.00E-47	[illegible]	[illegible]
comp30516_c0_seq6.p1				
comp30516_c0_seq6.p2	sp|P05132|KAPCA_MOUSE_cAMP-dependent_protein_kinase_catalytic_subunit_alpha_OS=Mus_musculus_GN=Prkaca_PE=1_SV=3	2.00E-47	[illegible]	[illegible]
comp30516_c0_seq6.p4	sp|Q39V40|GPMA_GEOMG_2,3-bisphosphoglycerate-dependent_phosphoglycerate_mutase_OS=Geobacter_metallireducens_(strain_GS-15_/_ATCC_53774_/_DSM_7210)_GN=gpmA_PE=3_SV=1	1.00E-47	[illegible]	[illegible]
comp30516_c0_seq8.p1	sp|P05132|KAPCA_MOUSE_cAMP-dependent_protein_kinase_catalytic_subunit_alpha_OS=Mus_musculus_GN=Prkaca_PE=1_SV=3	2.00E-47	[illegible]	[illegible]
comp30517_c0_seq1.p1	sp|A5PL98|DHSB_DANRE_Succinate_dehydrogenase_[ubiquinone]_iron-sulfur_subunit,_mitochondrial_OS=Danio_rerio_GN=sdhb_PE=2_SV=1	1.00E-124	[illegible]	[illegible]
comp30517_c0_seq4.p2				
comp30517_c1_seq2.p1				
comp30518_c0_seq1.p1				
comp30518_c0_seq2.p1	sp|Q9DGN1|STAG1_XENLA_Cohesin_subunit_SA-1_OS=Xenopus_laevis_GN=stag1_PE=1_SV=1	2.00E-12	[illegible]	[illegible]
comp30519_c0_seq2.p1				
comp30519_c0_seq4.p1				
comp30520_c0_seq1.p1				
comp30520_c0_seq2.p1				
comp30521_c0_seq1.p1	sp|Q53M11|HS219_ORYSJ_21.9_kDa_heat_shock_protein_OS=Oryza_sativa_subsp._japonica_GN=HSP21.9_PE=2_SV=1	1.00E-12	[illegible]	[illegible]
comp30524_c0_seq1.p1				
comp30525_c0_seq1.p1				
comp30525_c0_seq2.p1				
comp30526_c0_seq1.p1	sp|P59111|KCNH8_MOUSE_Potassium_voltage-gated_channel_subfamily_H_member_8_OS=Mus_musculus_GN=Kcnh8_PE=2_SV=2	7.00E-25	[illegible]	[illegible]
comp30526_c0_seq3.p1	sp|P59111|KCNH8_MOUSE_Potassium_voltage-gated_channel_subfamily_H_member_8_OS=Mus_musculus_GN=Kcnh8_PE=2_SV=2	7.00E-25	[illegible]	[illegible]
comp30527_c0_seq2.p1				
comp30527_c0_seq3.p1				
comp30528_c0_seq11.p1	sp|O45228|PROD_CAEEL_Proline_dehydrogenase_1,_mitochondrial_OS=Caenorhabditis_elegans_GN=B0513.5_PE=3_SV=2	5.00E-54	[illegible]	[illegible]
comp30528_c0_seq3.p1	sp|O45228|PROD_CAEEL_Proline_dehydrogenase_1,_mitochondrial_OS=Caenorhabditis_elegans_GN=B0513.5_PE=3_SV=2	2.00E-54	[illegible]	[illegible]
comp30528_c0_seq8.p1	sp|O45228|PROD_CAEEL_Proline_dehydrogenase_1,_mitochondrial_OS=Caenorhabditis_elegans_GN=B0513.5_PE=3_SV=2	5.00E-54	[illegible]	[illegible]

comp30531_c0_seq3.p1	sp|Q9XEE8|P2C30_ARATH_Probable_protein_phosphatase_2C_30_OS=Arabidopsis_thaliana_GN=PP2C5_PE=2_SV=1	3.00E-33	[illegible]	[illegible]
comp30531_c0_seq4.p1	sp|Q9FXE4|P2C14_ARATH_Probable_protein_phosphatase_2C_14_OS=Arabidopsis_thaliana_GN=At1g67820_PE=2_SV=2	2.00E-33	[illegible]	[illegible]
comp30531_c0_seq6.p1	sp|Q9XEE8|P2C30_ARATH_Probable_protein_phosphatase_2C_30_OS=Arabidopsis_thaliana_GN=PP2C5_PE=2_SV=1	2.00E-30	[illegible]	[illegible]
comp30532_c0_seq5.p1				
comp30532_c0_seq7.p1				
comp30533_c0_seq1.p1	sp|O75592|MYCB2_HUMAN_Probable_E3_ubiquitin-protein_ligase_MYCBP2_OS=Homo_sapiens_GN=MYCBP2_PE=1_SV=3	4.00E-22	[illegible]	[illegible]
comp30534_c0_seq2.p1				
comp30534_c0_seq3.p1				
comp30534_c0_seq4.p1				
comp30534_c0_seq4.p2				
comp30535_c0_seq4.p1				
comp30535_c0_seq6.p1				
comp30537_c0_seq1.p2				
comp30538_c0_seq1.p1				
comp30538_c0_seq1.p2				
comp30539_c0_seq1.p1	sp|Q54U63|LVSC_DICDI_BEACH_domain-containing_protein_lvsC_OS=Dictyostelium_discoideum_GN=lvsC_PE=4_SV=2	9.00E-99	GO:0005543,GO:0012505,GO:0016197,GO:0019898	[illegible]
comp30540_c0_seq3.p1	sp|P55737|HS902_ARATH_Heat_shock_protein_90-2_OS=Arabidopsis_thaliana_GN=HSP90-2_PE=1_SV=1	0	[illegible]	[illegible]
comp30540_c0_seq5.p1				
comp30540_c1_seq2.p1				
comp30541_c0_seq3.p1	sp|Q9M302|PP270_ARATH_Pentatricopeptide_repeat-containing_protein_At3g48810_OS=Arabidopsis_thaliana_GN=At3g48810_PE=2_SV=1	2.00E-18	GO:0003674,GO:0048445	[illegible]
comp30544_c0_seq2.p1				
comp30544_c0_seq2.p2	sp|Q29RA5|TIGRA_DANRE_Probable_fructose-2,6-bisphosphatase_TIGAR_A_OS=Danio_rerio_GN=tigara_PE=2_SV=1	1.00E-10	[illegible]	[illegible]
comp30545_c1_seq1.p1	sp|Q9NUE0|ZDH18_HUMAN_Palmitoyltransferase_ZDHHC18_OS=Homo_sapiens_GN=ZDHHC18_PE=2_SV=2	3.00E-41	[illegible]	[illegible]
comp30545_c2_seq2.p1	sp|Q5Z987|ATR_ORYSJ_Serine/threonine-protein_kinase_ATR_OS=Oryza_sativa_subsp._japonica_GN=Os06g0724700_PE=2_SV=1	3.00E-108	[illegible]	[illegible]
comp30545_c2_seq3.p1	sp|Q5Z987|ATR_ORYSJ_Serine/threonine-protein_kinase_ATR_OS=Oryza_sativa_subsp._japonica_GN=Os06g0724700_PE=2_SV=1	2.00E-127	[illegible]	[illegible]
comp30545_c4_seq1.p1				
comp30545_c4_seq2.p1				
comp30545_c4_seq3.p1	sp|P28760|SODM_BACCA_Superoxide_dismutase_[Mn]_OS=Bacillus_caldotenax_GN=sodA_PE=3_SV=2	1.00E-63	[illegible]	[illegible]
comp30545_c4_seq4.p1				
comp30545_c4_seq5.p1				
comp30546_c0_seq3.p1	sp|Q8N9H8|MUT7_HUMAN_Probable_exonuclease_mut-7_homolog_OS=Homo_sapiens_GN=EXD3_PE=1_SV=3	2.00E-12	[illegible]	[illegible]
comp30547_c0_seq6.p1				
comp30548_c0_seq10.p1				
comp30548_c0_seq4.p1				
comp30548_c0_seq7.p1				
comp30548_c0_seq9.p1	sp|P51960|MYBA_MOUSE_Myb-related_protein_A_OS=Mus_musculus_GN=Mybl1_PE=2_SV=2	2.00E-26	[illegible]	[illegible]
comp30549_c0_seq1.p1	sp|Q49YW0|SDCS_STAS1_Sodium-dependent_dicarboxylate_transporter_sdcS_OS=Staphylococcus_saprophyticus_subsp._saprophyticus_(strain_ATCC_15305_/_DSM_20229)_GN=sdcS_PE=3_SV=1	1.00E-33	[illegible]	[illegible]
comp30549_c0_seq2.p1	sp|Q49YW0|SDCS_STAS1_Sodium-dependent_dicarboxylate_transporter_sdcS_OS=Staphylococcus_saprophyticus_subsp._saprophyticus_(strain_ATCC_15305_/_DSM_20229)_GN=sdcS_PE=3_SV=1	7.00E-43	[illegible]	[illegible]
comp30550_c0_seq1.p1				
comp30550_c0_seq10.p1				
comp30550_c0_seq2.p2				
comp30550_c0_seq5.p2				
comp30550_c0_seq5.p3				
comp30550_c0_seq6.p1				
comp30550_c0_seq8.p1				
comp30551_c0_seq2.p1				
comp30551_c0_seq2.p5				
comp30551_c0_seq3.p1				
comp30551_c0_seq4.p1				
comp30552_c0_seq3.p1				
comp30552_c0_seq5.p1				
comp30553_c0_seq1.p1				
comp30553_c0_seq2.p1				
comp30553_c0_seq2.p3				
comp30553_c0_seq3.p1				
comp30553_c0_seq3.p3				
comp30553_c0_seq6.p1	sp|Q8BMG8|MFTC_MOUSE_Mitochondrial_folate_transporter/carrier_OS=Mus_musculus_GN=Slc25a32_PE=2_SV=1	9.00E-28	[illegible]	[illegible]
comp30553_c0_seq8.p1				
comp30553_c0_seq8.p3				
comp30553_c0_seq9.p1	sp|Q8BMG8|MFTC_MOUSE_Mitochondrial_folate_transporter/carrier_OS=Mus_musculus_GN=Slc25a32_PE=2_SV=1	2.00E-47	[illegible]	[illegible]
comp30554_c0_seq3.p1	sp|Q6PDG5|SMRC2_MOUSE_SWI/SNF_complex_subunit_SMARCC2_OS=Mus_musculus_GN=Smarcc2_PE=1_SV=2	8.00E-26	[illegible]	[illegible]
comp30554_c0_seq4.p1	sp|Q6PDG5|SMRC2_MOUSE_SWI/SNF_complex_subunit_SMARCC2_OS=Mus_musculus_GN=Smarcc2_PE=1_SV=2	6.00E-26	[illegible]	[illegible]
comp30555_c0_seq2.p1				
comp30556_c0_seq2.p1				
comp30556_c0_seq3.p1				
comp30556_c0_seq4.p1				
comp30556_c0_seq4.p3				
comp30557_c0_seq2.p1				
comp30557_c0_seq3.p1				
comp30557_c0_seq3.p2	sp|D4GGR2|TATD_PANAM_Tat-linked_quality_control_protein_TatD_OS=Pantoea_ananatis_(strain_LMG_20103)_GN=tatD_PE=3_SV=2	1.00E-42	[illegible]	[illegible]
comp30557_c0_seq5.p1				
comp30558_c0_seq3.p2				
comp30558_c0_seq3.p3				
comp30558_c0_seq3.p6				
comp30559_c0_seq3.p1				
comp30559_c0_seq4.p1				
comp3056_c1_seq1.p1	sp|P33607|NUOL_ECOLI_NADH-quinone_oxidoreductase_subunit_L_OS=Escherichia_coli_(strain_K12)_GN=nuoL_PE=1_SV=2	2.00E-60	[illegible]	[illegible]
comp30560_c0_seq4.p1	sp|O23087|ECA2_ARATH_Calcium-transporting_ATPase_2,_endoplasmic_reticulum-type_OS=Arabidopsis_thaliana_GN=ECA2_PE=2_SV=1	0	[illegible]	[illegible]
comp30560_c0_seq5.p1	sp|P90747|YE56_CAEEL_Probable_cation-transporting_ATPase_C10C6.6_OS=Caenorhabditis_elegans_GN=C10C6.6_PE=2_SV=3	2.00E-144	[illegible]	[illegible]
comp30560_c0_seq5.p4				
comp30562_c0_seq1.p1				
comp30562_c0_seq2.p1				
comp30563_c0_seq2.p1	sp|P10242|MYB_HUMAN_Transcriptional_activator_Myb_OS=Homo_sapiens_GN=MYB_PE=1_SV=2	2.00E-35	[illegible]	[illegible]
comp30564_c0_seq5.p1	sp|P16916|RHSA_ECOLI_Protein_rhsA_OS=Escherichia_coli_(strain_K12)_GN=rhsA_PE=3_SV=1	5.00E-82	GO:0097264	[illegible]
comp30565_c0_seq11.p1	sp|Q9C801|MOS2_ARATH_Protein_MOS2_OS=Arabidopsis_thaliana_GN=MOS2_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp30565_c0_seq11.p2				
comp30565_c0_seq3.p1	sp|Q9C801|MOS2_ARATH_Protein_MOS2_OS=Arabidopsis_thaliana_GN=MOS2_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp30565_c0_seq3.p2				
comp30565_c0_seq8.p1	sp|Q9C801|MOS2_ARATH_Protein_MOS2_OS=Arabidopsis_thaliana_GN=MOS2_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp30565_c0_seq8.p2				
comp30565_c0_seq9.p1	sp|Q9C801|MOS2_ARATH_Protein_MOS2_OS=Arabidopsis_thaliana_GN=MOS2_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp30565_c0_seq9.p2				
comp30566_c0_seq1.p1	sp|Q00874|DR100_ARATH_DNA-damage-repair/toleration_protein_DRT100_OS=Arabidopsis_thaliana_GN=DRT100_PE=2_SV=2	1.00E-22	[illegible]	[illegible]
comp30567_c0_seq1.p1	sp|O34524|YOCS_BACSU_Uncharacterized_sodium-dependent_transporter_yocS_OS=Bacillus_subtilis_GN=yocS_PE=3_SV=1	1.00E-48	[illegible]	[illegible]
comp30567_c0_seq2.p1				
comp30567_c0_seq3.p1				
comp30567_c0_seq5.p1				
comp30568_c0_seq3.p1	sp|P59277|SYP81_ARATH_Syntaxin-81_OS=Arabidopsis_thaliana_GN=SYP81_PE=2_SV=2	1.00E-14	[illegible]	[illegible]
comp30568_c0_seq5.p1				
comp30568_c0_seq8.p1				
comp30569_c1_seq3.p1				
comp30569_c1_seq5.p1				
comp30570_c0_seq3.p1				
comp30571_c0_seq4.p1				
comp30573_c0_seq2.p1	sp|Q43582|LSM4_TOBAC_Probable_U6_snRNA-associated_Sm-like_protein_LSm4_OS=Nicotiana_tabacum_PE=2_SV=1	5.00E-28	[illegible]	[illegible]
comp30573_c0_seq2.p4				
comp30573_c0_seq6.p1	sp|Q43582|LSM4_TOBAC_Probable_U6_snRNA-associated_Sm-like_protein_LSm4_OS=Nicotiana_tabacum_PE=2_SV=1	5.00E-28	[illegible]	[illegible]
comp30574_c0_seq1.p1				
comp30574_c0_seq2.p1				
comp30574_c0_seq2.p2				
comp30575_c0_seq2.p1				
comp30575_c0_seq2.p5				
comp30576_c0_seq1.p1	sp|A8XGH1|RPAB1_CAEBR_DNA-directed_RNA_polymerases_I,_II,_and_III_subunit_RPABC1_OS=Caenorhabditis_briggsae_GN=rpb-5_PE=3_SV=1	1.00E-56	[illegible]	[illegible]
comp30576_c0_seq2.p1	sp|Q5UPA0|YL025_MIMIV_Putative_ankyrin_repeat_protein_L25_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L25_PE=4_SV=1	8.00E-16		
comp30577_c0_seq2.p1				
comp30577_c0_seq3.p1				
comp30578_c0_seq1.p2				
comp30579_c0_seq2.p1				
comp30579_c0_seq4.p1				
comp30579_c0_seq4.p6				
comp30579_c0_seq4.p7				
comp30580_c0_seq1.p1				
comp30580_c0_seq2.p1	sp|P44573|OPDA_HAEIN_Oligopeptidase_A_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=prlC_PE=3_SV=1	2.00E-145	[illegible]	[illegible]
comp30580_c0_seq2.p2				
comp30581_c0_seq3.p1	sp|Q9SIK7|PSNB_ARATH_Presenilin-like_protein_At2g29900_OS=Arabidopsis_thaliana_GN=At2g29900_PE=2_SV=1	3.00E-30	[illegible]	[illegible]
comp30582_c1_seq6.p1	sp|Q1ZXG8|D1060_DICDI_Probable_tyrosine-protein_phosphatase_DG1060_OS=Dictyostelium_discoideum_GN=DG1060_PE=3_SV=1	1.00E-21	[illegible]	[illegible]
comp30582_c1_seq6.p2				
comp30583_c0_seq1.p1				
comp30583_c0_seq2.p2				
comp30583_c0_seq7.p1				
comp30583_c0_seq8.p2				
comp30583_c0_seq9.p1				
comp30583_c0_seq9.p2				
comp30584_c0_seq1.p1	sp|P02981|TCR3_ECOLX_Tetracycline_resistance_protein,_class_C_OS=Escherichia_coli_GN=tetA_PE=1_SV=1	4.00E-14	[illegible]	[illegible]
comp30584_c0_seq2.p1	sp|P02981|TCR3_ECOLX_Tetracycline_resistance_protein,_class_C_OS=Escherichia_coli_GN=tetA_PE=1_SV=1	4.00E-14	[illegible]	[illegible]
comp30584_c0_seq5.p1				
comp30584_c0_seq7.p1				
comp30585_c0_seq1.p1	sp|Q39639|PLSB_CUCSA_Glycerol-3-phosphate_acyltransferase,_chloroplastic_OS=Cucumis_sativus_PE=2_SV=1	1.00E-65	[illegible]	[illegible]
comp30586_c0_seq1.p2	sp|P02309|H4_YEAST_Histone_H4_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=HHF1_PE=1_SV=2	1.00E-36	[illegible]	[illegible]
comp30587_c0_seq1.p1				
comp30587_c0_seq2.p1				
comp30587_c0_seq2.p2				
comp30587_c0_seq3.p1				
comp30588_c0_seq1.p1				
comp30588_c0_seq1.p2	sp|Q55E58|PATS1_DICDI_Probable_serine/threonine-protein_kinase_pats1_OS=Dictyostelium_discoideum_GN=pats1_PE=3_SV=1	6.00E-13	[illegible]	[illegible]
comp30588_c0_seq6.p1				
comp30588_c0_seq6.p2				
comp30588_c0_seq6.p3				
comp3059_c0_seq1.p1	sp|P77414|WCAA_ECOLI_Putative_colanic_acid_biosynthesis_glycosyl_transferase_wcaA_OS=Escherichia_coli_(strain_K12)_GN=wcaA_PE=4_SV=1	1.00E-68	[illegible]	[illegible]
comp30590_c0_seq2.p1				
comp30590_c0_seq3.p1				
comp30590_c0_seq5.p1				
comp30590_c0_seq6.p1				
comp30591_c0_seq1.p1				
comp30591_c0_seq1.p4				
comp30591_c0_seq2.p1				
comp30591_c0_seq2.p2				
comp30591_c0_seq2.p5				
comp30592_c0_seq2.p1	sp|O46382|BIG1_BOVIN_Brefeldin_A-inhibited_guanine_nucleotide-exchange_protein_1_OS=Bos_taurus_GN=ARFGEF1_PE=1_SV=1	3.00E-26	[illegible]	[illegible]
comp30592_c0_seq2.p2				
comp30593_c0_seq1.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	2.00E-15	[illegible]	[illegible]
comp30594_c0_seq3.p3				
comp30595_c0_seq1.p1	sp|P31597|EAA3_RABIT_Excitatory_amino_acid_transporter_3_OS=Oryctolagus_cuniculus_GN=SLC1A1_PE=2_SV=1	8.00E-45	[illegible]	[illegible]
comp30596_c0_seq2.p1				
comp30596_c0_seq4.p1	sp|A4QN56|NAGT1_DANRE_Sodium-dependent_glucose_transporter_1_OS=Danio_rerio_GN=naglt1_PE=2_SV=1	5.00E-16	[illegible]	[illegible]
comp30597_c0_seq3.p1				
comp30597_c0_seq3.p6				
comp30597_c0_seq4.p1				
comp30597_c0_seq4.p6				
comp30598_c0_seq11.p1				
comp30598_c0_seq12.p1				
comp30598_c0_seq2.p1				
comp30598_c0_seq5.p1				
comp30599_c0_seq2.p1	sp|P0CM30|ATG2_CRYNJ_Autophagy-related_protein_2_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=ATG2_PE=3_SV=1	1.00E-43	[illegible]	[illegible]
comp30601_c0_seq1.p1				
comp30601_c0_seq1.p2				
comp30601_c0_seq2.p1				
comp30601_c0_seq2.p2				
comp30601_c0_seq4.p1				
comp30601_c0_seq4.p2				
comp30601_c0_seq6.p1				
comp30601_c0_seq6.p2				
comp30601_c0_seq7.p1				
comp30602_c0_seq3.p1				
comp30602_c0_seq3.p5				
comp30602_c0_seq4.p4				
comp30602_c0_seq4.p5				
comp30602_c0_seq6.p1	sp|P26294|PDS_SYNE7_15-cis-phytoene_desaturase_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=pds_PE=1_SV=1	9.00E-15	[illegible]	[illegible]
comp30603_c1_seq4.p1				
comp30603_c1_seq5.p1				
comp30603_c1_seq6.p1	sp|Q69ZN7|MYOF_MOUSE_Myoferlin_OS=Mus_musculus_GN=Myof_PE=1_SV=2	4.00E-16	[illegible]	[illegible]
comp30604_c0_seq4.p1				
comp30605_c0_seq3.p1	sp|Q2MHE4|HT1_ARATH_Serine/threonine-protein_kinase_HT1_OS=Arabidopsis_thaliana_GN=HT1_PE=1_SV=1	4.00E-37	[illegible]	[illegible]
comp30605_c1_seq1.p1				
comp30605_c1_seq3.p1	sp|Q2HJG2|PUF60_BOVIN_Poly(U)-binding-splicing_factor_PUF60_OS=Bos_taurus_GN=PUF60_PE=2_SV=1	2.00E-26	[illegible]	[illegible]
comp30606_c0_seq2.p1	sp|Q91WU6|ZDHC7_MOUSE_Palmitoyltransferase_ZDHHC7_OS=Mus_musculus_GN=Zdhhc7_PE=1_SV=1	7.00E-23	[illegible]	[illegible]
comp30606_c0_seq3.p1				
comp30606_c0_seq5.p1	sp|Q9NYG2|ZDHC3_HUMAN_Palmitoyltransferase_ZDHHC3_OS=Homo_sapiens_GN=ZDHHC3_PE=1_SV=1	9.00E-21	[illegible]	[illegible]
comp30606_c0_seq6.p1				
comp30606_c0_seq7.p2				
comp30607_c0_seq1.p1				
comp30607_c0_seq1.p2				
comp30608_c0_seq2.p1				
comp30608_c0_seq5.p1	sp|Q99385|VCX1_YEAST_Vacuolar_calcium_ion_transporter_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=VCX1_PE=1_SV=1	3.00E-68	[illegible]	[illegible]
comp30609_c0_seq2.p1				
comp30609_c0_seq5.p1				
comp30610_c0_seq1.p1				
comp30610_c0_seq1.p2				
comp30610_c0_seq1.p5				
comp30610_c0_seq8.p1				
comp30610_c0_seq8.p2				
comp30610_c0_seq8.p5				
comp30610_c0_seq9.p1				
comp30611_c0_seq2.p1	sp|O74462|TAF6_SCHPO_Transcription_initiation_factor_TFIID_subunit_6_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=taf6_PE=1_SV=1	3.00E-18	[illegible]	[illegible]
comp30611_c0_seq3.p1	sp|O74462|TAF6_SCHPO_Transcription_initiation_factor_TFIID_subunit_6_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=taf6_PE=1_SV=1	2.00E-43	[illegible]	[illegible]
comp30612_c0_seq2.p1	sp|Q9ATY5|UVH3_ARATH_DNA_repair_protein_UVH3_OS=Arabidopsis_thaliana_GN=UVH3_PE=2_SV=1	6.00E-71	[illegible]	[illegible]
comp30613_c0_seq1.p1				
comp30613_c0_seq1.p4				
comp30613_c0_seq2.p1	sp|Q61420|S35A1_MOUSE_CMP-sialic_acid_transporter_OS=Mus_musculus_GN=Slc35a1_PE=1_SV=2	8.00E-16	[illegible]	[illegible]
comp30613_c0_seq3.p2				
comp30616_c0_seq3.p1				
comp30617_c0_seq1.p1	sp|Q8R2N2|CIR1A_MOUSE_Cirhin_OS=Mus_musculus_GN=Cirh1a_PE=2_SV=3	8.00E-53	[illegible]	[illegible]
comp30617_c0_seq2.p1	sp|A4WNM9|MCTE_RHOS5_(3S)-malyl-CoA_thioesterase_OS=Rhodobacter_sphaeroides_(strain_ATCC_17025_/_ATH_2.4.3)_GN=mcl2_PE=3_SV=1	3.00E-75	[illegible]	[illegible]
comp30618_c0_seq2.p1				
comp30618_c0_seq3.p1				
comp30618_c0_seq4.p1				
comp30618_c0_seq4.p2				
comp30619_c0_seq2.p1	sp|Q8TD26|CHD6_HUMAN_Chromodomain-helicase-DNA-binding_protein_6_OS=Homo_sapiens_GN=CHD6_PE=1_SV=4	9.00E-21	[illegible]	[illegible]
comp30619_c1_seq3.p1	sp|Q8TDI0|CHD5_HUMAN_Chromodomain-helicase-DNA-binding_protein_5_OS=Homo_sapiens_GN=CHD5_PE=1_SV=1	9.00E-11	[illegible]	[illegible]
comp30619_c1_seq3.p3	sp|A2AJK6|CHD7_MOUSE_Chromodomain-helicase-DNA-binding_protein_7_OS=Mus_musculus_GN=Chd7_PE=2_SV=1	5.00E-53	[illegible]	[illegible]
comp30619_c1_seq5.p1	sp|Q8R050|ERF3A_MOUSE_Eukaryotic_peptide_chain_release_factor_GTP-binding_subunit_ERF3A_OS=Mus_musculus_GN=Gspt1_PE=1_SV=1	5.00E-147	[illegible]	[illegible]
comp30619_c1_seq6.p1	sp|Q8R050|ERF3A_MOUSE_Eukaryotic_peptide_chain_release_factor_GTP-binding_subunit_ERF3A_OS=Mus_musculus_GN=Gspt1_PE=1_SV=1	8.00E-131	[illegible]	[illegible]
comp30620_c1_seq1.p1				
comp30620_c1_seq3.p1				
comp30620_c1_seq5.p1				
comp30621_c0_seq2.p1				
comp30621_c0_seq2.p2				
comp30621_c0_seq3.p1				
comp30621_c0_seq4.p1	sp|P12270|TPR_HUMAN_Nucleoprotein_TPR_OS=Homo_sapiens_GN=TPR_PE=1_SV=3	6.00E-21	[illegible]	[illegible]
comp30622_c0_seq1.p1				
comp30622_c0_seq1.p2				
comp30622_c0_seq2.p1				
comp30622_c0_seq2.p2	sp|Q8IYR2|SMYD4_HUMAN_SET_and_MYND_domain-containing_protein_4_OS=Homo_sapiens_GN=SMYD4_PE=2_SV=3	2.00E-20	[illegible]	[illegible]
comp30622_c0_seq3.p1				
comp30622_c0_seq3.p2				
comp30622_c0_seq4.p1				
comp30622_c0_seq4.p2				
comp30622_c0_seq5.p1	sp|Q8IYR2|SMYD4_HUMAN_SET_and_MYND_domain-containing_protein_4_OS=Homo_sapiens_GN=SMYD4_PE=2_SV=3	4.00E-21	[illegible]	[illegible]
comp30623_c0_seq6.p1	sp|Q54NC0|HUS1_DICDI_Checkpoint_protein_hus1_homolog_OS=Dictyostelium_discoideum_GN=hus1_PE=3_SV=1	3.00E-21	[illegible]	[illegible]
comp30623_c0_seq7.p1	sp|Q5ZJM3|NGLY1_CHICK_Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine_amidase_OS=Gallus_gallus_GN=NGLY1_PE=2_SV=1	2.00E-37	[illegible]	[illegible]
comp30623_c0_seq7.p2	sp|Q54NC0|HUS1_DICDI_Checkpoint_protein_hus1_homolog_OS=Dictyostelium_discoideum_GN=hus1_PE=3_SV=1	1.00E-22	[illegible]	[illegible]
comp30625_c0_seq1.p1				
comp30625_c0_seq2.p1				
comp30625_c0_seq3.p1				
comp30625_c0_seq3.p2				
comp30628_c0_seq1.p1	sp|P54677|PI4K_DICDI_Phosphatidylinositol_4-kinase_OS=Dictyostelium_discoideum_GN=pikD_PE=3_SV=3	2.00E-65	[illegible]	[illegible]
comp30628_c0_seq3.p1				
comp30628_c0_seq3.p2	sp|P54677|PI4K_DICDI_Phosphatidylinositol_4-kinase_OS=Dictyostelium_discoideum_GN=pikD_PE=3_SV=3	4.00E-55	[illegible]	[illegible]
comp30629_c0_seq1.p1	sp|Q8H0T4|UPL2_ARATH_E3_ubiquitin-protein_ligase_UPL2_OS=Arabidopsis_thaliana_GN=UPL2_PE=1_SV=3	7.00E-27	[illegible]	[illegible]
comp30629_c0_seq2.p1	sp|Q92462|PUB1_SCHPO_E3_ubiquitin-protein_ligase_pub1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=pub1_PE=1_SV=2	3.00E-48	[illegible]	[illegible]
comp30630_c0_seq1.p1				
comp30630_c0_seq1.p2				
comp30630_c0_seq6.p1				
comp30630_c0_seq6.p2				
comp30631_c0_seq3.p2				
comp30631_c0_seq4.p1				
comp30632_c0_seq3.p1	sp|Q9SK50|TIC55_ARATH_Protein_TIC_55,_chloroplastic_OS=Arabidopsis_thaliana_GN=TIC55_PE=2_SV=1	7.00E-70	[illegible]	[illegible]
comp30633_c0_seq1.p1				
comp30634_c0_seq1.p1	sp|Q90678|PAFA_CHICK_Platelet-activating_factor_acetylhydrolase_OS=Gallus_gallus_GN=PLA2G7_PE=2_SV=1	1.00E-22	[illegible]	[illegible]
comp30635_c0_seq1.p2				
comp30636_c0_seq1.p1				
comp30636_c0_seq5.p1	sp|Q55793|CSD_SYNY3_Probable_cysteine_desulfurase_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=csd_PE=1_SV=1	4.00E-171	[illegible]	[illegible]
comp30637_c0_seq1.p1	sp|Q8W4E1|RH47_ARATH_DEAD-box_ATP-dependent_RNA_helicase_47,_mitochondrial_OS=Arabidopsis_thaliana_GN=RH47_PE=1_SV=2	9.00E-53	[illegible]	[illegible]
comp30639_c0_seq1.p1	sp|Q499P8|CP058_RAT_UPF0420_protein_C16orf58_homolog_OS=Rattus_norvegicus_PE=2_SV=1	1.00E-29	[illegible]	[illegible]
comp30639_c1_seq1.p1				
comp30639_c2_seq1.p1				
comp30639_c2_seq1.p2				
comp30639_c2_seq2.p1				
comp30639_c2_seq2.p2				
comp30640_c0_seq1.p1				
comp30640_c1_seq1.p1				
comp30640_c1_seq1.p2				
comp30641_c0_seq2.p1				
comp30642_c0_seq1.p1				
comp30642_c0_seq4.p1				
comp30643_c0_seq1.p1				
comp30643_c0_seq1.p3	sp|P0AFU2|YFBS_ECOLI_Uncharacterized_transporter_YfbS_OS=Escherichia_coli_(strain_K12)_GN=yfbS_PE=3_SV=1	2.00E-14	[illegible]	[illegible]
comp30643_c0_seq2.p1				
comp30643_c0_seq2.p2	sp|P0AFU2|YFBS_ECOLI_Uncharacterized_transporter_YfbS_OS=Escherichia_coli_(strain_K12)_GN=yfbS_PE=3_SV=1	2.00E-17	[illegible]	[illegible]
comp30643_c0_seq3.p1	sp|Q39593|SAC1_CHLRE_Putative_sulfur_deprivation_response_regulator_OS=Chlamydomonas_reinhardtii_GN=SAC1_PE=2_SV=1	2.00E-20	[illegible]	[illegible]
comp30643_c0_seq3.p2				
comp30644_c0_seq1.p1				
comp30645_c0_seq1.p1				
comp30645_c0_seq2.p1				
comp30645_c1_seq1.p1	sp|Q8GUI6|JMJ14_ARATH_Probable_lysine-specific_demethylase_JMJ14_OS=Arabidopsis_thaliana_GN=JMJ14_PE=1_SV=1	3.00E-26	[illegible]	[illegible]
comp30645_c1_seq2.p1	sp|Q8GUI6|JMJ14_ARATH_Probable_lysine-specific_demethylase_JMJ14_OS=Arabidopsis_thaliana_GN=JMJ14_PE=1_SV=1	4.00E-31	[illegible]	[illegible]
comp30646_c0_seq5.p1	sp|Q96AB6|NTAN1_HUMAN_Protein_N-terminal_asparagine_amidohydrolase_OS=Homo_sapiens_GN=NTAN1_PE=1_SV=3	5.00E-11	[illegible]	[illegible]
comp30647_c0_seq1.p1	sp|Q9H2U1|DHX36_HUMAN_Probable_ATP-dependent_RNA_helicase_DHX36_OS=Homo_sapiens_GN=DHX36_PE=1_SV=2	1.00E-103	[illegible]	[illegible]
comp30647_c0_seq2.p1	sp|Q9H2U1|DHX36_HUMAN_Probable_ATP-dependent_RNA_helicase_DHX36_OS=Homo_sapiens_GN=DHX36_PE=1_SV=2	1.00E-58	[illegible]	[illegible]
comp30647_c0_seq3.p1	sp|B2RR83|YTDC2_MOUSE_Probable_ATP-dependent_RNA_helicase_YTHDC2_OS=Mus_musculus_GN=Ythdc2_PE=2_SV=1	9.00E-79	[illegible]	[illegible]
comp30647_c0_seq5.p1				
comp30649_c0_seq3.p1				
comp30650_c0_seq2.p1	sp|Q5ZJN1|CT043_CHICK_UPF0549_protein_C20orf43_homolog_OS=Gallus_gallus_GN=RCJMB04_16p11_PE=2_SV=1	6.00E-23		
comp30651_c0_seq1.p1				
comp30652_c0_seq3.p1	sp|Q3EDF8|PPR28_ARATH_Pentatricopeptide_repeat-containing_protein_At1g09900_OS=Arabidopsis_thaliana_GN=At1g09900_PE=2_SV=1	6.00E-14	[illegible]	[illegible]
comp30652_c0_seq3.p2				
comp30652_c0_seq4.p1				
comp30653_c0_seq12.p1	sp|O14730|RIOK3_HUMAN_Serine/threonine-protein_kinase_RIO3_OS=Homo_sapiens_GN=RIOK3_PE=1_SV=2	9.00E-65	[illegible]	[illegible]
comp30653_c0_seq3.p5				
comp30653_c0_seq9.p5				
comp30654_c0_seq2.p1				
comp30655_c0_seq1.p1				
comp30655_c0_seq3.p1				
comp30655_c0_seq4.p1				
comp30655_c0_seq7.p2				
comp30655_c0_seq7.p3				
comp30655_c0_seq8.p1				
comp30656_c0_seq2.p1				
comp30656_c0_seq3.p1				
comp30656_c0_seq3.p2				
comp30656_c0_seq4.p1				
comp30656_c0_seq5.p1	sp|Q0WKV8|ULP2A_ARATH_Probable_ubiquitin-like-specific_protease_2A_OS=Arabidopsis_thaliana_GN=ULP2A_PE=2_SV=2	4.00E-15	[illegible]	[illegible]
comp30657_c0_seq1.p1	sp|A2RU49|AGPD1_HUMAN_Aminoglycoside_phosphotransferase_domain-containing_protein_1_OS=Homo_sapiens_GN=AGPHD1_PE=2_SV=2	1.00E-51	[illegible]	[illegible]
comp30657_c0_seq5.p1	sp|A9VE54|ITPA_MONBE_Inosine_triphosphate_pyrophosphatase_OS=Monosiga_brevicollis_GN=13033_PE=3_SV=1	7.00E-85	[illegible]	[illegible]
comp30659_c0_seq11.p1	sp|O96860|DYL2_DROME_Dynein_light_chain_2,_cytoplasmic_OS=Drosophila_melanogaster_GN=Cdlc2_PE=3_SV=1	4.00E-36	[illegible]	[illegible]
comp30659_c0_seq16.p1				
comp30659_c0_seq17.p1				
comp30659_c0_seq5.p1	sp|O96860|DYL2_DROME_Dynein_light_chain_2,_cytoplasmic_OS=Drosophila_melanogaster_GN=Cdlc2_PE=3_SV=1	4.00E-34	[illegible]	[illegible]
comp30659_c0_seq6.p2	sp|O96860|DYL2_DROME_Dynein_light_chain_2,_cytoplasmic_OS=Drosophila_melanogaster_GN=Cdlc2_PE=3_SV=1	9.00E-39	[illegible]	[illegible]
comp30659_c0_seq7.p1	sp|O96860|DYL2_DROME_Dynein_light_chain_2,_cytoplasmic_OS=Drosophila_melanogaster_GN=Cdlc2_PE=3_SV=1	5.00E-32	[illegible]	[illegible]
comp30659_c0_seq8.p1				
comp30659_c1_seq1.p1	sp|Q7Q5D4|S35B3_ANOGA_Adenosine_3'-phospho_5'-phosphosulfate_transporter_2_OS=Anopheles_gambiae_GN=Papst2_PE=3_SV=4	2.00E-34	[illegible]	[illegible]
comp30662_c0_seq3.p1	sp|A3BT52|RH29_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_29_OS=Oryza_sativa_subsp._japonica_GN=Os08g0416100_PE=2_SV=2	2.00E-158	[illegible]	[illegible]
comp30663_c0_seq3.p1	sp|Q3U4G0|CO041_MOUSE_Uncharacterized_protein_C15orf41_homolog_OS=Mus_musculus_PE=2_SV=2	6.00E-38	[illegible]	[illegible]
comp30664_c0_seq2.p1				
comp30664_c0_seq2.p2				
comp30664_c0_seq2.p3				
comp30664_c0_seq3.p1				
comp30664_c0_seq3.p2				
comp30664_c0_seq6.p1				
comp30665_c0_seq12.p1				
comp30666_c0_seq1.p1	sp|Q10270|MET16_SCHPO_Probable_phosphoadenosine_phosphosulfate_reductase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC13G7.06_PE=2_SV=1	8.00E-34	[illegible]	[illegible]
comp30666_c0_seq1.p2				
comp30666_c0_seq10.p1	sp|P54554|YQJQ_BACSU_Uncharacterized_oxidoreductase_yqjQ_OS=Bacillus_subtilis_GN=yqjQ_PE=3_SV=1	7.00E-11	[illegible]	[illegible]

comp30666_c0_seq14.p1		
comp30666_c0_seq14.p2	sp|P54554|YQJQ_BACSU_Uncharacterized_oxidoreductase_yqjQ_OS=Bacillus_subtilis_GN=yqjQ_PE=3_SV=1	9.00E-12
comp30666_c0_seq5.p1	sp|Q10270|MET16_SCHPO_Probable_phosphoadenosine_phosphosulfate_reductase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC13G7.06_PE=2_SV=1	8.00E-34
comp30666_c0_seq5.p3		
comp30666_c0_seq6.p1	sp|Q10270|MET16_SCHPO_Probable_phosphoadenosine_phosphosulfate_reductase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC13G7.06_PE=2_SV=1	6.00E-35
comp30668_c1_seq3.p1	sp|A4R8D7|MCES_MAGO7_mRNA_cap_guanine-N7_methyltransferase_OS=Magnaporthe_oryzae_(strain_70-15_/_ATCC_MYA-4617_/_FGSC_8958)_GN=ABD1_PE=3_SV=1	8.00E-31
comp30668_c1_seq3.p4		
comp30668_c1_seq5.p1	sp|A4R8D7|MCES_MAGO7_mRNA_cap_guanine-N7_methyltransferase_OS=Magnaporthe_oryzae_(strain_70-15_/_ATCC_MYA-4617_/_FGSC_8958)_GN=ABD1_PE=3_SV=1	8.00E-31
comp30668_c1_seq5.p2		
comp30668_c1_seq7.p1	sp|Q6Z9U7|MCES1_ORYSJ_mRNA_cap_guanine-N7_methyltransferase_1_OS=Oryza_sativa_subsp._japonica_GN=Os08g0180000_PE=2_SV=1	2.00E-34
comp30668_c1_seq8.p1	sp|Q6Z9U7|MCES1_ORYSJ_mRNA_cap_guanine-N7_methyltransferase_1_OS=Oryza_sativa_subsp._japonica_GN=Os08g0180000_PE=2_SV=1	7.00E-35
comp30668_c1_seq8.p3		
comp30669_c0_seq1.p1		
comp30669_c0_seq1.p2		
comp30671_c0_seq2.p1		
comp30673_c0_seq1.p1	sp|Q80ZK9|WDTC1_MOUSE_WD_and_tetratricopeptide_repeats_protein_1_OS=Mus_musculus_GN=Wdtc1_PE=1_SV=1	2.00E-21
comp30673_c0_seq2.p1	sp|Q3KPR1|C1D_XENLA_Nuclear_nucleic_acid-binding_protein_C1D_OS=Xenopus_laevis_GN=c1d_PE=2_SV=1	2.00E-22
comp30674_c0_seq2.p1	sp|Q04960|DNJH_CUCSA_DnaJ_protein_homolog_OS=Cucumis_sativus_GN=DNAJ1_PE=2_SV=1	3.00E-26
comp30674_c0_seq3.p1		
comp30674_c0_seq3.p2		
comp30674_c0_seq4.p1		
comp30674_c0_seq4.p2		
comp30675_c0_seq3.p1		
comp30675_c0_seq4.p1		
comp30676_c0_seq1.p1		
comp30676_c0_seq2.p2		
comp30676_c0_seq3.p1		
comp30676_c0_seq3.p2		
comp30677_c0_seq2.p1		
comp30677_c0_seq4.p1		
comp30678_c0_seq2.p1		
comp30678_c0_seq3.p1		
comp30679_c0_seq1.p1	sp|Q40593|VDE_TOBAC_Violaxanthin_de-epoxidase,_chloroplastic_OS=Nicotiana_tabacum_GN=VDE1_PE=2_SV=1	1.00E-21
comp30679_c0_seq3.p1		
comp30680_c0_seq1.p1	sp|Q07282|TCR5_ECOLX_Tetracycline_resistance_protein,_class_E_OS=Escherichia_coli_GN=tetA_PE=3_SV=1	1.00E-23
comp30683_c0_seq2.p1	sp|Q5FVC7|ACAP2_RAT_Arf-GAP_with_coiled-coil,_ANK_repeat_and_PH_domain-containing_protein_2_OS=Rattus_norvegicus_GN=Acap2_PE=2_SV=1	2.00E-49
comp30685_c0_seq1.p1	sp|Q9UNW9|NOVA2_HUMAN_RNA-binding_protein_Nova-2_OS=Homo_sapiens_GN=NOVA2_PE=1_SV=1	2.00E-14
comp30686_c0_seq1.p1		
comp30686_c0_seq6.p1		
comp30686_c0_seq7.p1		
comp30686_c0_seq8.p1		
comp30687_c0_seq2.p1	sp|Q54E41|HAOX_DICDI_Hydroxyacid_oxidase_OS=Dictyostelium_discoideum_GN=haox_PE=3_SV=1	4.00E-38
comp30687_c0_seq2.p2	sp|Q9UJM8|HAOX1_HUMAN_Hydroxyacid_oxidase_1_OS=Homo_sapiens_GN=HAO1_PE=1_SV=1	4.00E-39
comp30687_c0_seq2.p5		
comp30687_c0_seq3.p1	sp|Q9UJM8|HAOX1_HUMAN_Hydroxyacid_oxidase_1_OS=Homo_sapiens_GN=HAO1_PE=1_SV=1	3.00E-92
comp30688_c0_seq1.p1	sp|Q9Z0F5|CH25H_MOUSE_Cholesterol_25-hydroxylase_OS=Mus_musculus_GN=Ch25h_PE=1_SV=1	6.00E-28
comp30688_c0_seq3.p1	sp|Q4G017|NISCH_RAT_Nischarin_OS=Rattus_norvegicus_GN=Nisch_PE=2_SV=2	2.00E-13
comp30688_c0_seq4.p1		
comp30688_c0_seq4.p2	sp|Q4QQV7|CH25H_RAT_Cholesterol_25-hydroxylase_OS=Rattus_norvegicus_GN=Ch25h_PE=2_SV=1	1.00E-15
comp30688_c0_seq6.p1	sp|Q5PRC0|CH25H_DANRE_Cholesterol_25-hydroxylase-like_protein_OS=Danio_rerio_GN=ch25h_PE=2_SV=1	3.00E-23
comp30688_c0_seq7.p1		
comp30688_c0_seq7.p3	sp|Q4QQV7|CH25H_RAT_Cholesterol_25-hydroxylase_OS=Rattus_norvegicus_GN=Ch25h_PE=2_SV=1	1.00E-15
comp30688_c1_seq1.p1		
comp30689_c0_seq1.p1		
comp30689_c0_seq3.p1		
comp30689_c0_seq7.p1		
comp30690_c0_seq2.p1		
comp30690_c0_seq4.p1		
comp30690_c0_seq4.p2		
comp30691_c0_seq1.p1		
comp30691_c0_seq1.p2	sp|P02982|TCR1_ECOLX_Tetracycline_resistance_protein,_class_A_OS=Escherichia_coli_GN=tetA_PE=3_SV=2	1.00E-17
comp30692_c0_seq2.p1		
comp30693_c0_seq1.p1		
comp30694_c0_seq1.p1		
comp30695_c0_seq1.p1		
comp30695_c1_seq2.p1		
comp30695_c1_seq3.p1	sp|P0A5F6|Y1866_MYCBO_Putative_serine_esterase_Mb1866c_OS=Mycobacterium_bovis_GN=Mb1866c_PE=3_SV=1	1.00E-43
comp30695_c1_seq4.p1		
comp30696_c0_seq1.p2		
comp30696_c0_seq10.p1	sp|Q14BP6|YV012_MOUSE_Leucine-rich_repeat-containing_protein_LOC400891_homolog_OS=Mus_musculus_PE=2_SV=1	5.00E-11
comp30696_c0_seq14.p4		
comp30696_c0_seq2.p2		
comp30696_c0_seq2.p5		
comp30696_c0_seq3.p2		
comp30696_c0_seq4.p2		
comp30696_c0_seq4.p3		
comp30696_c0_seq4.p5		
comp30696_c0_seq5.p6		
comp30696_c0_seq6.p1	sp|Q14BP6|YV012_MOUSE_Leucine-rich_repeat-containing_protein_LOC400891_homolog_OS=Mus_musculus_PE=2_SV=1	7.00E-11
comp30696_c0_seq7.p4		
comp30696_c0_seq9.p1	sp|Q14BP6|YV012_MOUSE_Leucine-rich_repeat-containing_protein_LOC400891_homolog_OS=Mus_musculus_PE=2_SV=1	5.00E-11
comp30697_c0_seq1.p1	sp|Q96PY6|NEK1_HUMAN_Serine/threonine-protein_kinase_Nek1_OS=Homo_sapiens_GN=NEK1_PE=1_SV=2	7.00E-75
comp30698_c0_seq1.p1		
comp30698_c0_seq5.p1		
comp30698_c0_seq6.p1		
comp30699_c0_seq1.p1	sp|Q8TF05|PP4R1_HUMAN_Serine/threonine-protein_phosphatase_4_regulatory_subunit_1_OS=Homo_sapiens_GN=PPP4R1_PE=1_SV=1	2.00E-33
comp30700_c0_seq3.p1		
comp30700_c0_seq4.p1		
comp30700_c0_seq6.p1	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	3.00E-26
comp30701_c0_seq1.p1	sp|Q04217|DHR1_YEAST_Probable_ATP-dependent_RNA_helicase_DHR1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=ECM16_PE=1_SV=1	4.00E-82
comp30701_c0_seq1.p2	sp|P19582|DHOM_BACSU_Homoserine_dehydrogenase_OS=Bacillus_subtilis_GN=hom_PE=3_SV=2	2.00E-72
comp30702_c0_seq1.p1		
comp30703_c0_seq2.p1		
comp30704_c0_seq2.p1	sp|Q93YQ1|RTOR1_ARATH_Regulatory-associated_protein_of_TOR_1_OS=Arabidopsis_thaliana_GN=RAPTOR1_PE=1_SV=1	2.00E-19
comp30705_c0_seq2.p1	sp|Q9DBC0|SELO_MOUSE_Selenoprotein_O_OS=Mus_musculus_GN=Selo_PE=1_SV=4	4.00E-175
comp30706_c0_seq1.p1		
comp30707_c0_seq1.p1		
comp30708_c0_seq2.p1		
comp30709_c0_seq2.p1		
comp30709_c0_seq3.p1		
comp30710_c0_seq1.p1	sp|P42695|CNDD3_HUMAN_Condensin-2_complex_subunit_D3_OS=Homo_sapiens_GN=NCAPD3_PE=1_SV=2	1.00E-53
comp30711_c0_seq1.p1		
comp30713_c0_seq2.p1		
comp30713_c0_seq3.p1		
comp30713_c0_seq4.p1		
comp30713_c0_seq5.p1		
comp30713_c0_seq7.p1		
comp30714_c0_seq3.p1		
comp30714_c0_seq5.p1		
comp30714_c0_seq5.p2		
comp30715_c0_seq2.p1		
comp30715_c0_seq3.p1	sp|Q9FFN2|GLYT3_ARATH_Probable_glycosyltransferase_At5g03795_OS=Arabidopsis_thaliana_GN=At5g03795_PE=3_SV=2	7.00E-11
comp30716_c0_seq1.p1		
comp30716_c0_seq1.p3		
comp30716_c0_seq2.p1		
comp30716_c0_seq2.p3		
comp30717_c0_seq2.p1	sp|Q6TEL0|MTMR8_DANRE_Myotubularin-related_protein_8_OS=Danio_rerio_GN=mtmr8_PE=2_SV=1	1.00E-69
comp30717_c0_seq7.p1	sp|Q6TEL0|MTMR8_DANRE_Myotubularin-related_protein_8_OS=Danio_rerio_GN=mtmr8_PE=2_SV=1	1.00E-68
comp30717_c0_seq7.p4		
comp30718_c0_seq4.p1	sp|Q8GYX8|DNJ10_ARATH_Chaperone_protein_dnaJ_10_OS=Arabidopsis_thaliana_GN=ATJ10_PE=2_SV=2	1.00E-23
comp30719_c0_seq1.p2		
comp30719_c0_seq3.p1		
comp30720_c0_seq1.p1		
comp30720_c0_seq4.p1		
comp30721_c0_seq1.p1		
comp30722_c0_seq1.p1	sp|Q61IR6|MED14_CAEBR_Mediator_of_RNA_polymerase_II_transcription_subunit_14_OS=Caenorhabditis_briggsae_GN=rgr-1_PE=3_SV=3	3.00E-19
comp30722_c0_seq5.p1	sp|Q61IR6|MED14_CAEBR_Mediator_of_RNA_polymerase_II_transcription_subunit_14_OS=Caenorhabditis_briggsae_GN=rgr-1_PE=3_SV=3	1.00E-17
comp30723_c0_seq1.p1	sp|Q9CU62|SMC1A_MOUSE_Structural_maintenance_of_chromosomes_protein_1A_OS=Mus_musculus_GN=Smc1a_PE=1_SV=4	2.00E-143
comp30724_c0_seq1.p1		
comp30724_c1_seq1.p1		
comp30724_c2_seq2.p1		
comp30724_c2_seq2.p5		
comp30724_c2_seq3.p2		
comp30725_c0_seq2.p1	sp|P49256|LMAN2_CANFA_Vesicular_integral-membrane_protein_VIP36_OS=Canis_familiaris_GN=LMAN2_PE=1_SV=1	8.00E-21
comp30726_c0_seq2.p1		
comp30726_c0_seq2.p3	sp|A6URN9|PSA_METVS_Proteasome_subunit_alpha_OS=Methanococcus_vannielii_(strain_SB_/_ATCC_35089_/_DSM_1224)_GN=psmA_PE=3_SV=1	1.00E-11
comp30727_c0_seq2.p1		
comp30727_c0_seq2.p2		
comp30727_c0_seq3.p1	sp|Q28D01|WDR26_XENTR_WD_repeat-containing_protein_26_OS=Xenopus_tropicalis_GN=wdr26_PE=2_SV=2	8.00E-17
comp30728_c0_seq2.p1		
comp30728_c0_seq3.p1		
comp30729_c0_seq1.p1		
comp30729_c0_seq10.p1		
comp30729_c0_seq11.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	2.00E-17
comp30729_c0_seq3.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	1.00E-27
comp30729_c0_seq4.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	4.00E-11
comp30729_c0_seq5.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	1.00E-27
comp30729_c0_seq8.p1	sp|P22792|CPN2_HUMAN_Carboxypeptidase_N_subunit_2_OS=Homo_sapiens_GN=CPN2_PE=1_SV=3	5.00E-19
comp30731_c0_seq2.p1		
comp30731_c0_seq3.p1		
comp30732_c0_seq1.p1		
comp30732_c0_seq2.p1		
comp30732_c0_seq3.p1		
comp30732_c0_seq4.p1		
comp30732_c0_seq5.p1		
comp30732_c0_seq6.p1		
comp30733_c0_seq1.p1		
comp30733_c0_seq3.p1		
comp30734_c0_seq1.p1		
comp30735_c0_seq10.p1	sp|Q9XHH2|DNAL1_CHLRE_Dynein_light_chain_1,_axonemal_OS=Chlamydomonas_reinhardtii_GN=LC1_PE=1_SV=1	8.00E-64
comp30735_c0_seq10.p2	sp|B0KS71|RSMJ_PSEPG_Ribosomal_RNA_small_subunit_methyltransferase_J_OS=Pseudomonas_putida_(strain_GB-1)_GN=rsmJ_PE=3_SV=1	2.00E-19
comp30735_c0_seq12.p1		
comp30735_c0_seq12.p2		
comp30735_c0_seq12.p5	sp|C0Q148|RSMJ_SALPC_Ribosomal_RNA_small_subunit_methyltransferase_J_OS=Salmonella_paratyphi_C_(strain_RKS4594)_GN=rsmJ_PE=3_SV=2	4.00E-15
comp30735_c0_seq17.p1		
comp30735_c0_seq17.p2		
comp30735_c0_seq17.p5	sp|C0Q148|RSMJ_SALPC_Ribosomal_RNA_small_subunit_methyltransferase_J_OS=Salmonella_paratyphi_C_(strain_RKS4594)_GN=rsmJ_PE=3_SV=2	4.00E-15
comp30735_c0_seq19.p1		
comp30735_c0_seq2.p1	sp|B0KS71|RSMJ_PSEPG_Ribosomal_RNA_small_subunit_methyltransferase_J_OS=Pseudomonas_putida_(strain_GB-1)_GN=rsmJ_PE=3_SV=1	1.00E-27
comp30735_c0_seq2.p2		
comp30735_c0_seq24.p1		
comp30735_c0_seq24.p2		
comp30735_c0_seq3.p1	sp|B0KS71|RSMJ_PSEPG_Ribosomal_RNA_small_subunit_methyltransferase_J_OS=Pseudomonas_putida_(strain_GB-1)_GN=rsmJ_PE=3_SV=1	1.00E-27
comp30735_c0_seq3.p2		
comp30736_c0_seq3.p1	sp|Q8K2H6|APC10_MOUSE_Anaphase-promoting_complex_subunit_10_OS=Mus_musculus_GN=Anapc10_PE=2_SV=1	4.00E-49
comp30736_c0_seq4.p1	sp|Q8K2H6|APC10_MOUSE_Anaphase-promoting_complex_subunit_10_OS=Mus_musculus_GN=Anapc10_PE=2_SV=1	2.00E-24
comp30736_c0_seq5.p1		
comp30736_c0_seq5.p2	sp|Q8K2H6|APC10_MOUSE_Anaphase-promoting_complex_subunit_10_OS=Mus_musculus_GN=Anapc10_PE=2_SV=1	2.00E-24
comp30736_c0_seq5.p3		
comp30736_c0_seq6.p1		
comp30736_c0_seq9.p1		
comp30736_c0_seq9.p2	sp|Q8K2H6|APC10_MOUSE_Anaphase-promoting_complex_subunit_10_OS=Mus_musculus_GN=Anapc10_PE=2_SV=1	4.00E-51
comp30738_c0_seq2.p1	sp|Q54K57|TPSA_DICDI_Alpha,alpha-trehalose-phosphate_synthase_[UDP-forming]_A_OS=Dictyostelium_discoideum_GN=tpsA_PE=2_SV=1	0
comp30739_c0_seq2.p1		
comp30739_c0_seq3.p1		
comp30739_c0_seq3.p5		
comp30740_c1_seq1.p1	sp|Q31QR8|RPOD4_SYNE7_RNA_polymerase_sigma_factor_rpoD4_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=rpoD4_PE=3_SV=1	4.00E-24
comp30740_c1_seq12.p3		
comp30740_c1_seq13.p1		
comp30740_c1_seq14.p1		
comp30740_c1_seq14.p5		
comp30740_c1_seq19.p1		
comp30740_c1_seq19.p3		
comp30740_c1_seq2.p1	sp|Q51804|RPOS_VIBCH_RNA_polymerase_sigma_factor_rpoS_OS=Vibrio_cholerae_GN=rpoS_PE=3_SV=1	2.00E-19
comp30740_c1_seq20.p1		
comp30740_c1_seq21.p1	sp|Q31QR8|RPOD4_SYNE7_RNA_polymerase_sigma_factor_rpoD4_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=rpoD4_PE=3_SV=1	4.00E-25
comp30740_c1_seq22.p2		
comp30740_c1_seq22.p5		
comp30740_c1_seq23.p3		
comp30740_c1_seq23.p5		
comp30740_c1_seq24.p1	sp|Q31QG5|RPOD3_SYNE7_RNA_polymerase_sigma_factor_rpoD3_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=rpoD3_PE=3_SV=1	1.00E-19
comp30740_c1_seq9.p1		
comp30741_c0_seq1.p2		
comp30741_c0_seq5.p1	sp|Q5QN75|M2K1_ORYSJ_Mitogen-activated_protein_kinase_kinase_1_OS=Oryza_sativa_subsp._japonica_GN=MEK1_PE=1_SV=1	9.00E-19
comp30741_c0_seq6.p1		
comp30742_c0_seq1.p1		
comp30742_c1_seq2.p1		
comp30744_c0_seq1.p1		
comp30744_c0_seq2.p1		
comp30746_c0_seq3.p1		
comp30746_c0_seq9.p1	sp|Q75B82|NHP6_ASHGO_Non-histone_chromosomal_protein_6_OS=Ashbya_gossypii_(strain_ATCC_10895_/_CBS_109.51_/_FGSC_9923_/_NRRL_Y-1056)_GN=NHP6_PE=3_SV=1	1.00E-17
comp30747_c0_seq1.p1		
comp30747_c0_seq1.p7		
comp30747_c0_seq3.p1		
comp30749_c0_seq3.p1		
comp30750_c0_seq2.p1	sp|Q8BMD6|CN101_MOUSE_UPF0679_protein_C14orf101_homolog_OS=Mus_musculus_PE=2_SV=2	1.00E-25
comp30750_c0_seq3.p1	sp|Q8BMD6|CN101_MOUSE_UPF0679_protein_C14orf101_homolog_OS=Mus_musculus_PE=2_SV=2	1.00E-25
comp30751_c0_seq1.p1		
comp30751_c0_seq1.p2	sp|Q9M2S6|SDIR1_ARATH_E3_ubiquitin-protein_ligase_SDIR1_OS=Arabidopsis_thaliana_GN=SDIR1_PE=1_SV=1	4.00E-11
comp30751_c0_seq1.p3	sp|Q63528|RFA2_RAT_Replication_protein_A_32_kDa_subunit_OS=Rattus_norvegicus_GN=Rpa2_PE=2_SV=2	1.00E-29
comp30751_c0_seq1.p9		
comp30751_c0_seq2.p1		
comp30751_c0_seq2.p2	sp|Q9M2S6|SDIR1_ARATH_E3_ubiquitin-protein_ligase_SDIR1_OS=Arabidopsis_thaliana_GN=SDIR1_PE=1_SV=1	4.00E-11
comp30751_c0_seq2.p3		
comp30751_c0_seq2.p4	sp|Q63528|RFA2_RAT_Replication_protein_A_32_kDa_subunit_OS=Rattus_norvegicus_GN=Rpa2_PE=2_SV=2	1.00E-29
comp30751_c0_seq3.p1		
comp30751_c0_seq3.p2	sp|Q9M2S6|SDIR1_ARATH_E3_ubiquitin-protein_ligase_SDIR1_OS=Arabidopsis_thaliana_GN=SDIR1_PE=1_SV=1	4.00E-11
comp30751_c0_seq3.p3	sp|Q63528|RFA2_RAT_Replication_protein_A_32_kDa_subunit_OS=Rattus_norvegicus_GN=Rpa2_PE=2_SV=2	1.00E-29
comp30751_c0_seq3.p9		
comp30751_c0_seq4.p1		
comp30751_c0_seq4.p2	sp|Q9M2S6|SDIR1_ARATH_E3_ubiquitin-protein_ligase_SDIR1_OS=Arabidopsis_thaliana_GN=SDIR1_PE=1_SV=1	4.00E-11
comp30751_c0_seq4.p3		
comp30751_c0_seq4.p4	sp|Q63528|RFA2_RAT_Replication_protein_A_32_kDa_subunit_OS=Rattus_norvegicus_GN=Rpa2_PE=2_SV=2	1.00E-29
comp30752_c1_seq3.p1		
comp30752_c1_seq4.p1		
comp30752_c1_seq6.p1		
comp30753_c0_seq3.p1	sp|Q3T0W4|PP1R7_BOVIN_Protein_phosphatase_1_regulatory_subunit_7_OS=Bos_taurus_GN=PPP1R7_PE=1_SV=1	2.00E-50
comp30753_c0_seq5.p1	sp|Q3UM45|PP1R7_MOUSE_Protein_phosphatase_1_regulatory_subunit_7_OS=Mus_musculus_GN=Ppp1r7_PE=1_SV=2	2.00E-69
comp30754_c0_seq1.p1	sp|Q6BY27|DBP2_DEBHA_ATP-dependent_RNA_helicase_DBP2_OS=Debaryomyces_hansenii_(strain_ATCC_36239_/_CBS_767_/_JCM_1990_/_NBRC_0083_/_IGC_2968)_GN=DBP2_PE=3_SV=1	3.00E-128
comp30754_c0_seq1.p2	sp|Q6C4D4|DBP2_YARLI_ATP-dependent_RNA_helicase_DBP2_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=DBP2_PE=3_SV=1	1.00E-44
comp30754_c0_seq2.p1	sp|A1DGZ7|DBP2_NEOFI_ATP-dependent_RNA_helicase_dbp2_OS=Neosartorya_fischeri_(strain_ATCC_1020_/_DSM_3700_/_FGSC_A1164_/_NRRL_181)_GN=dbp2_PE=3_SV=1	0
comp30754_c0_seq3.p1	sp|A1C6C4|DBP2_ASPCL_ATP-dependent_RNA_helicase_dbp2_OS=Aspergillus_clavatus_(strain_ATCC_1007_/_CBS_513.65_/_DSM_816_/_NCTC_3887_/_NRRL_1)_GN=dbp2_PE=3_SV=1	7.00E-122
comp30754_c0_seq3.p2	sp|Q6C4D4|DBP2_YARLI_ATP-dependent_RNA_helicase_DBP2_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=DBP2_PE=3_SV=1	1.00E-44
comp30754_c0_seq3.p4		
comp30755_c0_seq3.p1		
comp30756_c0_seq1.p1	sp|Q8RX87|RFS6_ARATH_Probable_galactinol--sucrose_galactosyltransferase_6_OS=Arabidopsis_thaliana_GN=RFS6_PE=2_SV=2	5.00E-107
comp30756_c0_seq1.p2	sp|P52878|SERC_METBF_Phosphoserine_aminotransferase_OS=Methanosarcina_barkeri_(strain_Fusaro_/_DSM_804)_GN=serC_PE=1_SV=1	4.00E-152
comp30757_c0_seq1.p1		
comp30757_c0_seq3.p1		
comp30758_c0_seq3.p1		
comp30758_c0_seq4.p1		
comp30758_c0_seq7.p1		
comp30759_c0_seq1.p1		
comp30759_c0_seq1.p2		
comp30760_c0_seq2.p1	sp|Q5UPA0|YL025_MIMIV_Putative_ankyrin_repeat_protein_L25_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L25_PE=4_SV=1	2.00E-12
comp30760_c0_seq3.p1	sp|Q5UPA0|YL025_MIMIV_Putative_ankyrin_repeat_protein_L25_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L25_PE=4_SV=1	2.00E-12
comp30761_c0_seq1.p1	sp|Q87MD4|TRUC_VIBPA_tRNA_pseudouridine_synthase_C_OS=Vibrio_parahaemolyticus_GN=truC_PE=3_SV=1	1.00E-20
comp30763_c0_seq3.p1		
comp30763_c0_seq3.p2		
comp30765_c0_seq2.p1		
comp30765_c0_seq2.p2		
comp30765_c0_seq2.p3		
comp30765_c0_seq3.p1		
comp30765_c0_seq3.p2		
comp30765_c0_seq3.p4		
comp30765_c0_seq3.p5		
comp30765_c0_seq4.p1		
comp30765_c0_seq4.p2		
comp30765_c0_seq4.p3		
comp30765_c0_seq5.p1		
comp30765_c0_seq5.p2		
comp30765_c0_seq5.p3		
comp30765_c0_seq6.p1		
comp30765_c0_seq6.p2		
comp30765_c0_seq6.p4		
comp30765_c0_seq6.p5		
comp30765_c0_seq7.p1		
comp30765_c0_seq7.p2		
comp30765_c0_seq7.p4		
comp30765_c0_seq7.p5		
comp30766_c0_seq3.p1	sp|Q8PSE5|HTPX2_METMA_Protease_HtpX_homolog_2_OS=Methanosarcina_mazei_(strain_ATCC_BAA-159_/_DSM_3647_/_Goe1_/_Go1_/_JCM_11833_/_OCM_88)_GN=htpX2_PE=3_SV=1	5.00E-11
comp30766_c0_seq4.p1	sp|Q8K2Z8|UB2Q2_MOUSE_Ubiquitin-conjugating_enzyme_E2_Q2_OS=Mus_musculus_GN=Ube2q2_PE=2_SV=2	5.00E-26
comp30767_c0_seq3.p1	sp|O43379|WDR62_HUMAN_WD_repeat-containing_protein_62_OS=Homo_sapiens_GN=WDR62_PE=1_SV=4	4.00E-49
comp30769_c0_seq4.p1		
comp30770_c0_seq1.p1		
comp30771_c0_seq3.p1		
comp30772_c0_seq1.p1		
comp30772_c1_seq1.p1		
comp30772_c1_seq1.p5		
comp30773_c0_seq1.p2		
comp30773_c0_seq2.p1		
comp30773_c0_seq3.p1	sp|Q55680|Y005_SYNY3_Uncharacterized_protein_sll0005_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll0005_PE=3_SV=1	2.00E-82
comp30773_c0_seq5.p1	sp|Q55680|Y005_SYNY3_Uncharacterized_protein_sll0005_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll0005_PE=3_SV=1	7.00E-118
comp30774_c0_seq2.p1	sp|Q9UUJ6|NED1_SCHPO_Nuclear_elongation_and_deformation_protein_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ned1_PE=1_SV=1	6.00E-28
comp30774_c1_seq1.p1	sp|Q92539|LPIN2_HUMAN_Phosphatidate_phosphatase_LPIN2_OS=Homo_sapiens_GN=LPIN2_PE=1_SV=1	4.00E-12
comp30775_c0_seq12.p1		
comp30775_c0_seq13.p1	sp|Q8NFF2|NCKX4_HUMAN_Sodium/potassium/calcium_exchanger_4_OS=Homo_sapiens_GN=SLC24A4_PE=2_SV=2	1.00E-37
comp30775_c0_seq4.p1	sp|Q8NFF2|NCKX4_HUMAN_Sodium/potassium/calcium_exchanger_4_OS=Homo_sapiens_GN=SLC24A4_PE=2_SV=2	9.00E-23
comp30775_c0_seq6.p1	sp|Q9EPQ0|NCKX3_RAT_Sodium/potassium/calcium_exchanger_3_(Fragment)_OS=Rattus_norvegicus_GN=Slc24a3_PE=2_SV=1	1.00E-21
comp30777_c0_seq1.p1	sp|O88738|BIRC6_MOUSE_Baculoviral_IAP_repeat-containing_protein_6_OS=Mus_musculus_GN=Birc6_PE=1_SV=2	4.00E-53
comp30777_c0_seq4.p1		
comp30778_c0_seq4.p1		
comp30779_c2_seq2.p1		
comp30779_c2_seq3.p1	sp|Q7XJN0|RH17_ARATH_DEAD-box_ATP-dependent_RNA_helicase_17_OS=Arabidopsis_thaliana_GN=RH17_PE=2_SV=1	7.00E-53
comp30779_c2_seq3.p6	sp|Q0DLB9|RH17_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_17_OS=Oryza_sativa_subsp._japonica_GN=Os05g0110500_PE=2_SV=2	2.00E-18
comp30780_c0_seq1.p1	sp|O94537|PPK4_SCHPO_Serine/threonine-protein_kinase_ppk4_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ppk4_PE=2_SV=1	4.00E-76
comp30780_c0_seq2.p1	sp|P32361|IRE1_YEAST_Serine/threonine-protein_kinase/endoribonuclease_IRE1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=IRE1_PE=1_SV=2	7.00E-57
comp30780_c0_seq2.p2	sp|Q09499|IRE1_CAEEL_Serine/threonine-protein_kinase/endoribonuclease_ire-1_OS=Caenorhabditis_elegans_GN=ire-1_PE=2_SV=2	9.00E-14
comp30781_c0_seq5.p1		
comp30782_c0_seq1.p1		
comp30783_c0_seq5.p1		
comp30783_c0_seq5.p2		
comp30784_c0_seq2.p1	sp|Q8BTY2|S4A7_MOUSE_Sodium_bicarbonate_cotransporter_3_OS=Mus_musculus_GN=Slc4a7_PE=1_SV=2	5.00E-20
comp30784_c0_seq3.p1		
comp30784_c0_seq4.p1	sp|O18917|B3A3_RABIT_Anion_exchange_protein_3_OS=Oryctolagus_cuniculus_GN=SLC4A3_PE=2_SV=1	2.00E-70
comp30788_c0_seq2.p1	sp|Q9FIK7|THIC2_ARATH_Probable_acetyl-CoA_acetyltransferase,_cytosolic_2_OS=Arabidopsis_thaliana_GN=At5g47720_PE=2_SV=1	2.00E-144
comp30788_c0_seq4.p1	sp|Q9FIK7|THIC2_ARATH_Probable_acetyl-CoA_acetyltransferase,_cytosolic_2_OS=Arabidopsis_thaliana_GN=At5g47720_PE=2_SV=1	6.00E-71
comp30788_c0_seq5.p1	sp|Q8S4Y1|THIC1_ARATH_Acetyl-CoA_acetyltransferase,_cytosolic_1_OS=Arabidopsis_thaliana_GN=AAT1_PE=2_SV=1	1.00E-78
comp30790_c0_seq1.p1		
comp30790_c0_seq3.p1		
comp30790_c0_seq6.p1	sp|Q149N8|SHPRH_HUMAN_E3_ubiquitin-protein_ligase_SHPRH_OS=Homo_sapiens_GN=SHPRH_PE=1_SV=2	6.00E-45
comp30790_c0_seq7.p1	sp|Q149N8|SHPRH_HUMAN_E3_ubiquitin-protein_ligase_SHPRH_OS=Homo_sapiens_GN=SHPRH_PE=1_SV=2	6.00E-45
comp30790_c3_seq3.p1		
comp30790_c3_seq6.p1	sp|Q6P7K0|CMBL_XENTR_Carboxymethylenebutenolidase_homolog_OS=Xenopus_tropicalis_GN=cmbl_PE=2_SV=1	3.00E-12
comp30790_c3_seq7.p1	sp|Q6P7K0|CMBL_XENTR_Carboxymethylenebutenolidase_homolog_OS=Xenopus_tropicalis_GN=cmbl_PE=2_SV=1	2.00E-12
comp30791_c0_seq3.p1	sp|Q9LRE6|DPOD1_ORYSJ_DNA_polymerase_delta_catalytic_subunit_OS=Oryza_sativa_subsp._japonica_GN=POLD1_PE=2_SV=1	0

comp30791_c0_seq4.p1	sp|Q9P7M0|YOS3_SCHPO_ABC1_family_protein_C21C3.03,_mitochondrial_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC21C3.03_PE=2_SV=1	5.00E-54	GO:0005739,GO:0005739,GO:0005739,GO:0008150,GO:0008152,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016772,GO:0031966,GO:0031966
comp30792_c0_seq1.p1			
comp30792_c0_seq2.p1			
comp30793_c0_seq2.p1	sp|P27795|H2B_TRYCR_Histone_H2B_OS=Trypanosoma_cruzi_PE=3_SV=1	5.00E-33	GO:0000786,GO:0000786,GO:0003677,GO:0003677,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0046982
comp30794_c0_seq1.p1	sp|Q8L838|COG4_ARATH_Conserved_oligomeric_Golgi_complex_subunit_4_OS=Arabidopsis_thaliana_GN=COG4_PE=2_SV=1	2.00E-26	GO:0000139,GO:0005794,GO:0006810,GO:0015031,GO:0016020
comp30794_c0_seq3.p1	sp|Q8L838|COG4_ARATH_Conserved_oligomeric_Golgi_complex_subunit_4_OS=Arabidopsis_thaliana_GN=COG4_PE=2_SV=1	2.00E-24	GO:0000139,GO:0005794,GO:0006810,GO:0015031,GO:0016020
comp30795_c0_seq1.p1			
comp30796_c1_seq1.p1	sp|P0C165|NPHP3_DANRE_Nephrocystin-3_OS=Danio_rerio_GN=nphp3_PE=3_SV=1	2.00E-51	GO:0005929,GO:0005929,GO:0016055,GO:0042995,GO:0060271,GO:0072372
comp30796_c1_seq3.p1	sp|Q05090|KLC_STRPU_Kinesin_light_chain_OS=Strongylocentrotus_purpuratus_PE=2_SV=1	5.00E-34	GO:0003777,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005874,GO:0008152
comp30797_c0_seq3.p1	sp|A0JM23|NPHP3_XENTR_Nephrocystin-3_OS=Xenopus_tropicalis_GN=nphp3_PE=2_SV=2	2.00E-41	GO:0005929,GO:0005929,GO:0005929,GO:0016055,GO:0042995,GO:0060271,GO:0072372,GO:0090090,GO:2000095
comp30797_c0_seq6.p1	sp|A0JM23|NPHP3_XENTR_Nephrocystin-3_OS=Xenopus_tropicalis_GN=nphp3_PE=2_SV=2	2.00E-41	GO:0005929,GO:0005929,GO:0005929,GO:0016055,GO:0042995,GO:0060271,GO:0072372,GO:0090090,GO:2000095
comp30798_c0_seq2.p1	sp|Q9LYJ9|RH46_ARATH_DEAD-box_ATP-dependent_RNA_helicase_46_OS=Arabidopsis_thaliana_GN=RH46_PE=2_SV=2	6.00E-136	GO:0000166,GO:0003676,GO:0003723,GO:0004386,GO:0005524,GO:0005524,GO:0006200,GO:0008026,GO:0008152,GO:0008152,GO:0016787
comp30798_c0_seq2.p2	sp|Q96S44|PRPK_HUMAN_TP53-regulating_kinase_OS=Homo_sapiens_GN=TP53RK_PE=1_SV=2	5.00E-60	GO:0000166,GO:0000408,GO:0002039,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005829,GO:0006468,GO:0006468,GO:0008033,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016773,GO:0016787,GO:0070525
comp30798_c0_seq4.p1	sp|Q96S44|PRPK_HUMAN_TP53-regulating_kinase_OS=Homo_sapiens_GN=TP53RK_PE=1_SV=2	1.00E-38	GO:0000166,GO:0000408,GO:0002039,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005829,GO:0006468,GO:0006468,GO:0008033,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016773,GO:0016787,GO:0070525
comp30799_c0_seq2.p1			
comp30799_c0_seq3.p1	sp|Q16QL3|COQ2_AEDAE_4-hydroxybenzoate_polyprenyltransferase,_mitochondrial_OS=Aedes_aegypti_GN=coq2_PE=3_SV=1	1.00E-82	GO:0002083,GO:0004659,GO:0005666,GO:0005736,GO:0005739,GO:0005743,GO:0006360,GO:0006383,GO:0006744,GO:0006744,GO:0006744,GO:0006744,GO:0008299,GO:0008412,GO:0009058,GO:0016020,GO:0016021,GO:0016021,GO:0016740,GO:0031966,GO:0047293,GO:0003899
comp30799_c0_seq6.p1			
comp30799_c0_seq6.p3			
comp30801_c0_seq1.p1	sp|Q9NNW7|TRXR2_HUMAN_Thioredoxin_reductase_2,_mitochondrial_OS=Homo_sapiens_GN=TXNRD2_PE=1_SV=3	2.00E-94	GO:0000305,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0005515,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005759,GO:0007507,GO:0016491,GO:0016491,GO:0016668,GO:0030097,GO:0045454,GO:0050660,GO:0050661,GO:0055114,GO:0055114
comp30801_c0_seq1.p2	sp|O62768|TRXR1_BOVIN_Thioredoxin_reductase_1,_cytoplasmic_OS=Bos_taurus_GN=TXNRD1_PE=2_SV=3	2.00E-47	GO:0004791,GO:0004791,GO:0005737,GO:0005737,GO:0016491,GO:0016491,GO:0016668,GO:0045454,GO:0050660,GO:0050661,GO:0055114,GO:0055114
comp30802_c0_seq2.p1	sp|Q39YG6|ENGB_GEOMG_Probable_GTP-binding_protein_EngB_OS=Geobacter_metallireducens_(strain_GS-15_/_ATCC_53774_/_DSM_7210)_GN=engB_PE=3_SV=1	2.00E-35	GO:0000166,GO:0000287,GO:0000917,GO:0000917,GO:0000917,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0006184,GO:0007049,GO:0046872,GO:0046872,GO:0051301
comp30802_c0_seq3.p1	sp|Q39YG6|ENGB_GEOMG_Probable_GTP-binding_protein_EngB_OS=Geobacter_metallireducens_(strain_GS-15_/_ATCC_53774_/_DSM_7210)_GN=engB_PE=3_SV=1	2.00E-35	GO:0000166,GO:0000287,GO:0000917,GO:0000917,GO:0000917,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0006184,GO:0007049,GO:0046872,GO:0046872,GO:0051301
comp30803_c0_seq3.p1	sp|O04212|Y2090_ARATH_Putative_ABC1_protein_At2g40090_OS=Arabidopsis_thaliana_GN=At2g40090_PE=2_SV=2	2.00E-94	GO:0005215,GO:0006810,GO:0008152,GO:0016772
comp30803_c0_seq4.p2			
comp30803_c0_seq8.p1	sp|O04212|Y2090_ARATH_Putative_ABC1_protein_At2g40090_OS=Arabidopsis_thaliana_GN=At2g40090_PE=2_SV=2	2.00E-93	GO:0005215,GO:0006810,GO:0008152,GO:0016772
comp30804_c0_seq1.p1	sp|A2AWA9|RBGP1_MOUSE_Rab_GTPase-activating_protein_1_OS=Mus_musculus_GN=Rabgap1_PE=2_SV=1	1.00E-18	GO:0005096,GO:0005097,GO:0005737,GO:0005815,GO:0005829,GO:0005856,GO:0007049,GO:0032313,GO:0032851,GO:0043547
comp30804_c0_seq1.p2			
comp30804_c0_seq1.p3	sp|Q54NK8|GPN3_DICDI_GPN-loop_GTPase_3_homolog_OS=Dictyostelium_discoideum_GN=gpn3_PE=3_SV=1	3.00E-71	GO:0000166,GO:0000166,GO:0005525,GO:0005575,GO:0008150,GO:0008152,GO:0016787
comp30804_c0_seq4.p1	sp|A2AWA9|RBGP1_MOUSE_Rab_GTPase-activating_protein_1_OS=Mus_musculus_GN=Rabgap1_PE=2_SV=1	1.00E-18	GO:0005096,GO:0005097,GO:0005737,GO:0005815,GO:0005829,GO:0005856,GO:0007049,GO:0032313,GO:0032851,GO:0043547
comp30804_c0_seq4.p2			
comp30804_c0_seq4.p3	sp|Q54NK8|GPN3_DICDI_GPN-loop_GTPase_3_homolog_OS=Dictyostelium_discoideum_GN=gpn3_PE=3_SV=1	3.00E-71	GO:0000166,GO:0000166,GO:0005525,GO:0005575,GO:0008150,GO:0008152,GO:0016787
comp30805_c0_seq1.p1			
comp30805_c0_seq3.p1	sp|Q2YDC9|PDCD2_BOVIN_Programmed_cell_death_protein_2_OS=Bos_taurus_GN=PDCD2_PE=2_SV=1	7.00E-57	GO:0003677,GO:0005634,GO:0005634,GO:0005737,GO:0006915,GO:0019899,GO:0046872,GO:0070062
comp30805_c0_seq5.p1			
comp30806_c0_seq1.p2			
comp30806_c1_seq1.p1			
comp30807_c0_seq2.p1			
comp30807_c0_seq4.p1	sp|Q8R1F6|HID1_MOUSE_Protein_hid-1_homolog_OS=Mus_musculus_PE=1_SV=1	5.00E-124	GO:0000138,GO:0000138,GO:0000139,GO:0003674,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005794,GO:0005794,GO:0005797,GO:0005797,GO:0005881,GO:0005881,GO:0006886,GO:0006886,GO:0016020,GO:0031001,GO:0031001,GO:0070062,GO:0090498,GO:0090498
comp30807_c0_seq4.p2			
comp30808_c0_seq1.p1			
comp30808_c0_seq1.p2	sp|P78599|DCOR_CANAL_Ornithine_decarboxylase_OS=Candida_albicans_(strain_SC5314_/_ATCC_MYA-2876)_GN=SPE1_PE=3_SV=1	4.00E-13	GO:0003824,GO:0004586,GO:0004586,GO:0004586,GO:0006596,GO:0006596,GO:0006596,GO:0006596,GO:0016829,GO:0016831,GO:0033387
comp30808_c0_seq2.p1			
comp30808_c0_seq3.p1			
comp30809_c0_seq1.p1			
comp30809_c0_seq2.p1			
comp30809_c0_seq3.p2			
comp30810_c0_seq1.p1			
comp30810_c0_seq2.p1			
comp30810_c0_seq3.p5			
comp30810_c0_seq4.p1			
comp30811_c0_seq2.p1			
comp30811_c0_seq4.p1			
comp30812_c1_seq1.p2	sp|Q99LG4|TTC5_MOUSE_Tetratricopeptide_repeat_protein_5_OS=Mus_musculus_GN=Ttc5_PE=1_SV=2	2.00E-19	GO:0003677,GO:0003682,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0006281,GO:0006974,GO:0045944
comp30813_c0_seq1.p1	sp|P00244|FER1_APHFL_Ferredoxin-1_OS=Aphanizomenon_flos-aquae_PE=1_SV=2	4.00E-24	GO:0009055,GO:0022900,GO:0046872,GO:0051536,GO:0051536,GO:0051537,GO:0051537,GO:0055114
comp30813_c0_seq3.p1	sp|P20654|PP1_EMENI_Serine/threonine-protein_phosphatase_PP1_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=bimG_PE=2_SV=1	0	GO:0000022,GO:0004721,GO:0004721,GO:0005730,GO:0005816,GO:0007049,GO:0007059,GO:0007067,GO:0008152,GO:0008152,GO:0016311,GO:0016311,GO:0016787,GO:0016787,GO:0030010,GO:0030428,GO:0046872,GO:0051211,GO:0051301
comp30813_c0_seq6.p1			
comp30814_c0_seq1.p1			
comp30814_c0_seq2.p1			
comp30816_c0_seq1.p1			
comp30816_c0_seq3.p1	sp|Q6NZP1|ZRAB3_MOUSE_Zinc_finger_Ran-binding_domain-containing_protein_3_OS=Mus_musculus_GN=Zranb3_PE=1_SV=1	5.00E-39	GO:0000166,GO:0000733,GO:0000737,GO:0003676,GO:0003677,GO:0003824,GO:0004386,GO:0004518,GO:0004519,GO:0004519,GO:0004520,GO:0004520,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0006281,GO:0006281,GO:0006281,GO:0006974,GO:0006974,GO:0006974,GO:0008152,GO:0008270,GO:0009411,GO:0009411,GO:0016787,GO:0031297,GO:0031297,GO:0036292,GO:0036292,GO:0036310,GO:0036310,GO:0043596,GO:0043596,GO:0045910,GO:0045910,GO:0046872,GO:0048478,GO:0048478,GO:0070530,GO:0070530,GO:0003678
comp30817_c0_seq2.p1			
comp30818_c0_seq3.p1	sp|Q54GH3|TOM1_DICDI_Target_of_Myb_protein_1_OS=Dictyostelium_discoideum_GN=tom1_PE=1_SV=1	2.00E-16	GO:0005515,GO:0005515,GO:0005515,GO:0005622,GO:0005737,GO:0005737,GO:0005737,GO:0006810,GO:0006886,GO:0015031,GO:0016020,GO:0016020,GO:0035091,GO:0043130
comp30818_c0_seq5.p1	sp|Q9ZV48|TPS11_ARATH_Probable_alpha,alpha-trehalose-phosphate_synthase_[UDP-forming]_11_OS=Arabidopsis_thaliana_GN=TPS11_PE=2_SV=1	9.00E-103	GO:0003824,GO:0005739,GO:0005829,GO:0005992,GO:0008152,GO:0016740,GO:0016757,GO:0003825,GO:0004805
comp30818_c0_seq7.p1	sp|Q9LRA7|TPS9_ARATH_Probable_alpha,alpha-trehalose-phosphate_synthase_[UDP-forming]_9_OS=Arabidopsis_thaliana_GN=TPS9_PE=1_SV=1	9.00E-42	GO:0003824,GO:0005992,GO:0008152,GO:0009744,GO:0009750,GO:0016740,GO:0016757,GO:0003825,GO:0004805
comp30819_c0_seq2.p1	sp|Q47944|SDH_GLUOY_L-sorbose_1-dehydrogenase_OS=Gluconobacter_oxydans_PE=3_SV=1	6.00E-39	GO:0006066,GO:0008812,GO:0016491,GO:0016614,GO:0050660,GO:0055114
comp30820_c0_seq3.p1			
comp30820_c0_seq4.p1			
comp30820_c1_seq1.p2			

comp30915_c0_seq9.p1	sp|Q9BZL6|KPCD2_HUMAN_Serine/threonine-protein_kinase_D2_OS=Homo_sapiens_GN=PRKD2_PE=1_SV=2	2.00E-37	GO:0000166,GO:0001525,GO:0001938,GO:0001938,GO:0002376,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004674,GO:0004697,GO:0004697,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005794,GO:0005794,GO:0005886,GO:0005886,GO:0006468,GO:0006468,GO:0007155,GO:0008219,GO:0010595,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0018105,GO:0030949,GO:0032743,GO:0032743,GO:0032757,GO:0032793,GO:0033138,GO:0035556,GO:0035556,GO:0035924,GO:0035924,GO:0035924,GO:0038033,GO:0038033,GO:0043536,GO:0043536,GO:0045743,GO:0045766,GO:0045766,GO:0045766,GO:0045785,GO:0045944,GO:0045944,GO:0046777,GO:0046777,GO:0046872,GO:0048010,GO:0050852,GO:0050862,GO:0050862,GO:0051091,GO:0051092,GO:0051092,GO:0061154,GO:0070374,GO:0070374,GO:0089700,GO:1901727,GO:1902533,GO:2000573,GO:2000573,GO:2001028	nucleotide binding,angiogenesis,positive regulation of endothelial cell proliferation,positive regulation of endothelial cell proliferation,immune system process,protein kinase activity,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein kinase C activity,protein kinase C activity,protein binding,protein binding,ATP binding,ATP binding,nucleus,nucleus,nucleus,nucleoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,Golgi apparatus,Golgi apparatus,plasma membrane,plasma membrane,protein phosphorylation,protein phosphorylation,cell adhesion,cell death,positive regulation of endothelial cell migration,membrane,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-serine phosphorylation,positive regulation of vascular endothelial growth factor receptor signaling pathway,positive regulation of interleukin-2 production,positive regulation of interleukin-2 production,positive regulation of interleukin-8 production,positive regulation of CREB transcription factor activity,positive regulation of peptidyl-serine phosphorylation,intracellular signal transduction,intracellular signal transduction,cellular response to vascular endothelial growth factor stimulus,cellular response to vascular endothelial growth factor stimulus,positive regulation of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling pathway,positive regulation of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling pathway,positive regulation of blood vessel endothelial cell migration,positive regulation of blood vessel endothelial cell migration,positive regulation of fibroblast growth factor receptor signaling pathway,positive regulation of angiogenesis,positive regulation of angiogenesis,positive regulation of angiogenesis,positive regulation of cell adhesion,positive regulation of transcription from RNA polymerase II promoter,positive regulation of transcription from RNA polymerase II promoter,protein autophosphorylation,protein autophosphorylation,metal ion binding,vascular endothelial growth factor receptor signaling pathway,T cell receptor signaling pathway,positive regulation of T cell receptor signaling pathway,positive regulation of T cell receptor signaling pathway,positive regulation of sequence-specific DNA binding transcription factor activity,positive regulation of NF-kappaB transcription factor activity,positive regulation of NF-kappaB transcription factor activity,endothelial tube morphogenesis,positive regulation of ERK1 and ERK2 cascade,positive regulation of ERK1 and ERK2 cascade,protein kinase D signaling,positive regulation of histone deacetylase activity,positive regulation of intracellular signal transduction,positive regulation of DNA biosynthetic process,positive regulation of DNA biosynthetic process,positive regulation of endothelial cell chemotaxis
comp30916_c0_seq1.p1	sp|Q6DI37|UBCP1_DANRE_Ubiquitin-like_domain-containing_CTD_phosphatase_1_OS=Danio_rerio_GN=ublcp1_PE=2_SV=1	6.00E-47	GO:0004721,GO:0004721,GO:0004721,GO:0005634,GO:0005634,GO:0005634,GO:0008152,GO:0016311,GO:0016311,GO:0016311,GO:0016787	phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,nucleus,nucleus,nucleus,metabolic process,dephosphorylation,dephosphorylation,dephosphorylation,hydrolase activity
comp30916_c0_seq1.p4				
comp30916_c0_seq2.p1	sp|P38875|GPI16_YEAST_GPI_transamidase_component_GPI16_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=GPI16_PE=1_SV=2	1.00E-27	GO:0003923,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005783,GO:0005789,GO:0006506,GO:0006506,GO:0016020,GO:0016021,GO:0016255,GO:0016255,GO:0042765,GO:0042765,GO:0003923	GPI-anchor transamidase activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,endoplasmic reticulum,endoplasmic reticulum membrane,GPI anchor biosynthetic process,GPI anchor biosynthetic process,membrane,integral component of membrane,attachment of GPI anchor to protein,attachment of GPI anchor to protein,GPI-anchor transamidase complex,GPI-anchor transamidase complex,GPI-anchor transamidase activity
comp30917_c0_seq1.p1				
comp30917_c1_seq1.p1	sp|Q924W7|ST5_MOUSE_Suppression_of_tumorigenicity_5_protein_OS=Mus_musculus_GN=St5_PE=2_SV=1	3.00E-14	GO:0005085,GO:0005575,GO:0017112,GO:0017112,GO:0032851,GO:0070374	guanyl-nucleotide exchange factor activity,cellular_component,Rab guanyl-nucleotide exchange factor activity,Rab guanyl-nucleotide exchange factor activity,positive regulation of Rab GTPase activity,positive regulation of ERK1 and ERK2 cascade
comp30917_c1_seq1.p4				
comp30918_c0_seq1.p1				
comp30918_c0_seq7.p1	sp|Q9QXN5|MIOX_MOUSE_Inositol_oxygenase_OS=Mus_musculus_GN=Miox_PE=1_SV=2	4.00E-19	GO:0004033,GO:0004033,GO:0005506,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0008199,GO:0008199,GO:0016234,GO:0016491,GO:0016491,GO:0016491,GO:0016651,GO:0016701,GO:0019310,GO:0019310,GO:0046872,GO:0050113,GO:0050113,GO:0050113,GO:0050661,GO:0055114,GO:0055114,GO:0070062	aldo-keto reductase (NADP) activity,aldo-keto reductase (NADP) activity,iron ion binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,ferric iron binding,ferric iron binding,inclusion body,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on NAD(P)H,oxidoreductase activity, acting on single donors with incorporation of molecular oxygen,inositol catabolic process,inositol catabolic process,metal ion binding,inositol oxygenase activity,inositol oxygenase activity,inositol oxygenase activity,NADP binding,oxidation-reduction process,oxidation-reduction process,extracellular vesicular exosome
comp30920_c0_seq2.p1				
comp30920_c0_seq2.p5	sp|Q54UU1|TPPC4_DICDI_Trafficking_protein_particle_complex_subunit_4_OS=Dictyostelium_discoideum_GN=trappc4_PE=3_SV=1	1.00E-40	GO:0005783,GO:0005783,GO:0005794,GO:0005794,GO:0005801,GO:0006810,GO:0006810,GO:0006888,GO:0006888,GO:0016192,GO:0017112,GO:0030008,GO:0032851,GO:0044351	endoplasmic reticulum,endoplasmic reticulum,Golgi apparatus,Golgi apparatus,cis-Golgi network,transport,transport,ER to Golgi vesicle-mediated transport,ER to Golgi vesicle-mediated transport,vesicle-mediated transport,Rab guanyl-nucleotide exchange factor activity,TRAPP complex,positive regulation of Rab GTPase activity,macropinocytosis
comp30921_c0_seq2.p1	sp|P29620|CDKD1_ORYSJ_Cyclin-dependent_kinase_D-1_OS=Oryza_sativa_subsp._japonica_GN=CDKD-1_PE=1_SV=1	4.00E-105	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004693,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006468,GO:0007049,GO:0008353,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0051301,GO:0051726	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,cyclin-dependent protein serine/threonine kinase activity,ATP binding,ATP binding,nucleus,nucleus,protein phosphorylation,cell cycle,RNA polymerase II carboxy-terminal domain kinase activity,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,cell division,regulation of cell cycle
comp30922_c0_seq5.p1				
comp30922_c0_seq6.p1				
comp30923_c0_seq1.p1	sp|Q05865|FOLC_BACSU_Folylpolyglutamate_synthase_OS=Bacillus_subtilis_GN=folC_PE=3_SV=2	2.00E-45	GO:0000166,GO:0004326,GO:0004326,GO:0005524,GO:0005524,GO:0006730,GO:0009058,GO:0009396,GO:0016874,GO:0016874,GO:0046901	nucleotide binding,tetrahydrofolylpolyglutamate synthase activity,tetrahydrofolylpolyglutamate synthase activity,ATP binding,ATP binding,one-carbon metabolic process,biosynthetic process,folic acid-containing compound biosynthetic process,ligase activity,ligase activity,tetrahydrofolylpolyglutamate biosynthetic process
comp30923_c0_seq3.p1	sp|Q05865|FOLC_BACSU_Folylpolyglutamate_synthase_OS=Bacillus_subtilis_GN=folC_PE=3_SV=2	1.00E-40	GO:0000166,GO:0004326,GO:0004326,GO:0005524,GO:0005524,GO:0006730,GO:0009058,GO:0009396,GO:0016874,GO:0016874,GO:0046901	nucleotide binding,tetrahydrofolylpolyglutamate synthase activity,tetrahydrofolylpolyglutamate synthase activity,ATP binding,ATP binding,one-carbon metabolic process,biosynthetic process,folic acid-containing compound biosynthetic process,ligase activity,ligase activity,tetrahydrofolylpolyglutamate biosynthetic process
comp30925_c0_seq2.p1	sp|Q8GVC7|PKZ1_PHYIN_Serine/threonine-protein_kinase_PKZ1_OS=Phytophthora_infestans_GN=PKZ1_PE=1_SV=1	1.00E-45	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp30926_c0_seq2.p1				
comp30927_c0_seq3.p1	sp|Q505D1|ANR28_MOUSE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_A_OS=Mus_musculus_GN=Ankrd28_PE=1_SV=1	2.00E-15	GO:0005575,GO:0005634,GO:0005654,GO:0008150	cellular_component,nucleus,nucleoplasm,biological_process
comp30927_c1_seq1.p1	sp|Q94A08|RFS2_ARATH_Probable_galactinol--sucrose_galactosyltransferase_2_OS=Arabidopsis_thaliana_GN=RFS2_PE=2_SV=2	6.00E-101	GO:0003824,GO:0005975,GO:0006979,GO:0009506,GO:0016740,GO:0016757,GO:0034484,GO:0052692,GO:0080167,GO:0047274	catalytic activity,carbohydrate metabolic process,response to oxidative stress,plasmodesma,transferase activity,transferase activity, transferring glycosyl groups,raffinose catabolic process,raffinose alpha-galactosidase activity,response to karrikin,galactinol-sucrose galactosyltransferase activity
comp30928_c0_seq1.p1				
comp30928_c0_seq1.p5				
comp30928_c0_seq3.p2	sp|Q9SR77|HBPL1_ARATH_Heme-binding-like_protein_At3g10130,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g10130_PE=1_SV=1	2.00E-15	GO:0008150,GO:0009507,GO:0009507,GO:0009507,GO:0009535,GO:0009536,GO:0010287,GO:0010287,GO:0010287	biological_process,chloroplast,chloroplast,chloroplast,chloroplast thylakoid membrane,plastid,plastoglobule,plastoglobule,plastoglobule
comp30928_c0_seq4.p1	sp|Q9SR77|HBPL1_ARATH_Heme-binding-like_protein_At3g10130,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g10130_PE=1_SV=1	5.00E-23	GO:0008150,GO:0009507,GO:0009507,GO:0009507,GO:0009535,GO:0009536,GO:0010287,GO:0010287,GO:0010287	biological_process,chloroplast,chloroplast,chloroplast,chloroplast thylakoid membrane,plastid,plastoglobule,plastoglobule,plastoglobule
comp30928_c1_seq1.p2				
comp30929_c0_seq3.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	3.00E-26	GO:0005576,GO:0005618,GO:0005618,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0019867	extracellular region,cell wall,cell wall,cell outer membrane,cell outer membrane,membrane,integral component of membrane,outer membrane
comp30929_c0_seq4.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	3.00E-26	GO:0005576,GO:0005618,GO:0005618,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0019867	extracellular region,cell wall,cell wall,cell outer membrane,cell outer membrane,membrane,integral component of membrane,outer membrane
comp30930_c0_seq1.p1				
comp30932_c0_seq11.p1				
comp30932_c0_seq11.p3	sp|Q63055|ARFRP_RAT_ADP-ribosylation_factor-related_protein_1_OS=Rattus_norvegicus_GN=Arfrp1_PE=2_SV=1	1.00E-53	GO:0000166,GO:0005525,GO:0005525,GO:0005622,GO:0005794,GO:0005794,GO:0005794,GO:0005802,GO:0007264,GO:0007369,GO:0016020,GO:0034067,GO:0042147,GO:0043001	nucleotide binding,GTP binding,GTP binding,intracellular,Golgi apparatus,Golgi apparatus,Golgi apparatus,trans-Golgi network,small GTPase mediated signal transduction,gastrulation,membrane,protein localization to Golgi apparatus,retrograde transport, endosome to Golgi,Golgi to plasma membrane protein transport
comp30932_c0_seq16.p1				
comp30932_c0_seq16.p3	sp|Q63055|ARFRP_RAT_ADP-ribosylation_factor-related_protein_1_OS=Rattus_norvegicus_GN=Arfrp1_PE=2_SV=1	1.00E-53	GO:0000166,GO:0005525,GO:0005525,GO:0005622,GO:0005794,GO:0005794,GO:0005794,GO:0005802,GO:0007264,GO:0007369,GO:0016020,GO:0034067,GO:0042147,GO:0043001	nucleotide binding,GTP binding,GTP binding,intracellular,Golgi apparatus,Golgi apparatus,Golgi apparatus,trans-Golgi network,small GTPase mediated signal transduction,gastrulation,membrane,protein localization to Golgi apparatus,retrograde transport, endosome to Golgi,Golgi to plasma membrane protein transport
comp30932_c0_seq19.p1				
comp30932_c0_seq19.p3	sp|Q63055|ARFRP_RAT_ADP-ribosylation_factor-related_protein_1_OS=Rattus_norvegicus_GN=Arfrp1_PE=2_SV=1	1.00E-53	GO:0000166,GO:0005525,GO:0005525,GO:0005622,GO:0005794,GO:0005794,GO:0005794,GO:0005802,GO:0007264,GO:0007369,GO:0016020,GO:0034067,GO:0042147,GO:0043001	nucleotide binding,GTP binding,GTP binding,intracellular,Golgi apparatus,Golgi apparatus,Golgi apparatus,trans-Golgi network,small GTPase mediated signal transduction,gastrulation,membrane,protein localization to Golgi apparatus,retrograde transport, endosome to Golgi,Golgi to plasma membrane protein transport
comp30932_c0_seq20.p1				
comp30932_c0_seq20.p3	sp|Q63055|ARFRP_RAT_ADP-ribosylation_factor-related_protein_1_OS=Rattus_norvegicus_GN=Arfrp1_PE=2_SV=1	1.00E-53	GO:0000166,GO:0005525,GO:0005525,GO:0005622,GO:0005794,GO:0005794,GO:0005794,GO:0005802,GO:0007264,GO:0007369,GO:0016020,GO:0034067,GO:0042147,GO:0043001	nucleotide binding,GTP binding,GTP binding,intracellular,Golgi apparatus,Golgi apparatus,Golgi apparatus,trans-Golgi network,small GTPase mediated signal transduction,gastrulation,membrane,protein localization to Golgi apparatus,retrograde transport, endosome to Golgi,Golgi to plasma membrane protein transport
comp30932_c0_seq21.p1				
comp30932_c0_seq21.p3	sp|Q63055|ARFRP_RAT_ADP-ribosylation_factor-related_protein_1_OS=Rattus_norvegicus_GN=Arfrp1_PE=2_SV=1	1.00E-53	GO:0000166,GO:0005525,GO:0005525,GO:0005622,GO:0005794,GO:0005794,GO:0005794,GO:0005802,GO:0007264,GO:0007369,GO:0016020,GO:0034067,GO:0042147,GO:0043001	nucleotide binding,GTP binding,GTP binding,intracellular,Golgi apparatus,Golgi apparatus,Golgi apparatus,trans-Golgi network,small GTPase mediated signal transduction,gastrulation,membrane,protein localization to Golgi apparatus,retrograde transport, endosome to Golgi,Golgi to plasma membrane protein transport
comp30932_c0_seq22.p1				
comp30932_c0_seq22.p3	sp|Q63055|ARFRP_RAT_ADP-ribosylation_factor-related_protein_1_OS=Rattus_norvegicus_GN=Arfrp1_PE=2_SV=1	1.00E-53	GO:0000166,GO:0005525,GO:0005525,GO:0005622,GO:0005794,GO:0005794,GO:0005794,GO:0005802,GO:0007264,GO:0007369,GO:0016020,GO:0034067,GO:0042147,GO:0043001	nucleotide binding,GTP binding,GTP binding,intracellular,Golgi apparatus,Golgi apparatus,Golgi apparatus,trans-Golgi network,small GTPase mediated signal transduction,gastrulation,membrane,protein localization to Golgi apparatus,retrograde transport, endosome to Golgi,Golgi to plasma membrane protein transport
comp30932_c0_seq8.p1	sp|Q63055|ARFRP_RAT_ADP-ribosylation_factor-related_protein_1_OS=Rattus_norvegicus_GN=Arfrp1_PE=2_SV=1	9.00E-49	GO:0000166,GO:0005525,GO:0005525,GO:0005622,GO:0005794,GO:0005794,GO:0005794,GO:0005802,GO:0007264,GO:0007369,GO:0016020,GO:0034067,GO:0042147,GO:0043001	nucleotide binding,GTP binding,GTP binding,intracellular,Golgi apparatus,Golgi apparatus,Golgi apparatus,trans-Golgi network,small GTPase mediated signal transduction,gastrulation,membrane,protein localization to Golgi apparatus,retrograde transport, endosome to Golgi,Golgi to plasma membrane protein transport
comp30933_c0_seq1.p1				
comp30933_c0_seq1.p2	sp|Q54Z24|PITH1_DICDI_PITH_domain-containing_protein_1_OS=Dictyostelium_discoideum_GN=DDB_G0277951_PE=3_SV=1	2.00E-38	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp30934_c0_seq3.p1				
comp30934_c0_seq7.p1				
comp30936_c0_seq1.p1				
comp30936_c0_seq1.p4	sp|F4HUK6|AAE1_ARATH_Probable_acyl-activating_enzyme_1,_peroxisomal_OS=Arabidopsis_thaliana_GN=AAE1_PE=2_SV=1	2.00E-19	GO:0003824,GO:0005777,GO:0005777,GO:0005777,GO:0006629,GO:0006631,GO:0008152,GO:0015996,GO:0016874	catalytic activity,peroxisome,peroxisome,peroxisome,lipid metabolic process,fatty acid metabolic process,metabolic process,chlorophyll catabolic process,ligase activity
comp30936_c0_seq2.p1	sp|F4HUK6|AAE1_ARATH_Probable_acyl-activating_enzyme_1,_peroxisomal_OS=Arabidopsis_thaliana_GN=AAE1_PE=2_SV=1	4.00E-123	GO:0003824,GO:0005777,GO:0005777,GO:0005777,GO:0006629,GO:0006631,GO:0008152,GO:0015996,GO:0016874	catalytic activity,peroxisome,peroxisome,peroxisome,lipid metabolic process,fatty acid metabolic process,metabolic process,chlorophyll catabolic process,ligase activity
comp30936_c0_seq2.p2				
comp30936_c0_seq8.p1				
comp30937_c0_seq3.p1				
comp30937_c0_seq3.p2				
comp30937_c1_seq1.p1				
comp30937_c1_seq1.p5				
comp30937_c1_seq2.p1				
comp30938_c0_seq1.p1				
comp30938_c0_seq2.p1	sp|Q5F3K4|WDR48_CHICK_WD_repeat-containing_protein_48_OS=Gallus_gallus_GN=WDR48_PE=2_SV=1	5.00E-43	GO:0000724,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005764,GO:0005764,GO:0006974,GO:0007283,GO:0007338,GO:0008584,GO:0016579,GO:0016579,GO:0035264,GO:0043231,GO:0043588,GO:0048568,GO:0048705,GO:0048872,GO:0050679,GO:0072520,GO:1902525	double-strand break repair via homologous recombination,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,lysosome,lysosome,cellular response to DNA damage stimulus,spermatogenesis,single fertilization,male gonad development,protein deubiquitination,protein deubiquitination,multicellular organism growth,intracellular membrane-bounded organelle,skin development,embryonic organ development,skeletal system morphogenesis,homeostasis of number of cells,positive regulation of epithelial cell proliferation,seminiferous tubule development,regulation of protein monoubiquitination
comp30939_c0_seq16.p2				
comp30939_c0_seq17.p3	sp|Q9ZU95|NUD17_ARATH_Nudix_hydrolase_17,_mitochondrial_OS=Arabidopsis_thaliana_GN=NUDT17_PE=2_SV=1	9.00E-11	GO:0005739,GO:0005739,GO:0008152,GO:0008152,GO:0016787,GO:0016787,GO:0046872	mitochondrion,mitochondrion,metabolic process,metabolic process,hydrolase activity,hydrolase activity,metal ion binding
comp30939_c0_seq5.p2				
comp30939_c0_seq6.p2				
comp30940_c0_seq8.p1				
comp30940_c1_seq1.p1				
comp30940_c1_seq1.p2	sp|Q6AY19|ADCK4_RAT_Uncharacterized_aarF_domain-containing_protein_kinase_4_OS=Rattus_norvegicus_GN=Adck4_PE=2_SV=1	2.00E-132	GO:0004674,GO:0005737,GO:0005737,GO:0005739,GO:0005739,GO:0005886,GO:0005886,GO:0006468,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0031966	protein serine/threonine kinase activity,cytoplasm,cytoplasm,mitochondrion,mitochondrion,plasma membrane,plasma membrane,protein phosphorylation,membrane,integral component of membrane,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,mitochondrial membrane
comp30941_c1_seq4.p1	sp|P94400|YCIC_BACSU_Putative_metal_chaperone_YciC_OS=Bacillus_subtilis_GN=yciC_PE=2_SV=1	4.00E-50	GO:0000166,GO:0005525	nucleotide binding,GTP binding
comp30941_c1_seq5.p1	sp|P94400|YCIC_BACSU_Putative_metal_chaperone_YciC_OS=Bacillus_subtilis_GN=yciC_PE=2_SV=1	4.00E-50	GO:0000166,GO:0005525	nucleotide binding,GTP binding
comp30941_c1_seq6.p1	sp|P31521|P47K_PSECL_47_kDa_protein_OS=Pseudomonas_chlororaphis_PE=3_SV=1	2.00E-17	GO:0000166,GO:0005524	nucleotide binding,ATP binding
comp30942_c0_seq1.p1				
comp30943_c0_seq1.p1				
comp30943_c0_seq4.p1				
comp30943_c0_seq6.p1				
comp30943_c0_seq7.p1				
comp30945_c1_seq1.p1				
comp30946_c0_seq1.p2				
comp30947_c0_seq5.p1	sp|P44426|BIOA_HAEIN_Adenosylmethionine-8-amino-7-oxononanoate_aminotransferase_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=bioA_PE=3_SV=1	1.00E-33	GO:0003824,GO:0004015,GO:0004015,GO:0004015,GO:0005737,GO:0005737,GO:0005737,GO:0008483,GO:0008483,GO:0009102,GO:0009102,GO:0009102,GO:0009102,GO:0016740,GO:0030170,GO:0030170	catalytic activity,adenosylmethionine-8-amino-7-oxononanoate transaminase activity,adenosylmethionine-8-amino-7-oxononanoate transaminase activity,adenosylmethionine-8-amino-7-oxononanoate transaminase activity,cytoplasm,cytoplasm,cytoplasm,transaminase activity,transaminase activity,biotin biosynthetic process,biotin biosynthetic process,biotin biosynthetic process,biotin biosynthetic process,transferase activity,pyridoxal phosphate binding,pyridoxal phosphate binding
comp30948_c0_seq3.p1	sp|P14735|IDE_HUMAN_Insulin-degrading_enzyme_OS=Homo_sapiens_GN=IDE_PE=1_SV=4	1.00E-50	GO:0000166,GO:0001540,GO:0001948,GO:0003824,GO:0003824,GO:0004222,GO:0004222,GO:0004222,GO:0005102,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005576,GO:0005576,GO:0005615,GO:0005615,GO:0005634,GO:0005634,GO:0005654,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0005777,GO:0005782,GO:0005829,GO:0005829,GO:0005829,GO:0005886,GO:0005886,GO:0006200,GO:0006508,GO:0006508,GO:0006508,GO:0006508,GO:0008152,GO:0008233,GO:0008237,GO:0008270,GO:0008286,GO:0008340,GO:0009986,GO:0009986,GO:0010815,GO:0010815,GO:0010992,GO:0016020,GO:0016032,GO:0016787,GO:0016887,GO:0017046,GO:0031597,GO:0031626,GO:0032461,GO:0042277,GO:0042447,GO:0042803,GO:0042803,GO:0043130,GO:0043559,GO:0043559,GO:0043559,GO:0044257,GO:0045861,GO:0046872,GO:0046872,GO:0050435,GO:0050435,GO:0051260,GO:0051289,GO:0051291,GO:0051603,GO:0051603,GO:1901142,GO:1901143,GO:1901143,GO:0005634	nucleotide binding,beta-amyloid binding,glycoprotein binding,catalytic activity,catalytic activity,metalloendopeptidase activity,metalloendopeptidase activity,metalloendopeptidase activity,receptor binding,protein binding,protein binding,ATP binding,ATP binding,extracellular region,extracellular region,extracellular space,extracellular space,nucleus,nucleus,nucleoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,mitochondrion,peroxisome,peroxisomal matrix,cytosol,cytosol,cytosol,plasma membrane,plasma membrane,ATP catabolic process,proteolysis,proteolysis,proteolysis,proteolysis,metabolic process,peptidase activity,metallopeptidase activity,zinc ion binding,insulin receptor signaling pathway,determination of adult lifespan,cell surface,cell surface,bradykinin catabolic process,bradykinin catabolic process,ubiquitin homeostasis,membrane,viral process,hydrolase activity,ATPase activity,peptide hormone binding,cytosolic proteasome complex,beta-endorphin binding,positive regulation of protein oligomerization,peptide binding,hormone catabolic process,protein homodimerization activity,protein homodimerization activity,ubiquitin binding,insulin binding,insulin binding,insulin binding,cellular protein catabolic process,negative regulation of proteolysis,metal ion binding,metal ion binding,beta-amyloid metabolic process,beta-amyloid metabolic process,protein homooligomerization,protein homotetramerization,protein heterooligomerization,proteolysis involved in cellular protein catabolic process,proteolysis involved in cellular protein catabolic process,insulin metabolic process,insulin catabolic process,insulin catabolic process,nucleus
comp30948_c0_seq6.p1	sp|P14735|IDE_HUMAN_Insulin-degrading_enzyme_OS=Homo_sapiens_GN=IDE_PE=1_SV=4	0	GO:0000166,GO:0001540,GO:0001948,GO:0003824,GO:0003824,GO:0004222,GO:0004222,GO:0004222,GO:0005102,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005576,GO:0005576,GO:0005615,GO:0005615,GO:0005634,GO:0005634,GO:0005654,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0005777,GO:0005782,GO:0005829,GO:0005829,GO:0005829,GO:0005886,GO:0005886,GO:0006200,GO:0006508,GO:0006508,GO:0006508,GO:0006508,GO:0008152,GO:0008233,GO:0008237,GO:0008270,GO:0008286,GO:0008340,GO:0009986,GO:0009986,GO:0010815,GO:0010815,GO:0010992,GO:0016020,GO:0016032,GO:0016787,GO:0016887,GO:0017046,GO:0031597,GO:0031626,GO:0032461,GO:0042277,GO:0042447,GO:0042803,GO:0042803,GO:0043130,GO:0043559,GO:0043559,GO:0043559,GO:0044257,GO:0045861,GO:0046872,GO:0046872,GO:0050435,GO:0050435,GO:0051260,GO:0051289,GO:0051291,GO:0051603,GO:0051603,GO:1901142,GO:1901143,GO:1901143,GO:0005634	nucleotide binding,beta-amyloid binding,glycoprotein binding,catalytic activity,catalytic activity,metalloendopeptidase activity,metalloendopeptidase activity,metalloendopeptidase activity,receptor binding,protein binding,protein binding,ATP binding,ATP binding,extracellular region,extracellular region,extracellular space,extracellular space,nucleus,nucleus,nucleoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,mitochondrion,peroxisome,peroxisomal matrix,cytosol,cytosol,cytosol,plasma membrane,plasma membrane,ATP catabolic process,proteolysis,proteolysis,proteolysis,proteolysis,metabolic process,peptidase activity,metallopeptidase activity,zinc ion binding,insulin receptor signaling pathway,determination of adult lifespan,cell surface,cell surface,bradykinin catabolic process,bradykinin catabolic process,ubiquitin homeostasis,membrane,viral process,hydrolase activity,ATPase activity,peptide hormone binding,cytosolic proteasome complex,beta-endorphin binding,positive regulation of protein oligomerization,peptide binding,hormone catabolic process,protein homodimerization activity,protein homodimerization activity,ubiquitin binding,insulin binding,insulin binding,insulin binding,cellular protein catabolic process,negative regulation of proteolysis,metal ion binding,metal ion binding,beta-amyloid metabolic process,beta-amyloid metabolic process,protein homooligomerization,protein homotetramerization,protein heterooligomerization,proteolysis involved in cellular protein catabolic process,proteolysis involved in cellular protein catabolic process,insulin metabolic process,insulin catabolic process,insulin catabolic process,nucleus
comp30948_c0_seq6.p4				
comp30949_c0_seq5.p1				
comp30949_c0_seq6.p1				
comp30950_c0_seq1.p1				
comp30950_c0_seq4.p1				
comp30952_c0_seq1.p1	sp|Q9TW32|PPIB_DICDI_Peptidyl-prolyl_cis-trans_isomerase_B_OS=Dictyostelium_discoideum_GN=cypB_PE=1_SV=1	2.00E-14	GO:0000413,GO:0000413,GO:0003755,GO:0003755,GO:0003755,GO:0005783,GO:0006457,GO:0016853,GO:0042277,GO:0043231,GO:0043231,GO:0044351	protein peptidyl-prolyl isomerization,protein peptidyl-prolyl isomerization,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,endoplasmic reticulum,protein folding,isomerase activity,peptide binding,intracellular membrane-bounded organelle,intracellular membrane-bounded organelle,macropinocytosis
comp30952_c0_seq2.p1				
comp30952_c0_seq3.p1				
comp30952_c0_seq3.p2				
comp30953_c0_seq5.p1				
comp30954_c0_seq6.p1	sp|O06423|MGTA_MYCTU_GDP-mannose-dependent_alpha-mannosyltransferase_OS=Mycobacterium_tuberculosis_GN=mgtA_PE=1_SV=1	3.00E-26		
comp30954_c0_seq6.p2	sp|Q5FVF1|F10C1_RAT_Protein_FRA10AC1_homolog_OS=Rattus_norvegicus_GN=Fra10ac1_PE=2_SV=1	3.00E-28	GO:0005634,GO:0005634	nucleus,nucleus
comp30954_c0_seq6.p6				
comp30955_c0_seq1.p1				
comp30955_c0_seq2.p1				
comp30956_c0_seq3.p1	sp|D4DEN7|CARP_TRIVH_Probable_vacuolar_protease_A_OS=Trichophyton_verrucosum_(strain_HKI_0517)_GN=PEP2_PE=3_SV=1	3.00E-43	GO:0004190,GO:0004190,GO:0005576,GO:0005576,GO:0005773,GO:0005775,GO:0006508,GO:0006508,GO:0008233,GO:0009405,GO:0016787	aspartic-type endopeptidase activity,aspartic-type endopeptidase activity,extracellular region,extracellular region,vacuole,vacuolar lumen,proteolysis,proteolysis,peptidase activity,pathogenesis,hydrolase activity
comp30956_c0_seq3.p2	sp|O23627|SYGM1_ARATH_Glycine--tRNA_ligase_1,_mitochondrial_OS=Arabidopsis_thaliana_GN=GLYRS-1_PE=2_SV=1	0	GO:0000166,GO:0000166,GO:0004812,GO:0004812,GO:0004820,GO:0004820,GO:0004820,GO:0004820,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0005739,GO:0005739,GO:0005768,GO:0005794,GO:0005802,GO:0005829,GO:0006094,GO:0006412,GO:0006418,GO:0006426,GO:0006426,GO:0007010,GO:0010498,GO:0015966,GO:0016874,GO:0046686,GO:0046983	nucleotide binding,nucleotide binding,aminoacyl-tRNA ligase activity,aminoacyl-tRNA ligase activity,glycine-tRNA ligase activity,glycine-tRNA ligase activity,glycine-tRNA ligase activity,glycine-tRNA ligase activity,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,mitochondrion,mitochondrion,mitochondrion,endosome,Golgi apparatus,trans-Golgi network,cytosol,gluconeogenesis,translation,tRNA aminoacylation for protein translation,glycyl-tRNA aminoacylation,glycyl-tRNA aminoacylation,cytoskeleton organization,proteasomal protein catabolic process,diadenosine tetraphosphate biosynthetic process,ligase activity,response to cadmium ion,protein dimerization activity
comp30957_c0_seq5.p1	sp|Q16AA3|ENGB_ROSDO_Probable_GTP-binding_protein_EngB_OS=Roseobacter_denitrificans_(strain_ATCC_33942_/_OCh_114)_GN=engB_PE=3_SV=1	4.00E-32	GO:0000166,GO:0000287,GO:0000917,GO:0000917,GO:0000917,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0006184,GO:0007049,GO:0046872,GO:0046872,GO:0051301	nucleotide binding,magnesium ion binding,barrier septum assembly,barrier septum assembly,barrier septum assembly,GTPase activity,GTP binding,GTP binding,GTP binding,GTP catabolic process,cell cycle,metal ion binding,metal ion binding,cell division
comp30957_c0_seq6.p1	sp|Q16AA3|ENGB_ROSDO_Probable_GTP-binding_protein_EngB_OS=Roseobacter_denitrificans_(strain_ATCC_33942_/_OCh_114)_GN=engB_PE=3_SV=1	3.00E-32	GO:0000166,GO:0000287,GO:0000917,GO:0000917,GO:0000917,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0006184,GO:0007049,GO:0046872,GO:0046872,GO:0051301	nucleotide binding,magnesium ion binding,barrier septum assembly,barrier septum assembly,barrier septum assembly,GTPase activity,GTP binding,GTP binding,GTP binding,GTP catabolic process,cell cycle,metal ion binding,metal ion binding,cell division
comp30958_c0_seq6.p1	sp|Q2VF18|DCL2_CRYPA_Dicer-like_protein_2_OS=Cryphonectria_parasitica_GN=DCL-2_PE=3_SV=1	7.00E-16	GO:0000166,GO:0003676,GO:0003723,GO:0003723,GO:0004386,GO:0004525,GO:0005524,GO:0005524,GO:0006396,GO:0016787,GO:0016891,GO:0046872,GO:0050688,GO:0051607,GO:0090501,GO:0090502,GO:0090502	nucleotide binding,nucleic acid binding,RNA binding,RNA binding,helicase activity,ribonuclease III activity,ATP binding,ATP binding,RNA processing,hydrolase activity,endoribonuclease activity, producing 5'-phosphomonoesters,metal ion binding,regulation of defense response to virus,defense response to virus,RNA phosphodiester bond hydrolysis,RNA phosphodiester bond hydrolysis, endonucleolytic,RNA phosphodiester bond hydrolysis, endonucleolytic
comp30958_c0_seq6.p3				
comp30960_c0_seq1.p1	sp|Q9FKI0|FIMB2_ARATH_Fimbrin-like_protein_2_OS=Arabidopsis_thaliana_GN=FIM2_PE=2_SV=1	1.00E-19	GO:0003779,GO:0005737,GO:0005829,GO:0005856,GO:0005856,GO:0009846,GO:0009860,GO:0030036,GO:0030048,GO:0051015,GO:0051645,GO:0051646,GO:0060151	actin binding,cytoplasm,cytosol,cytoskeleton,cytoskeleton,pollen germination,pollen tube growth,actin cytoskeleton organization,actin filament-based movement,actin filament binding,Golgi localization,mitochondrion localization,peroxisome localization
comp30960_c0_seq1.p3				
comp30960_c0_seq4.p1	sp|Q9FKI0|FIMB2_ARATH_Fimbrin-like_protein_2_OS=Arabidopsis_thaliana_GN=FIM2_PE=2_SV=1	1.00E-19	GO:0003779,GO:0005737,GO:0005829,GO:0005856,GO:0005856,GO:0009846,GO:0009860,GO:0030036,GO:0030048,GO:0051015,GO:0051645,GO:0051646,GO:0060151	actin binding,cytoplasm,cytosol,cytoskeleton,cytoskeleton,pollen germination,pollen tube growth,actin cytoskeleton organization,actin filament-based movement,actin filament binding,Golgi localization,mitochondrion localization,peroxisome localization
comp30961_c1_seq2.p1				
comp30961_c1_seq2.p3	sp|Q9DAA6|EXOS1_MOUSE_Exosome_complex_component_CSL4_OS=Mus_musculus_GN=Exosc1_PE=2_SV=1	5.00E-35	GO:0000176,GO:0000178,GO:0000178,GO:0000178,GO:0003723,GO:0003723,GO:0003723,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0005730,GO:0005737,GO:0005737,GO:0005737,GO:0006364,GO:0004532	nuclear exosome (RNase complex),exosome (RNase complex),exosome (RNase complex),exosome (RNase complex),RNA binding,RNA binding,RNA binding,protein binding,nucleus,nucleus,nucleus,nucleolus,nucleolus,nucleolus,cytoplasm,cytoplasm,cytoplasm,rRNA processing,exoribonuclease activity
comp30963_c0_seq7.p1				
comp30963_c0_seq8.p1	sp|Q32PP1|CE045_DANRE_UPF0544_protein_C5orf45_homolog_OS=Danio_rerio_GN=zgc:123335_PE=2_SV=1	2.00E-11	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp30964_c0_seq7.p1				
comp30964_c0_seq9.p1				
comp30966_c0_seq2.p1				
comp30966_c0_seq6.p1	sp|Q7ZWY2|PIHD1_XENLA_PIH1_domain-containing_protein_1_OS=Xenopus_laevis_GN=pih1d1_PE=2_SV=1	3.00E-11		
comp30966_c0_seq6.p2				
comp30967_c0_seq2.p1	sp|Q55750|MFD_SYNY3_Transcription-repair-coupling_factor_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=mfd_PE=3_SV=1	4.00E-69	GO:0000166,GO:0000166,GO:0000716,GO:0003676,GO:0003677,GO:0003677,GO:0003684,GO:0004386,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0006281,GO:0006281,GO:0006355,GO:0006974,GO:0016787,GO:0016787	nucleotide binding,nucleotide binding,transcription-coupled nucleotide-excision repair, DNA damage recognition,nucleic acid binding,DNA binding,DNA binding,damaged DNA binding,helicase activity,helicase activity,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,DNA repair,DNA repair,regulation of transcription, DNA-templated,cellular response to DNA damage stimulus,hydrolase activity,hydrolase activity
comp30967_c1_seq1.p1	sp|Q55750|MFD_SYNY3_Transcription-repair-coupling_factor_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=mfd_PE=3_SV=1	7.00E-47	GO:0000166,GO:0000166,GO:0000716,GO:0003676,GO:0003677,GO:0003677,GO:0003684,GO:0004386,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0006281,GO:0006281,GO:0006355,GO:0006974,GO:0016787,GO:0016787	nucleotide binding,nucleotide binding,transcription-coupled nucleotide-excision repair, DNA damage recognition,nucleic acid binding,DNA binding,DNA binding,damaged DNA binding,helicase activity,helicase activity,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,DNA repair,DNA repair,regulation of transcription, DNA-templated,cellular response to DNA damage stimulus,hydrolase activity,hydrolase activity
comp30968_c0_seq2.p1				
comp30968_c0_seq4.p1	sp|Q5R443|S38A1_PONAB_Sodium-coupled_neutral_amino_acid_transporter_1_OS=Pongo_abelii_GN=SLC38A1_PE=2_SV=1	8.00E-13	GO:0005886,GO:0005886,GO:0006810,GO:0006811,GO:0006814,GO:0006865,GO:0015293,GO:0016020,GO:0016021,GO:0055085	plasma membrane,plasma membrane,transport,ion transport,sodium ion transport,amino acid transport,symporter activity,membrane,integral component of membrane,transmembrane transport
comp30968_c0_seq5.p1	sp|A8KBL5|S38AB_DANRE_Putative_sodium-coupled_neutral_amino_acid_transporter_11_OS=Danio_rerio_GN=slc38a11_PE=2_SV=2	5.00E-14	GO:0003333,GO:0005783,GO:0006810,GO:0006811,GO:0006814,GO:0006865,GO:0015171,GO:0016020,GO:0016020,GO:0016021	amino acid transmembrane transport,endoplasmic reticulum,transport,ion transport,sodium ion transport,amino acid transport,amino acid transmembrane transporter activity,membrane,membrane,integral component of membrane
comp30969_c0_seq3.p2				
comp30969_c0_seq5.p1				
comp30969_c0_seq6.p1				
comp30970_c0_seq2.p1				
comp30971_c0_seq4.p1				
comp30971_c0_seq4.p2				
comp30971_c0_seq5.p1				
comp30971_c0_seq6.p1				
comp30972_c0_seq2.p1				
comp30973_c0_seq1.p1				
comp30973_c0_seq1.p2				
comp30973_c0_seq2.p1				
comp30973_c0_seq3.p1				
comp30974_c0_seq4.p1	sp|B0G126|FYV1_DICDI_1-phosphatidylinositol_3-phosphate_5-kinase_OS=Dictyostelium_discoideum_GN=pip5k3_PE=3_SV=1	1.00E-37	GO:0000166,GO:0000285,GO:0000285,GO:0005524,GO:0005524,GO:0006644,GO:0016301,GO:0016307,GO:0016310,GO:0016740,GO:0044267,GO:0046488,GO:0046854,GO:0046854,GO:0046854,GO:0046872,GO:0046872	nucleotide binding,1-phosphatidylinositol-3-phosphate 5-kinase activity,1-phosphatidylinositol-3-phosphate 5-kinase activity,ATP binding,ATP binding,phospholipid metabolic process,kinase activity,phosphatidylinositol phosphate kinase activity,phosphorylation,transferase activity,cellular protein metabolic process,phosphatidylinositol metabolic process,phosphatidylinositol phosphorylation,phosphatidylinositol phosphorylation,phosphatidylinositol phosphorylation,metal ion binding,metal ion binding
comp30974_c0_seq4.p2	sp|P34756|FAB1_YEAST_1-phosphatidylinositol_3-phosphate_5-kinase_FAB1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=FAB1_PE=1_SV=3	2.00E-30	GO:0000166,GO:0000285,GO:0000285,GO:0000285,GO:0000285,GO:0000329,GO:0000329,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005768,GO:0005773,GO:0005774,GO:0010008,GO:0010008,GO:0010008,GO:0016020,GO:0016301,GO:0016307,GO:0016310,GO:0016740,GO:0032266,GO:0044267,GO:0046488,GO:0046854,GO:0046854,GO:0046854,GO:0046872,GO:0046872,GO:0070772,GO:0070772	nucleotide binding,1-phosphatidylinositol-3-phosphate 5-kinase activity,1-phosphatidylinositol-3-phosphate 5-kinase activity,1-phosphatidylinositol-3-phosphate 5-kinase activity,1-phosphatidylinositol-3-phosphate 5-kinase activity,fungal-type vacuole membrane,fungal-type vacuole membrane,protein binding,protein binding,protein binding,ATP binding,ATP binding,endosome,vacuole,vacuolar membrane,endosome membrane,endosome membrane,endosome membrane,membrane,kinase activity,phosphatidylinositol phosphate kinase activity,phosphorylation,transferase activity,phosphatidylinositol-3-phosphate binding,cellular protein metabolic process,phosphatidylinositol metabolic process,phosphatidylinositol phosphorylation,phosphatidylinositol phosphorylation,phosphatidylinositol phosphorylation,metal ion binding,metal ion binding,PAS complex,PAS complex
comp30974_c0_seq5.p1				
comp30974_c0_seq7.p1	sp|B0G126|FYV1_DICDI_1-phosphatidylinositol_3-phosphate_5-kinase_OS=Dictyostelium_discoideum_GN=pip5k3_PE=3_SV=1	1.00E-37	GO:0000166,GO:0000285,GO:0000285,GO:0005524,GO:0005524,GO:0006644,GO:0016301,GO:0016307,GO:0016310,GO:0016740,GO:0044267,GO:0046488,GO:0046854,GO:0046854,GO:0046854,GO:0046872,GO:0046872	nucleotide binding,1-phosphatidylinositol-3-phosphate 5-kinase activity,1-phosphatidylinositol-3-phosphate 5-kinase activity,ATP binding,ATP binding,phospholipid metabolic process,kinase activity,phosphatidylinositol phosphate kinase activity,phosphorylation,transferase activity,cellular protein metabolic process,phosphatidylinositol metabolic process,phosphatidylinositol phosphorylation,phosphatidylinositol phosphorylation,phosphatidylinositol phosphorylation,metal ion binding,metal ion binding
comp30974_c0_seq7.p2	sp|P34756|FAB1_YEAST_1-phosphatidylinositol_3-phosphate_5-kinase_FAB1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=FAB1_PE=1_SV=3	2.00E-30	GO:0000166,GO:0000285,GO:0000285,GO:0000285,GO:0000285,GO:0000329,GO:0000329,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005768,GO:0005773,GO:0005774,GO:0010008,GO:0010008,GO:0010008,GO:0016020,GO:0016301,GO:0016307,GO:0016310,GO:0016740,GO:0032266,GO:0044267,GO:0046488,GO:0046854,GO:0046854,GO:0046854,GO:0046872,GO:0046872,GO:0070772,GO:0070772	nucleotide binding,1-phosphatidylinositol-3-phosphate 5-kinase activity,1-phosphatidylinositol-3-phosphate 5-kinase activity,1-phosphatidylinositol-3-phosphate 5-kinase activity,1-phosphatidylinositol-3-phosphate 5-kinase activity,fungal-type vacuole membrane,fungal-type vacuole membrane,protein binding,protein binding,protein binding,ATP binding,ATP binding,endosome,vacuole,vacuolar membrane,endosome membrane,endosome membrane,endosome membrane,membrane,kinase activity,phosphatidylinositol phosphate kinase activity,phosphorylation,transferase activity,phosphatidylinositol-3-phosphate binding,cellular protein metabolic process,phosphatidylinositol metabolic process,phosphatidylinositol phosphorylation,phosphatidylinositol phosphorylation,phosphatidylinositol phosphorylation,metal ion binding,metal ion binding,PAS complex,PAS complex
comp30975_c0_seq2.p1				
comp30975_c0_seq3.p1				
comp30975_c0_seq3.p2	sp|B1MFT1|GLPK_MYCA9_Glycerol_kinase_OS=Mycobacterium_abscessus_(strain_ATCC_19977_/_DSM_44196)_GN=glpK_PE=3_SV=1	1.00E-12	GO:0000166,GO:0004370,GO:0004370,GO:0004370,GO:0004370,GO:0005524,GO:0005524,GO:0005975,GO:0006071,GO:0006071,GO:0006072,GO:0006072,GO:0016301,GO:0016310,GO:0016740,GO:0016773,GO:0019563	nucleotide binding,glycerol kinase activity,glycerol kinase activity,glycerol kinase activity,glycerol kinase activity,ATP binding,ATP binding,carbohydrate metabolic process,glycerol metabolic process,glycerol metabolic process,glycerol-3-phosphate metabolic process,glycerol-3-phosphate metabolic process,kinase activity,phosphorylation,transferase activity,phosphotransferase activity, alcohol group as acceptor,glycerol catabolic process
comp30975_c0_seq4.p1				
comp30975_c0_seq4.p2				
comp30975_c1_seq1.p1	sp|Q9LFU5|TRM1_ARATH_Probable_tRNA_(guanine(26)-N(2))-dimethyltransferase_1_OS=Arabidopsis_thaliana_GN=At5g15810_PE=2_SV=3	3.00E-13	GO:0000049,GO:0003723,GO:0003723,GO:0004809,GO:0008033,GO:0008033,GO:0008168,GO:0016740,GO:0030488,GO:0032259	tRNA binding,RNA binding,RNA binding,tRNA (guanine-N2-)-methyltransferase activity,tRNA processing,tRNA processing,methyltransferase activity,transferase activity,tRNA methylation,methylation
comp30975_c1_seq2.p1	sp|Q9LFU5|TRM1_ARATH_Probable_tRNA_(guanine(26)-N(2))-dimethyltransferase_1_OS=Arabidopsis_thaliana_GN=At5g15810_PE=2_SV=3	2.00E-13	GO:0000049,GO:0003723,GO:0003723,GO:0004809,GO:0008033,GO:0008033,GO:0008168,GO:0016740,GO:0030488,GO:0032259	tRNA binding,RNA binding,RNA binding,tRNA (guanine-N2-)-methyltransferase activity,tRNA processing,tRNA processing,methyltransferase activity,transferase activity,tRNA methylation,methylation
comp30975_c1_seq2.p2				
comp30975_c1_seq3.p1	sp|Q9LFU5|TRM1_ARATH_Probable_tRNA_(guanine(26)-N(2))-dimethyltransferase_1_OS=Arabidopsis_thaliana_GN=At5g15810_PE=2_SV=3	2.00E-33	GO:0000049,GO:0003723,GO:0003723,GO:0004809,GO:0008033,GO:0008033,GO:0008168,GO:0016740,GO:0030488,GO:0032259	tRNA binding,RNA binding,RNA binding,tRNA (guanine-N2-)-methyltransferase activity,tRNA processing,tRNA processing,methyltransferase activity,transferase activity,tRNA methylation,methylation
comp30975_c1_seq3.p2				
comp30975_c1_seq5.p1	sp|Q3TX08|TRM1_MOUSE_tRNA_(guanine(26)-N(2))-dimethyltransferase_OS=Mus_musculus_GN=Trmt1_PE=1_SV=2	1.00E-61	GO:0000049,GO:0003723,GO:0003723,GO:0004809,GO:0005575,GO:0008033,GO:0008033,GO:0008150,GO:0008168,GO:0016740,GO:0030488,GO:0032259,GO:0044822,GO:0046872,GO:0046872	tRNA binding,RNA binding,RNA binding,tRNA (guanine-N2-)-methyltransferase activity,cellular_component,tRNA processing,tRNA processing,biological_process,methyltransferase activity,transferase activity,tRNA methylation,methylation,poly(A) RNA binding,metal ion binding,metal ion binding
comp30975_c1_seq5.p2				
comp30975_c1_seq7.p1	sp|Q9LFU5|TRM1_ARATH_Probable_tRNA_(guanine(26)-N(2))-dimethyltransferase_1_OS=Arabidopsis_thaliana_GN=At5g15810_PE=2_SV=3	2.00E-33	GO:0000049,GO:0003723,GO:0003723,GO:0004809,GO:0008033,GO:0008033,GO:0008168,GO:0016740,GO:0030488,GO:0032259	tRNA binding,RNA binding,RNA binding,tRNA (guanine-N2-)-methyltransferase activity,tRNA processing,tRNA processing,methyltransferase activity,transferase activity,tRNA methylation,methylation
comp30975_c1_seq7.p2	sp|Q3TX08|TRM1_MOUSE_tRNA_(guanine(26)-N(2))-dimethyltransferase_OS=Mus_musculus_GN=Trmt1_PE=1_SV=2	2.00E-30	GO:0000049,GO:0003723,GO:0003723,GO:0004809,GO:0005575,GO:0008033,GO:0008033,GO:0008150,GO:0008168,GO:0016740,GO:0030488,GO:0032259,GO:0044822,GO:0046872,GO:0046872	tRNA binding,RNA binding,RNA binding,tRNA (guanine-N2-)-methyltransferase activity,cellular_component,tRNA processing,tRNA processing,biological_process,methyltransferase activity,transferase activity,tRNA methylation,methylation,poly(A) RNA binding,metal ion binding,metal ion binding
comp30975_c1_seq9.p1	sp|Q3TX08|TRM1_MOUSE_tRNA_(guanine(26)-N(2))-dimethyltransferase_OS=Mus_musculus_GN=Trmt1_PE=1_SV=2	2.00E-72	GO:0000049,GO:0003723,GO:0003723,GO:0004809,GO:0005575,GO:0008033,GO:0008033,GO:0008150,GO:0008168,GO:0016740,GO:0030488,GO:0032259,GO:0044822,GO:0046872,GO:0046872	tRNA binding,RNA binding,RNA binding,tRNA (guanine-N2-)-methyltransferase activity,cellular_component,tRNA processing,tRNA processing,biological_process,methyltransferase activity,transferase activity,tRNA methylation,methylation,poly(A) RNA binding,metal ion binding,metal ion binding
comp30976_c0_seq1.p1				
comp30976_c0_seq2.p1	sp|Q5JSP0|FGD3_HUMAN_FYVE,_RhoGEF_and_PH_domain-containing_protein_3_OS=Homo_sapiens_GN=FGD3_PE=1_SV=1	3.00E-25	GO:0001726,GO:0005085,GO:0005085,GO:0005089,GO:0005737,GO:0005737,GO:0005737,GO:0005794,GO:0005829,GO:0005829,GO:0005829,GO:0005856,GO:0005856,GO:0007010,GO:0007264,GO:0008360,GO:0030027,GO:0030036,GO:0031267,GO:0032321,GO:0035023,GO:0043065,GO:0043088,GO:0043547,GO:0043547,GO:0046847,GO:0046872,GO:0046872,GO:0048011,GO:0048011,GO:0051056,GO:0097190	ruffle,guanyl-nucleotide exchange factor activity,guanyl-nucleotide exchange factor activity,Rho guanyl-nucleotide exchange factor activity,cytoplasm,cytoplasm,cytoplasm,Golgi apparatus,cytosol,cytosol,cytosol,cytoskeleton,cytoskeleton,cytoskeleton organization,small GTPase mediated signal transduction,regulation of cell shape,lamellipodium,actin cytoskeleton organization,small GTPase binding,positive regulation of Rho GTPase activity,regulation of Rho protein signal transduction,positive regulation of apoptotic process,regulation of Cdc42 GTPase activity,positive regulation of GTPase activity,positive regulation of GTPase activity,filopodium assembly,metal ion binding,metal ion binding,neurotrophin TRK receptor signaling pathway,neurotrophin TRK receptor signaling pathway,regulation of small GTPase mediated signal transduction,apoptotic signaling pathway
comp30976_c0_seq4.p1				
comp30977_c0_seq1.p1				
comp30977_c0_seq1.p2				
comp30977_c0_seq1.p4				
comp30978_c0_seq1.p1	sp|O75366|AVIL_HUMAN_Advillin_OS=Homo_sapiens_GN=AVIL_PE=1_SV=3	3.00E-14	GO:0003779,GO:0003779,GO:0003779,GO:0005737,GO:0005856,GO:0005856,GO:0007010,GO:0007399,GO:0010976,GO:0010976,GO:0010976,GO:0015629,GO:0030424,GO:0042995,GO:0042995,GO:0042995,GO:0043005,GO:0051693,GO:0060271	actin binding,actin binding,actin binding,cytoplasm,cytoskeleton,cytoskeleton,cytoskeleton organization,nervous system development,positive regulation of neuron projection development,positive regulation of neuron projection development,positive regulation of neuron projection development,actin cytoskeleton,axon,cell projection,cell projection,cell projection,neuron projection,actin filament capping,cilium morphogenesis
comp30978_c0_seq1.p9				
comp30978_c0_seq2.p1	sp|O75366|AVIL_HUMAN_Advillin_OS=Homo_sapiens_GN=AVIL_PE=1_SV=3	2.00E-14	GO:0003779,GO:0003779,GO:0003779,GO:0005737,GO:0005856,GO:0005856,GO:0007010,GO:0007399,GO:0010976,GO:0010976,GO:0010976,GO:0015629,GO:0030424,GO:0042995,GO:0042995,GO:0042995,GO:0043005,GO:0051693,GO:0060271	actin binding,actin binding,actin binding,cytoplasm,cytoskeleton,cytoskeleton,cytoskeleton organization,nervous system development,positive regulation of neuron projection development,positive regulation of neuron projection development,positive regulation of neuron projection development,actin cytoskeleton,axon,cell projection,cell projection,cell projection,neuron projection,actin filament capping,cilium morphogenesis
comp30978_c0_seq2.p2	sp|P34268|FLII_CAEEL_Protein_flightless-1_homolog_OS=Caenorhabditis_elegans_GN=fli-1_PE=2_SV=2	7.00E-11	GO:0003779,GO:0005634,GO:0007275	actin binding,nucleus,multicellular organismal development
comp30978_c0_seq2.p9				
comp30979_c0_seq1.p1	sp|Q3AKH0|GATA_SYNSC_Glutamyl-tRNA(Gln)_amidotransferase_subunit_A_OS=Synechococcus_sp._(strain_CC9605)_GN=gatA_PE=3_SV=1	2.00E-98	GO:0000166,GO:0005524,GO:0006412,GO:0006412,GO:0006412,GO:0016874,GO:0016884,GO:0050567,GO:0050567	nucleotide binding,ATP binding,translation,translation,translation,ligase activity,carbon-nitrogen ligase activity, with glutamine as amido-N-donor,glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity,glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity
comp30979_c0_seq1.p2				
comp30979_c0_seq3.p1				
comp30979_c0_seq8.p1				
comp30980_c0_seq2.p1	sp|Q5RGT6|ANGE2_DANRE_Protein_angel_homolog_2_OS=Danio_rerio_GN=angel2_PE=2_SV=1	2.00E-16	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp30980_c0_seq2.p3				
comp30980_c0_seq3.p1	sp|Q5RGT6|ANGE2_DANRE_Protein_angel_homolog_2_OS=Danio_rerio_GN=angel2_PE=2_SV=1	1.00E-13	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp30981_c0_seq2.p1				
comp30982_c0_seq2.p1				
comp30982_c0_seq3.p1				
comp30983_c0_seq3.p1				
comp30983_c0_seq3.p2	sp|Q653T6|SPS1_ORYSJ_Solanesyl-diphosphate_synthase_1,_mitochondrial_OS=Oryza_sativa_subsp._japonica_GN=SPS1_PE=1_SV=1	3.00E-74	GO:0004659,GO:0005739,GO:0005739,GO:0005739,GO:0006744,GO:0006744,GO:0008299,GO:0008299,GO:0008299,GO:0009507,GO:0009536,GO:0009790,GO:0016740,GO:0016740,GO:0046872,GO:0046872,GO:0050347,GO:0050347,GO:0052923,GO:0052924	prenyltransferase activity,mitochondrion,mitochondrion,mitochondrion,ubiquinone biosynthetic process,ubiquinone biosynthetic process,isoprenoid biosynthetic process,isoprenoid biosynthetic process,isoprenoid biosynthetic process,chloroplast,plastid,embryo development,transferase activity,transferase activity,metal ion binding,metal ion binding,trans-octaprenyltranstransferase activity,trans-octaprenyltranstransferase activity,all-trans-nonaprenyl-diphosphate synthase (geranyl-diphosphate specific) activity,all-trans-nonaprenyl-diphosphate synthase (geranylgeranyl-diphosphate specific) activity
comp30984_c0_seq1.p1				
comp30984_c0_seq4.p1	sp|Q5EFZ4|VAC8_PICPA_Vacuolar_protein_8_OS=Pichia_pastoris_GN=VAC8_PE=3_SV=3	5.00E-12	GO:0005773,GO:0005774,GO:0016020	vacuole,vacuolar membrane,membrane
comp30985_c0_seq1.p1				
comp30987_c0_seq2.p1				
comp30987_c0_seq3.p1				
comp30988_c0_seq1.p1				
comp30988_c0_seq1.p2				
comp30989_c0_seq2.p1				
comp30991_c1_seq2.p1	sp|P27216|ANX13_HUMAN_Annexin_A13_OS=Homo_sapiens_GN=ANXA13_PE=1_SV=3	1.00E-24	GO:0001786,GO:0005509,GO:0005544,GO:0005544,GO:0005615,GO:0005654,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0016020,GO:0016323,GO:0016323,GO:0016324,GO:0016324,GO:0030154,GO:0042997,GO:0042998,GO:0042998,GO:0045121,GO:0045121,GO:0070062,GO:0070062,GO:0070382,GO:1901611,GO:0031210	phosphatidylserine binding,calcium ion binding,calcium-dependent phospholipid binding,calcium-dependent phospholipid binding,extracellular space,nucleoplasm,plasma membrane,plasma membrane,plasma membrane,plasma membrane,membrane,basolateral plasma membrane,basolateral plasma membrane,apical plasma membrane,apical plasma membrane,cell differentiation,negative regulation of Golgi to plasma membrane protein transport,positive regulation of Golgi to plasma membrane protein transport,positive regulation of Golgi to plasma membrane protein transport,membrane raft,membrane raft,extracellular vesicular exosome,extracellular vesicular exosome,exocytic vesicle,phosphatidylglycerol binding,phosphatidylcholine binding
comp30991_c1_seq3.p1	sp|P79134|ANXA6_BOVIN_Annexin_A6_OS=Bos_taurus_GN=ANXA6_PE=1_SV=2	4.00E-64	GO:0001725,GO:0001786,GO:0003418,GO:0004872,GO:0005262,GO:0005509,GO:0005525,GO:0005544,GO:0005544,GO:0005544,GO:0005737,GO:0005737,GO:0005737,GO:0005765,GO:0005829,GO:0005886,GO:0005925,GO:0006816,GO:0006816,GO:0006937,GO:0006937,GO:0008201,GO:0008289,GO:0015276,GO:0015485,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0019899,GO:0030061,GO:0031214,GO:0031902,GO:0031988,GO:0034220,GO:0035374,GO:0042470,GO:0042584,GO:0042802,GO:0042802,GO:0042803,GO:0048306,GO:0048306,GO:0048306,GO:0048306,GO:0048471,GO:0048471,GO:0051015,GO:0051260,GO:0051283,GO:0070062,GO:0070509,GO:0070588	stress fiber,phosphatidylserine binding,growth plate cartilage chondrocyte differentiation,receptor activity,calcium channel activity,calcium ion binding,GTP binding,calcium-dependent phospholipid binding,calcium-dependent phospholipid binding,calcium-dependent phospholipid binding,cytoplasm,cytoplasm,cytoplasm,lysosomal membrane,cytosol,plasma membrane,focal adhesion,calcium ion transport,calcium ion transport,regulation of muscle contraction,regulation of muscle contraction,heparin binding,lipid binding,ligand-gated ion channel activity,cholesterol binding,membrane,membrane,membrane,integral component of membrane,integral component of membrane,enzyme binding,mitochondrial crista,biomineral tissue development,late endosome membrane,membrane-bounded vesicle,ion transmembrane transport,chondroitin sulfate binding,melanosome,chromaffin granule membrane,identical protein binding,identical protein binding,protein homodimerization activity,calcium-dependent protein binding,calcium-dependent protein binding,calcium-dependent protein binding,calcium-dependent protein binding,perinuclear region of cytoplasm,perinuclear region of cytoplasm,actin filament binding,protein homooligomerization,negative regulation of sequestering of calcium ion,extracellular vesicular exosome,calcium ion import,calcium ion transmembrane transport
comp30991_c2_seq3.p1				
comp30992_c1_seq5.p1	sp|Q83WC3|SDMT_APHHA_Sarcosine/dimethylglycine_N-methyltransferase_OS=Aphanothece_halophytica_PE=1_SV=1	8.00E-21	GO:0008152,GO:0008168,GO:0008168,GO:0016740,GO:0019286,GO:0019286,GO:0032259,GO:0032259,GO:0052729,GO:0052729,GO:0052730	metabolic process,methyltransferase activity,methyltransferase activity,transferase activity,glycine betaine biosynthetic process from glycine,glycine betaine biosynthetic process from glycine,methylation,methylation,dimethylglycine N-methyltransferase activity,dimethylglycine N-methyltransferase activity,sarcosine N-methyltransferase activity
comp30993_c0_seq3.p1				
comp30993_c1_seq3.p2				
comp30995_c0_seq1.p1				
comp30995_c0_seq2.p1				
comp30996_c0_seq10.p2				
comp30996_c0_seq3.p1	sp|Q9EPL8|IPO7_MOUSE_Importin-7_OS=Mus_musculus_GN=Ipo7_PE=1_SV=2	3.00E-100	GO:0005515,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006606,GO:0006810,GO:0006886,GO:0008536,GO:0015031,GO:0016020,GO:0042393,GO:0045087	protein binding,nucleus,nucleus,cytoplasm,cytoplasm,protein import into nucleus,transport,intracellular protein transport,Ran GTPase binding,protein transport,membrane,histone binding,innate immune response
comp30996_c0_seq7.p1	sp|Q9EPL8|IPO7_MOUSE_Importin-7_OS=Mus_musculus_GN=Ipo7_PE=1_SV=2	2.00E-99	GO:0005515,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006606,GO:0006810,GO:0006886,GO:0008536,GO:0015031,GO:0016020,GO:0042393,GO:0045087	protein binding,nucleus,nucleus,cytoplasm,cytoplasm,protein import into nucleus,transport,intracellular protein transport,Ran GTPase binding,protein transport,membrane,histone binding,innate immune response
comp30996_c0_seq8.p1				
comp30997_c0_seq3.p1				
comp30997_c0_seq4.p1				
comp30998_c1_seq2.p1				
comp30999_c0_seq1.p1				
comp30999_c0_seq1.p2	sp|Q9P7U1|YI7F_SCHPO_Uncharacterized_AIM2_family_protein_C977.15_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC977.15_PE=2_SV=1	6.00E-26	GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0008150,GO:0008152,GO:0016787	nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytosol,biological_process,metabolic process,hydrolase activity
comp30999_c0_seq3.p1	sp|Q9P7U1|YI7F_SCHPO_Uncharacterized_AIM2_family_protein_C977.15_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC977.15_PE=2_SV=1	6.00E-26	GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0008150,GO:0008152,GO:0016787	nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytosol,biological_process,metabolic process,hydrolase activity
comp30999_c0_seq4.p1	sp|Q9P7U1|YI7F_SCHPO_Uncharacterized_AIM2_family_protein_C977.15_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC977.15_PE=2_SV=1	6.00E-26	GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0008150,GO:0008152,GO:0016787	nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytosol,biological_process,metabolic process,hydrolase activity
comp30999_c0_seq4.p2				
comp30999_c0_seq4.p3				
comp30999_c0_seq8.p1	sp|Q9P7U1|YI7F_SCHPO_Uncharacterized_AIM2_family_protein_C977.15_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC977.15_PE=2_SV=1	6.00E-15	GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0008150,GO:0008152,GO:0016787	nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytosol,biological_process,metabolic process,hydrolase activity
comp31000_c0_seq1.p1	sp|P33279|E2AK1_RABIT_Eukaryotic_translation_initiation_factor_2-alpha_kinase_1_OS=Oryctolagus_cuniculus_GN=EIF2AK1_PE=1_SV=1	2.00E-22	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004694,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0006417,GO:0006468,GO:0006950,GO:0008285,GO:0009605,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0017148,GO:0018105,GO:0020037,GO:0042803,GO:0046777,GO:0046986	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,eukaryotic translation initiation factor 2alpha kinase activity,protein binding,protein binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,regulation of translation,protein phosphorylation,response to stress,negative regulation of cell proliferation,response to external stimulus,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,negative regulation of translation,peptidyl-serine phosphorylation,heme binding,protein homodimerization activity,protein autophosphorylation,negative regulation of hemoglobin biosynthetic process
comp31000_c1_seq1.p1	sp|Q6NSR8|PEPL1_MOUSE_Probable_aminopeptidase_NPEPL1_OS=Mus_musculus_GN=Npepl1_PE=2_SV=1	9.00E-108	GO:0004177,GO:0004177,GO:0005622,GO:0005634,GO:0005737,GO:0006508,GO:0006508,GO:0008150,GO:0008233,GO:0008235,GO:0016787,GO:0019538,GO:0030145,GO:0046872	aminopeptidase activity,aminopeptidase activity,intracellular,nucleus,cytoplasm,proteolysis,proteolysis,biological_process,peptidase activity,metalloexopeptidase activity,hydrolase activity,protein metabolic process,manganese ion binding,metal ion binding
comp31001_c0_seq1.p1	sp|P52551|MYBB_XENLA_Myb-related_protein_B_OS=Xenopus_laevis_GN=mybl2_PE=2_SV=2	4.00E-38	GO:0003677,GO:0003677,GO:0003682,GO:0003700,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0007049	DNA binding,DNA binding,chromatin binding,sequence-specific DNA binding transcription factor activity,nucleus,nucleus,transcription, DNA-templated,regulation of transcription, DNA-templated,cell cycle
comp31002_c0_seq3.p1				
comp31002_c0_seq4.p2				
comp31002_c0_seq5.p1				
comp31002_c0_seq5.p2				
comp31003_c0_seq1.p1				
comp31003_c0_seq2.p1				
comp31003_c0_seq3.p1				
comp31004_c0_seq2.p1				
comp31005_c0_seq11.p1				
comp31005_c0_seq12.p1	sp|Q6ZNF0|PAPL_HUMAN_Iron/zinc_purple_acid_phosphatase-like_protein_OS=Homo_sapiens_GN=PAPL_PE=2_SV=2	3.00E-39	GO:0003993,GO:0003993,GO:0005576,GO:0005576,GO:0008152,GO:0008152,GO:0016311,GO:0016311,GO:0016787,GO:0016787,GO:0046872,GO:0046872	acid phosphatase activity,acid phosphatase activity,extracellular region,extracellular region,metabolic process,metabolic process,dephosphorylation,dephosphorylation,hydrolase activity,hydrolase activity,metal ion binding,metal ion binding
comp31005_c0_seq4.p1	sp|Q12546|PPA_ASPFI_Acid_phosphatase_OS=Aspergillus_ficuum_GN=aphA_PE=1_SV=1	2.00E-31	GO:0003993,GO:0003993,GO:0005576,GO:0005576,GO:0008152,GO:0008152,GO:0016311,GO:0016311,GO:0016787,GO:0016787,GO:0046872	acid phosphatase activity,acid phosphatase activity,extracellular region,extracellular region,metabolic process,metabolic process,dephosphorylation,dephosphorylation,hydrolase activity,hydrolase activity,metal ion binding
comp31005_c0_seq4.p2				
comp31006_c0_seq1.p1				
comp31009_c0_seq4.p1				
comp31010_c1_seq1.p1				
comp31011_c0_seq1.p1				
comp31011_c0_seq10.p2				
comp31011_c0_seq3.p1				
comp31011_c0_seq5.p1				
comp31011_c0_seq6.p2				
comp31011_c0_seq9.p1				
comp31012_c0_seq7.p1				
comp31012_c0_seq8.p1				
comp31013_c0_seq1.p1				
comp31013_c0_seq2.p1				
comp31013_c0_seq6.p1				
comp31014_c0_seq2.p1	sp|A5PJS2|S5A1_BOVIN_3-oxo-5-alpha-steroid_4-dehydrogenase_1_OS=Bos_taurus_GN=SRD5A1_PE=2_SV=1	2.00E-72	GO:0003865,GO:0003865,GO:0005737,GO:0005783,GO:0005789,GO:0006629,GO:0006702,GO:0007548,GO:0008202,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016491,GO:0016627,GO:0030154,GO:0031090,GO:0043231,GO:0047751,GO:0055114,GO:0055114	3-oxo-5-alpha-steroid 4-dehydrogenase activity,3-oxo-5-alpha-steroid 4-dehydrogenase activity,cytoplasm,endoplasmic reticulum,endoplasmic reticulum membrane,lipid metabolic process,androgen biosynthetic process,sex differentiation,steroid metabolic process,membrane,membrane,integral component of membrane,integral component of membrane,oxidoreductase activity,oxidoreductase activity, acting on the CH-CH group of donors,cell differentiation,organelle membrane,intracellular membrane-bounded organelle,cholestenone 5-alpha-reductase activity,oxidation-reduction process,oxidation-reduction process
comp31016_c0_seq2.p1				
comp31017_c0_seq2.p1	sp|P35564|CALX_MOUSE_Calnexin_OS=Mus_musculus_GN=Canx_PE=1_SV=1	6.00E-112	GO:0001948,GO:0005509,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005783,GO:0005789,GO:0005789,GO:0005789,GO:0005790,GO:0005791,GO:0005840,GO:0006457,GO:0007568,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0030246,GO:0030424,GO:0032839,GO:0034185,GO:0035255,GO:0042470,GO:0043025,GO:0043197,GO:0043209,GO:0043234,GO:0044822,GO:0046872,GO:0048488,GO:0051082,GO:0061077,GO:0070062,GO:0071556,GO:0072583	glycoprotein binding,calcium ion binding,protein binding,protein binding,protein binding,cytoplasm,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,endoplasmic reticulum membrane,endoplasmic reticulum membrane,smooth endoplasmic reticulum,rough endoplasmic reticulum,ribosome,protein folding,aging,membrane,membrane,membrane,integral component of membrane,integral component of membrane,carbohydrate binding,axon,dendrite cytoplasm,apolipoprotein binding,ionotropic glutamate receptor binding,melanosome,neuronal cell body,dendritic spine,myelin sheath,protein complex,poly(A) RNA binding,metal ion binding,synaptic vesicle endocytosis,unfolded protein binding,chaperone-mediated protein folding,extracellular vesicular exosome,integral component of lumenal side of endoplasmic reticulum membrane,clathrin-mediated endocytosis
comp31017_c0_seq2.p2				
comp31018_c0_seq1.p1				
comp31018_c0_seq1.p3				
comp31018_c0_seq1.p4	sp|Q9FMM0|UBC18_ARATH_Probable_ubiquitin-conjugating_enzyme_E2_18_OS=Arabidopsis_thaliana_GN=UBC18_PE=2_SV=1	1.00E-30	GO:0000166,GO:0000209,GO:0005524,GO:0005634,GO:0005737,GO:0016567,GO:0016874,GO:0016881,GO:0019787,GO:0031625,GO:0043161,GO:0061630	nucleotide binding,protein polyubiquitination,ATP binding,nucleus,cytoplasm,protein ubiquitination,ligase activity,acid-amino acid ligase activity,small conjugating protein transferase activity,ubiquitin protein ligase binding,proteasome-mediated ubiquitin-dependent protein catabolic process,ubiquitin protein ligase activity
comp31018_c0_seq4.p1				
comp31018_c0_seq5.p1	sp|P23133|TODF_PSEP1_2-hydroxy-6-oxo-2,4-heptadienoate_hydrolase_OS=Pseudomonas_putida_(strain_F1_/_ATCC_700007)_GN=todF_PE=3_SV=2	3.00E-12	GO:0003824,GO:0016787,GO:0019439,GO:0042203,GO:0052689	catalytic activity,hydrolase activity,aromatic compound catabolic process,toluene catabolic process,carboxylic ester hydrolase activity
comp31018_c0_seq5.p3	sp|Q9FMM0|UBC18_ARATH_Probable_ubiquitin-conjugating_enzyme_E2_18_OS=Arabidopsis_thaliana_GN=UBC18_PE=2_SV=1	1.00E-30	GO:0000166,GO:0000209,GO:0005524,GO:0005634,GO:0005737,GO:0016567,GO:0016874,GO:0016881,GO:0019787,GO:0031625,GO:0043161,GO:0061630	nucleotide binding,protein polyubiquitination,ATP binding,nucleus,cytoplasm,protein ubiquitination,ligase activity,acid-amino acid ligase activity,small conjugating protein transferase activity,ubiquitin protein ligase binding,proteasome-mediated ubiquitin-dependent protein catabolic process,ubiquitin protein ligase activity
comp31019_c0_seq1.p1	sp|Q6AYN2|TMM66_RAT_Transmembrane_protein_66_OS=Rattus_norvegicus_GN=Tmem66_PE=2_SV=1	1.00E-16	GO:0005783,GO:0005789,GO:0006810,GO:0006811,GO:0006816,GO:0015279,GO:0016020,GO:0016021,GO:0030176,GO:0030176,GO:0070588,GO:2001256,GO:2001256	endoplasmic reticulum,endoplasmic reticulum membrane,transport,ion transport,calcium ion transport,store-operated calcium channel activity,membrane,integral component of membrane,integral component of endoplasmic reticulum membrane,integral component of endoplasmic reticulum membrane,calcium ion transmembrane transport,regulation of store-operated calcium entry,regulation of store-operated calcium entry
comp31019_c1_seq1.p1				
comp31019_c1_seq13.p1				
comp31019_c1_seq16.p1				
comp31019_c1_seq16.p8				
comp31020_c0_seq2.p1				
comp31020_c0_seq2.p2	sp|Q5R8J8|DNJB4_PONAB_DnaJ_homolog_subfamily_B_member_4_OS=Pongo_abelii_GN=DNAJB4_PE=2_SV=1	1.00E-39	GO:0006457,GO:0051082	protein folding,unfolded protein binding
comp31021_c0_seq4.p1	sp|O46606|DDHD1_BOVIN_Phospholipase_DDHD1_OS=Bos_taurus_GN=DDHD1_PE=1_SV=1	3.00E-30	GO:0005737,GO:0005737,GO:0006629,GO:0016042,GO:0016787,GO:0046872	cytoplasm,cytoplasm,lipid metabolic process,lipid catabolic process,hydrolase activity,metal ion binding
comp31022_c0_seq2.p1				
comp31023_c0_seq3.p1				
comp31023_c0_seq4.p1	sp|P70805|ALGG_AZOVI_Poly(beta-D-mannuronate)_C5_epimerase_OS=Azotobacter_vinelandii_GN=algG_PE=2_SV=1	6.00E-17	GO:0016853,GO:0042121,GO:0042121,GO:0042597,GO:0042597	isomerase activity,alginic acid biosynthetic process,alginic acid biosynthetic process,periplasmic space,periplasmic space
comp31024_c0_seq2.p1	sp|O95551|TYDP2_HUMAN_Tyrosyl-DNA_phosphodiesterase_2_OS=Homo_sapiens_GN=TDP2_PE=1_SV=1	1.00E-30	GO:0000287,GO:0000287,GO:0000287,GO:0003697,GO:0003714,GO:0004518,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005730,GO:0005737,GO:0005737,GO:0005737,GO:0006281,GO:0006302,GO:0006302,GO:0006974,GO:0007166,GO:0016605,GO:0016605,GO:0016787,GO:0030145,GO:0036317,GO:0045171,GO:0046872,GO:0070260,GO:0070260,GO:0070260,GO:0070260,GO:0090305,GO:1903507	magnesium ion binding,magnesium ion binding,magnesium ion binding,single-stranded DNA binding,transcription corepressor activity,nuclease activity,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,nucleoplasm,nucleolus,cytoplasm,cytoplasm,cytoplasm,DNA repair,double-strand break repair,double-strand break repair,cellular response to DNA damage stimulus,cell surface receptor signaling pathway,PML body,PML body,hydrolase activity,manganese ion binding,tyrosyl-RNA phosphodiesterase activity,intercellular bridge,metal ion binding,5'-tyrosyl-DNA phosphodiesterase activity,5'-tyrosyl-DNA phosphodiesterase activity,5'-tyrosyl-DNA phosphodiesterase activity,5'-tyrosyl-DNA phosphodiesterase activity,nucleic acid phosphodiester bond hydrolysis,negative regulation of nucleic acid-templated transcription
comp31024_c0_seq5.p2	sp|Q5XJA0|TYDP2_DANRE_Tyrosyl-DNA_phosphodiesterase_2_OS=Danio_rerio_GN=tdp2_PE=2_SV=3	5.00E-26	GO:0000287,GO:0003697,GO:0004518,GO:0005634,GO:0005634,GO:0006281,GO:0006302,GO:0006974,GO:0007275,GO:0007368,GO:0007369,GO:0016605,GO:0016605,GO:0016787,GO:0030145,GO:0046872,GO:0070260,GO:0090305	magnesium ion binding,single-stranded DNA binding,nuclease activity,nucleus,nucleus,DNA repair,double-strand break repair,cellular response to DNA damage stimulus,multicellular organismal development,determination of left/right symmetry,gastrulation,PML body,PML body,hydrolase activity,manganese ion binding,metal ion binding,5'-tyrosyl-DNA phosphodiesterase activity,nucleic acid phosphodiester bond hydrolysis
comp31024_c0_seq7.p1	sp|O95551|TYDP2_HUMAN_Tyrosyl-DNA_phosphodiesterase_2_OS=Homo_sapiens_GN=TDP2_PE=1_SV=1	1.00E-30	GO:0000287,GO:0000287,GO:0000287,GO:0003697,GO:0003714,GO:0004518,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005730,GO:0005737,GO:0005737,GO:0005737,GO:0006281,GO:0006302,GO:0006302,GO:0006974,GO:0007166,GO:0016605,GO:0016605,GO:0016787,GO:0030145,GO:0036317,GO:0045171,GO:0046872,GO:0070260,GO:0070260,GO:0070260,GO:0070260,GO:0090305,GO:1903507	magnesium ion binding,magnesium ion binding,magnesium ion binding,single-stranded DNA binding,transcription corepressor activity,nuclease activity,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,nucleoplasm,nucleolus,cytoplasm,cytoplasm,cytoplasm,DNA repair,double-strand break repair,double-strand break repair,cellular response to DNA damage stimulus,cell surface receptor signaling pathway,PML body,PML body,hydrolase activity,manganese ion binding,tyrosyl-RNA phosphodiesterase activity,intercellular bridge,metal ion binding,5'-tyrosyl-DNA phosphodiesterase activity,5'-tyrosyl-DNA phosphodiesterase activity,5'-tyrosyl-DNA phosphodiesterase activity,5'-tyrosyl-DNA phosphodiesterase activity,nucleic acid phosphodiester bond hydrolysis,negative regulation of nucleic acid-templated transcription
comp31025_c0_seq1.p1	sp|Q08BC4|CD037_DANRE_Uncharacterized_protein_C4orf37_homolog_OS=Danio_rerio_GN=zgc:153987_PE=2_SV=1	6.00E-30	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp31025_c0_seq1.p2				
comp31025_c0_seq4.p1	sp|Q08BC4|CD037_DANRE_Uncharacterized_protein_C4orf37_homolog_OS=Danio_rerio_GN=zgc:153987_PE=2_SV=1	6.00E-30	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp31025_c0_seq4.p2				
comp31026_c0_seq1.p1				
comp31027_c0_seq1.p1	sp|Q9QZD4|XPF_MOUSE_DNA_repair_endonuclease_XPF_OS=Mus_musculus_GN=Ercc4_PE=2_SV=3	1.00E-63	GO:0000014,GO:0000109,GO:0000109,GO:0000110,GO:0000110,GO:0000712,GO:0000723,GO:0000724,GO:0000724,GO:0000737,GO:0000737,GO:0000781,GO:0000784,GO:0001094,GO:0003676,GO:0003677,GO:0003677,GO:0003684,GO:0003684,GO:0003697,GO:0003697,GO:0004518,GO:0004518,GO:0004519,GO:0004519,GO:0004520,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005669,GO:0006259,GO:0006281,GO:0006281,GO:0006281,GO:0006289,GO:0006289,GO:0006295,GO:0006296,GO:0006296,GO:0006974,GO:0008022,GO:0009411,GO:0009650,GO:0010834,GO:0016787,GO:0032205,GO:0033683,GO:0043566,GO:0047485,GO:1901255	single-stranded DNA endodeoxyribonuclease activity,nucleotide-excision repair complex,nucleotide-excision repair complex,nucleotide-excision repair factor 1 complex,nucleotide-excision repair factor 1 complex,resolution of meiotic recombination intermediates,telomere maintenance,double-strand break repair via homologous recombination,double-strand break repair via homologous recombination,DNA catabolic process, endonucleolytic,DNA catabolic process, endonucleolytic,chromosome, telomeric region,nuclear chromosome, telomeric region,TFIID-class transcription factor binding,nucleic acid binding,DNA binding,DNA binding,damaged DNA binding,damaged DNA binding,single-stranded DNA binding,single-stranded DNA binding,nuclease activity,nuclease activity,endonuclease activity,endonuclease activity,endodeoxyribonuclease activity,protein binding,nucleus,nucleus,nucleus,transcription factor TFIID complex,DNA metabolic process,DNA repair,DNA repair,DNA repair,nucleotide-excision repair,nucleotide-excision repair,nucleotide-excision repair, DNA incision, 3'-to lesion,nucleotide-excision repair, DNA incision, 5'-to lesion,nucleotide-excision repair, DNA incision, 5'-to lesion,cellular response to DNA damage stimulus,protein C-terminus binding,response to UV,UV protection,telomere maintenance via telomere shortening,hydrolase activity,negative regulation of telomere maintenance,nucleotide-excision repair, DNA incision,structure-specific DNA binding,protein N-terminus binding,nucleotide-excision repair involved in interstrand cross-link repair
comp31028_c1_seq12.p1				
comp31028_c1_seq14.p1				
comp31028_c1_seq14.p2				
comp31028_c1_seq15.p1				
comp31028_c1_seq16.p1				
comp31028_c1_seq16.p2				
comp31028_c1_seq2.p1				
comp31028_c1_seq22.p1				
comp31028_c1_seq24.p1				
comp31028_c1_seq24.p2				
comp31028_c1_seq25.p1				
comp31028_c1_seq7.p1				
comp31028_c1_seq8.p1				
comp31028_c1_seq8.p2				
comp31030_c0_seq4.p1	sp|P80235|CACM_YEAST_Putative_mitochondrial_carnitine_O-acetyltransferase_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YAT1_PE=1_SV=2	3.00E-103	GO:0004092,GO:0004092,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0006066,GO:0006629,GO:0006631,GO:0006810,GO:0009437,GO:0016020,GO:0016740,GO:0016746,GO:0016746	carnitine O-acetyltransferase activity,carnitine O-acetyltransferase activity,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,alcohol metabolic process,lipid metabolic process,fatty acid metabolic process,transport,carnitine metabolic process,membrane,transferase activity,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups
comp31030_c0_seq5.p1	sp|Q00614|CACP_CANTR_Carnitine_O-acetyltransferase,_mitochondrial_OS=Candida_tropicalis_GN=CAT2_PE=3_SV=1	3.00E-15	GO:0004092,GO:0005739,GO:0005743,GO:0005743,GO:0005777,GO:0005777,GO:0006629,GO:0006631,GO:0006810,GO:0016020,GO:0016740,GO:0016746,GO:0016746	carnitine O-acetyltransferase activity,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,peroxisome,peroxisome,lipid metabolic process,fatty acid metabolic process,transport,membrane,transferase activity,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups
comp31030_c0_seq5.p3				
comp31030_c0_seq6.p1	sp|P80235|CACM_YEAST_Putative_mitochondrial_carnitine_O-acetyltransferase_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YAT1_PE=1_SV=2	4.00E-98	GO:0004092,GO:0004092,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0006066,GO:0006629,GO:0006631,GO:0006810,GO:0009437,GO:0016020,GO:0016740,GO:0016746,GO:0016746	carnitine O-acetyltransferase activity,carnitine O-acetyltransferase activity,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,alcohol metabolic process,lipid metabolic process,fatty acid metabolic process,transport,carnitine metabolic process,membrane,transferase activity,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups
comp31031_c0_seq12.p1	sp|Q12603|XYNA_DICTH_Beta-1,4-xylanase_OS=Dictyoglomus_thermophilum_GN=xynA_PE=3_SV=1	2.00E-46	GO:0000272,GO:0004553,GO:0005576,GO:0005576,GO:0005975,GO:0005975,GO:0008152,GO:0016787,GO:0016798,GO:0031176,GO:0045493,GO:0045493	polysaccharide catabolic process,hydrolase activity, hydrolyzing O-glycosyl compounds,extracellular region,extracellular region,carbohydrate metabolic process,carbohydrate metabolic process,metabolic process,hydrolase activity,hydrolase activity, acting on glycosyl bonds,endo-1,4-beta-xylanase activity,xylan catabolic process,xylan catabolic process
comp31031_c0_seq2.p1				
comp31031_c0_seq5.p1	sp|P07986|GUX_CELFI_Exoglucanase/xylanase_OS=Cellulomonas_fimi_GN=cex_PE=1_SV=1	3.00E-37	GO:0000272,GO:0003824,GO:0004553,GO:0005975,GO:0005975,GO:0008152,GO:0008152,GO:0016162,GO:0016787,GO:0016798,GO:0030245,GO:0030246,GO:0030247,GO:0031176,GO:0045493	polysaccharide catabolic process,catalytic activity,hydrolase activity, hydrolyzing O-glycosyl compounds,carbohydrate metabolic process,carbohydrate metabolic process,metabolic process,metabolic process,cellulose 1,4-beta-cellobiosidase activity,hydrolase activity,hydrolase activity, acting on glycosyl bonds,cellulose catabolic process,carbohydrate binding,polysaccharide binding,endo-1,4-beta-xylanase activity,xylan catabolic process
comp31031_c0_seq6.p1	sp|P07986|GUX_CELFI_Exoglucanase/xylanase_OS=Cellulomonas_fimi_GN=cex_PE=1_SV=1	6.00E-59	GO:0000272,GO:0003824,GO:0004553,GO:0005975,GO:0005975,GO:0008152,GO:0008152,GO:0016162,GO:0016787,GO:0016798,GO:0030245,GO:0030246,GO:0030247,GO:0031176,GO:0045493	polysaccharide catabolic process,catalytic activity,hydrolase activity, hydrolyzing O-glycosyl compounds,carbohydrate metabolic process,carbohydrate metabolic process,metabolic process,metabolic process,cellulose 1,4-beta-cellobiosidase activity,hydrolase activity,hydrolase activity, acting on glycosyl bonds,cellulose catabolic process,carbohydrate binding,polysaccharide binding,endo-1,4-beta-xylanase activity,xylan catabolic process
comp31031_c0_seq8.p1	sp|Q12603|XYNA_DICTH_Beta-1,4-xylanase_OS=Dictyoglomus_thermophilum_GN=xynA_PE=3_SV=1	5.00E-46	GO:0000272,GO:0004553,GO:0005576,GO:0005576,GO:0005975,GO:0005975,GO:0008152,GO:0016787,GO:0016798,GO:0031176,GO:0045493,GO:0045493	polysaccharide catabolic process,hydrolase activity, hydrolyzing O-glycosyl compounds,extracellular region,extracellular region,carbohydrate metabolic process,carbohydrate metabolic process,metabolic process,hydrolase activity,hydrolase activity, acting on glycosyl bonds,endo-1,4-beta-xylanase activity,xylan catabolic process,xylan catabolic process
comp31032_c0_seq1.p1	sp|Q9SCW4|HFB2A_ARATH_Heat_stress_transcription_factor_B-2a_OS=Arabidopsis_thaliana_GN=HSFB2A_PE=2_SV=1	3.00E-12	GO:0002679,GO:0003677,GO:0003700,GO:0003700,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0006355,GO:0006355,GO:0009408,GO:0010200,GO:0010200,GO:0035556,GO:0043565	respiratory burst involved in defense response,DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,nucleus,nucleus,nucleus,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,response to heat,response to chitin,response to chitin,intracellular signal transduction,sequence-specific DNA binding
comp31032_c0_seq4.p1	sp|P41151|HFA1A_ARATH_Heat_stress_transcription_factor_A-1a_OS=Arabidopsis_thaliana_GN=HSFA1A_PE=1_SV=2	4.00E-12	GO:0003677,GO:0003677,GO:0003700,GO:0003700,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0006355,GO:0009408,GO:0009408,GO:0009408,GO:0009408,GO:0043565	DNA binding,DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,response to heat,response to heat,response to heat,response to heat,sequence-specific DNA binding
comp31033_c0_seq1.p1	sp|Q6Z690|LDL1_ORYSJ_Lysine-specific_histone_demethylase_1_homolog_1_OS=Oryza_sativa_subsp._japonica_GN=Os02g0755200_PE=2_SV=1	2.00E-45	GO:0003677,GO:0003677,GO:0005634,GO:0006351,GO:0006355,GO:0016491,GO:0016491,GO:0016491,GO:0016568,GO:0016568,GO:0016575,GO:0048364,GO:0051568,GO:0055114,GO:0055114,GO:0055114	DNA binding,DNA binding,nucleus,transcription, DNA-templated,regulation of transcription, DNA-templated,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,chromatin modification,chromatin modification,histone deacetylation,root development,histone H3-K4 methylation,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp31033_c1_seq2.p1				
comp31033_c1_seq4.p1	sp|Q9JI13|SAS10_MOUSE_Something_about_silencing_protein_10_OS=Mus_musculus_GN=Utp3_PE=1_SV=1	2.00E-16	GO:0000462,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0007275,GO:0007420,GO:0016568,GO:0032040,GO:0044822	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),protein binding,nucleus,nucleus,nucleus,nucleolus,nucleolus,multicellular organismal development,brain development,chromatin modification,small-subunit processome,poly(A) RNA binding
comp31034_c0_seq5.p1				
comp31035_c0_seq1.p1				
comp31035_c0_seq3.p1	sp|Q6IV78|TAZ_SAISC_Tafazzin_OS=Saimiri_sciureus_GN=TAZ_PE=3_SV=1	2.00E-28	GO:0006644,GO:0008152,GO:0016020,GO:0016020,GO:0016021,GO:0016746	phospholipid metabolic process,metabolic process,membrane,membrane,integral component of membrane,transferase activity, transferring acyl groups
comp31035_c0_seq5.p1	sp|Q6IV78|TAZ_SAISC_Tafazzin_OS=Saimiri_sciureus_GN=TAZ_PE=3_SV=1	5.00E-28	GO:0006644,GO:0008152,GO:0016020,GO:0016020,GO:0016021,GO:0016746	phospholipid metabolic process,metabolic process,membrane,membrane,integral component of membrane,transferase activity, transferring acyl groups
comp31035_c0_seq6.p1				
comp31035_c0_seq9.p3				
comp31036_c0_seq2.p1	sp|O70472|TM131_MOUSE_Transmembrane_protein_131_OS=Mus_musculus_GN=Tmem131_PE=1_SV=2	1.00E-27	GO:0003674,GO:0005575,GO:0008150,GO:0016020,GO:0016020,GO:0016021	molecular_function,cellular_component,biological_process,membrane,membrane,integral component of membrane
comp31036_c0_seq3.p2				
comp31037_c0_seq5.p1				
comp31038_c0_seq1.p1				
comp31038_c0_seq4.p1	sp|C0LGE0|Y1765_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At1g07650_OS=Arabidopsis_thaliana_GN=At1g07650_PE=1_SV=1	6.00E-14	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,protein phosphorylation,membrane,membrane,integral component of membrane,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp31040_c1_seq1.p1	sp|Q31ME3|RPOD2_SYNE7_RNA_polymerase_sigma_factor_rpoD2_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=rpoD2_PE=1_SV=1	5.00E-50	GO:0003677,GO:0003677,GO:0003700,GO:0005737,GO:0005737,GO:0006351,GO:0006352,GO:0006355,GO:0006355,GO:0006355,GO:0016987,GO:0016987	DNA binding,DNA binding,sequence-specific DNA binding transcription factor activity,cytoplasm,cytoplasm,transcription, DNA-templated,DNA-templated transcription, initiation,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,sigma factor activity,sigma factor activity
comp31040_c1_seq1.p3				
comp31040_c2_seq2.p1	sp|Q6PEH4|DIEXF_DANRE_Digestive_organ_expansion_factor_OS=Danio_rerio_GN=diexf_PE=2_SV=2	8.00E-94	GO:0000462,GO:0003674,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005730,GO:0007275,GO:0019843,GO:0030163,GO:0031017,GO:0031648,GO:0032040,GO:0034511,GO:0035265,GO:0035265,GO:0048546,GO:0090594	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),molecular_function,nucleus,nucleus,nucleus,nucleus,nucleolus,multicellular organismal development,rRNA binding,protein catabolic process,exocrine pancreas development,protein destabilization,small-subunit processome,U3 snoRNA binding,organ growth,organ growth,digestive tract morphogenesis,inflammatory response to wounding
comp31040_c2_seq3.p1				
comp31040_c2_seq4.p1	sp|Q6PEH4|DIEXF_DANRE_Digestive_organ_expansion_factor_OS=Danio_rerio_GN=diexf_PE=2_SV=2	5.00E-82	GO:0000462,GO:0003674,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005730,GO:0007275,GO:0019843,GO:0030163,GO:0031017,GO:0031648,GO:0032040,GO:0034511,GO:0035265,GO:0035265,GO:0048546,GO:0090594	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),molecular_function,nucleus,nucleus,nucleus,nucleus,nucleolus,multicellular organismal development,rRNA binding,protein catabolic process,exocrine pancreas development,protein destabilization,small-subunit processome,U3 snoRNA binding,organ growth,organ growth,digestive tract morphogenesis,inflammatory response to wounding
comp31041_c0_seq1.p1	sp|Q4IPX8|SYM1_GIBZE_Protein_SYM1_OS=Gibberella_zeae_(strain_PH-1_/_ATCC_MYA-4620_/_FGSC_9075_/_NRRL_31084)_GN=SYM1_PE=3_SV=1	6.00E-12	GO:0005739,GO:0005743,GO:0005743,GO:0016020,GO:0016021,GO:0016021	mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,membrane,integral component of membrane,integral component of membrane
comp31042_c0_seq1.p1				
comp31043_c0_seq2.p1				
comp31043_c0_seq2.p2				
comp31043_c0_seq4.p1				
comp31043_c0_seq6.p1				
comp31043_c0_seq6.p2				
comp31043_c0_seq7.p1				
comp31043_c1_seq1.p1	sp|Q9SZ67|WRK19_ARATH_Probable_WRKY_transcription_factor_19_OS=Arabidopsis_thaliana_GN=WRKY19_PE=2_SV=1	4.00E-44	GO:0000166,GO:0003677,GO:0003700,GO:0003700,GO:0003700,GO:0004672,GO:0004674,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0006355,GO:0006468,GO:0006952,GO:0007165,GO:0009556,GO:0009941,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0043531,GO:0043565,GO:0052543,GO:0061025	nucleotide binding,DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,protein kinase activity,protein serine/threonine kinase activity,protein binding,ATP binding,ATP binding,nucleus,nucleus,nucleus,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,protein phosphorylation,defense response,signal transduction,microsporogenesis,chloroplast envelope,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,ADP binding,sequence-specific DNA binding,callose deposition in cell wall,membrane fusion
comp31044_c0_seq4.p1				
comp31044_c0_seq5.p1				
comp31045_c0_seq2.p1				
comp31045_c0_seq4.p1				
comp31046_c0_seq2.p2	sp|Q55GU0|Y9955_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0267514_OS=Dictyostelium_discoideum_GN=DDB_G0267514_PE=3_SV=1	2.00E-18	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005575,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,cellular_component,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp31047_c0_seq3.p1	sp|Q54TS4|YIPF1_DICDI_Protein_YIPF1_homolog_OS=Dictyostelium_discoideum_GN=yipf1_PE=3_SV=1	1.00E-11	GO:0003674,GO:0008150,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0044351	molecular_function,biological_process,membrane,membrane,membrane,integral component of membrane,macropinocytosis
comp31050_c0_seq1.p1				
comp31050_c0_seq1.p2				
comp31050_c0_seq2.p1				
comp31050_c0_seq3.p1				
comp31050_c0_seq4.p1				
comp31050_c0_seq4.p2				
comp31050_c0_seq5.p1				
comp31050_c0_seq5.p2				
comp31050_c0_seq6.p1				
comp31050_c0_seq7.p1				
comp31050_c0_seq7.p2				
comp31050_c0_seq8.p1				
comp31051_c2_seq10.p1				
comp31051_c2_seq12.p1				
comp31051_c2_seq14.p1				
comp31051_c2_seq15.p1				
comp31051_c2_seq3.p1				
comp31053_c0_seq1.p1				

comp31054_c0_seq6.p1	sp|Q568K5|NAA40_DANRE_N-alpha-acetyltransferase_40_OS=Danio_rerio_GN=naa40_PE=2_SV=1	8.00E-16	GO:0005575,GO:0008080,GO:0008152,GO:0008152,GO:0008152,GO:0016740,GO:0016746	cellular_component,N-acetyltransferase activity,metabolic process,metabolic process,metabolic process,transferase activity,transferase activity, transferring acyl groups
comp31054_c0_seq6.p3				
comp31056_c0_seq5.p1				
comp31056_c0_seq5.p2	sp|Q5S7T7|TIM50_PHYIN_Mitochondrial_import_inner_membrane_translocase_subunit_TIM50_OS=Phytophthora_infestans_GN=TIM50_PE=2_SV=1	1.00E-37	GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0005744,GO:0006810,GO:0006810,GO:0015031,GO:0015031,GO:0016020,GO:0016021	mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane presequence translocase complex,transport,transport,protein transport,protein transport,membrane,integral component of membrane
comp31057_c0_seq1.p1				
comp31057_c0_seq3.p1				
comp31057_c0_seq5.p1				
comp31058_c0_seq2.p1				
comp31059_c0_seq2.p1	sp|Q6ZI17|OML2_ORYSJ_Protein_MEI2-like_2_OS=Oryza_sativa_subsp._japonica_GN=ML2_PE=2_SV=1	6.00E-50	GO:0000166,GO:0003676,GO:0003723	nucleotide binding,nucleic acid binding,RNA binding
comp31059_c0_seq3.p1	sp|Q6ZI17|OML2_ORYSJ_Protein_MEI2-like_2_OS=Oryza_sativa_subsp._japonica_GN=ML2_PE=2_SV=1	9.00E-50	GO:0000166,GO:0003676,GO:0003723	nucleotide binding,nucleic acid binding,RNA binding
comp31059_c0_seq4.p1				
comp31061_c0_seq1.p1	sp|O96099|FAD5B_DICDI_Delta(5)_fatty_acid_desaturase_B_OS=Dictyostelium_discoideum_GN=fadB_PE=1_SV=1	8.00E-13	GO:0005506,GO:0005886,GO:0006629,GO:0006629,GO:0006631,GO:0006633,GO:0006633,GO:0006636,GO:0016020,GO:0016020,GO:0016021,GO:0016491,GO:0016491,GO:0016717,GO:0020037,GO:0046872,GO:0055114,GO:0055114,GO:0055114	iron ion binding,plasma membrane,lipid metabolic process,lipid metabolic process,fatty acid metabolic process,fatty acid biosynthetic process,fatty acid biosynthetic process,unsaturated fatty acid biosynthetic process,membrane,membrane,integral component of membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water,heme binding,metal ion binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp31061_c0_seq2.p1	sp|O96099|FAD5B_DICDI_Delta(5)_fatty_acid_desaturase_B_OS=Dictyostelium_discoideum_GN=fadB_PE=1_SV=1	8.00E-13	GO:0005506,GO:0005886,GO:0006629,GO:0006629,GO:0006631,GO:0006633,GO:0006633,GO:0006636,GO:0016020,GO:0016020,GO:0016021,GO:0016491,GO:0016491,GO:0016717,GO:0020037,GO:0046872,GO:0055114,GO:0055114,GO:0055114	iron ion binding,plasma membrane,lipid metabolic process,lipid metabolic process,fatty acid metabolic process,fatty acid biosynthetic process,fatty acid biosynthetic process,unsaturated fatty acid biosynthetic process,membrane,membrane,integral component of membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water,heme binding,metal ion binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp31062_c0_seq3.p1				
comp31062_c0_seq4.p1	sp|Q9YHB5|CND3_XENLA_Condensin_complex_subunit_3_OS=Xenopus_laevis_GN=ncapg_PE=1_SV=1	5.00E-30	GO:0000796,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0005737,GO:0005737,GO:0005829,GO:0007049,GO:0007067,GO:0007076,GO:0030261,GO:0051301	condensin complex,nucleus,nucleus,chromosome,chromosome,cytoplasm,cytoplasm,cytosol,cell cycle,mitotic nuclear division,mitotic chromosome condensation,chromosome condensation,cell division
comp31062_c0_seq5.p1				
comp31063_c0_seq2.p1				
comp31063_c0_seq2.p2				
comp31063_c0_seq3.p1				
comp31063_c0_seq4.p1				
comp31063_c0_seq4.p2				
comp31065_c0_seq1.p1				
comp31067_c0_seq2.p1				
comp31067_c0_seq3.p1				
comp31068_c0_seq2.p1	sp|Q8NFD2|ANKK1_HUMAN_Ankyrin_repeat_and_protein_kinase_domain-containing_protein_1_OS=Homo_sapiens_GN=ANKK1_PE=1_SV=1	2.00E-27	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp31068_c0_seq3.p1	sp|Q8NFD2|ANKK1_HUMAN_Ankyrin_repeat_and_protein_kinase_domain-containing_protein_1_OS=Homo_sapiens_GN=ANKK1_PE=1_SV=1	2.00E-27	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp31069_c1_seq1.p1				
comp31069_c1_seq6.p1	sp|B5WWZ8|FAO1_LOTJA_Long-chain-alcohol_oxidase_FAO1_OS=Lotus_japonicus_GN=FAO1_PE=1_SV=1	6.00E-71	GO:0006066,GO:0009409,GO:0016020,GO:0016020,GO:0016021,GO:0016491,GO:0016614,GO:0046577,GO:0046577,GO:0046577,GO:0050660,GO:0055114,GO:0055114,GO:0055114	alcohol metabolic process,response to cold,membrane,membrane,integral component of membrane,oxidoreductase activity,oxidoreductase activity, acting on CH-OH group of donors,long-chain-alcohol oxidase activity,long-chain-alcohol oxidase activity,long-chain-alcohol oxidase activity,flavin adenine dinucleotide binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp31070_c0_seq5.p1				
comp31071_c0_seq5.p1				
comp31071_c0_seq6.p1				
comp31071_c0_seq7.p1				
comp31071_c0_seq8.p1				
comp31072_c0_seq1.p1				
comp31073_c0_seq1.p1				
comp31073_c0_seq5.p1				
comp31074_c0_seq1.p1				
comp31074_c0_seq10.p1				
comp31074_c0_seq10.p4				
comp31074_c0_seq4.p1				
comp31074_c0_seq4.p4				
comp31074_c0_seq6.p1				
comp31076_c0_seq2.p1				
comp31076_c2_seq1.p1	sp|Q9VR91|HERC2_DROME_Probable_E3_ubiquitin-protein_ligase_HERC2_OS=Drosophila_melanogaster_GN=HERC2_PE=1_SV=3	7.00E-32	GO:0004842,GO:0004842,GO:0005575,GO:0005634,GO:0005737,GO:0005737,GO:0005814,GO:0005856,GO:0016567,GO:0016567,GO:0016874,GO:0020037,GO:0042787,GO:0046872	ubiquitin-protein transferase activity,ubiquitin-protein transferase activity,cellular_component,nucleus,cytoplasm,cytoplasm,centriole,cytoskeleton,protein ubiquitination,protein ubiquitination,ligase activity,heme binding,protein ubiquitination involved in ubiquitin-dependent protein catabolic process,metal ion binding
comp31076_c2_seq2.p1	sp|B3H615|ING2_ARATH_PHD_finger_protein_ING2_OS=Arabidopsis_thaliana_GN=ING2_PE=1_SV=1	5.00E-24	GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0008270,GO:0016568,GO:0016568,GO:0035064,GO:0035064,GO:0040008,GO:0046872	nucleus,nucleus,nucleus,nucleus,transcription, DNA-templated,regulation of transcription, DNA-templated,zinc ion binding,chromatin modification,chromatin modification,methylated histone binding,methylated histone binding,regulation of growth,metal ion binding
comp31076_c2_seq3.p1				
comp31076_c2_seq4.p1	sp|O60306|AQR_HUMAN_Intron-binding_protein_aquarius_OS=Homo_sapiens_GN=AQR_PE=1_SV=4	7.00E-132	GO:0000398,GO:0000398,GO:0003723,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005681,GO:0005681,GO:0006397,GO:0008380,GO:0016020,GO:0044822,GO:0044822,GO:0071013	mRNA splicing, via spliceosome,mRNA splicing, via spliceosome,RNA binding,protein binding,nucleus,nucleus,nucleus,nucleoplasm,spliceosomal complex,spliceosomal complex,mRNA processing,RNA splicing,membrane,poly(A) RNA binding,poly(A) RNA binding,catalytic step 2 spliceosome
comp31076_c3_seq1.p1	sp|Q8CFQ3|AQR_MOUSE_Intron-binding_protein_aquarius_OS=Mus_musculus_GN=Aqr_PE=2_SV=2	1.00E-94	GO:0000398,GO:0003723,GO:0005634,GO:0005634,GO:0005634,GO:0005681,GO:0005681,GO:0006397,GO:0008150,GO:0008380,GO:0016020,GO:0044822,GO:0071013	mRNA splicing, via spliceosome,RNA binding,nucleus,nucleus,nucleus,spliceosomal complex,spliceosomal complex,mRNA processing,biological_process,RNA splicing,membrane,poly(A) RNA binding,catalytic step 2 spliceosome
comp31077_c0_seq1.p1	sp|Q58DU0|MMTA2_BOVIN_Multiple_myeloma_tumor-associated_protein_2_homolog_OS=Bos_taurus_GN=MMTAG2_PE=2_SV=1	2.00E-27	GO:0044822	poly(A) RNA binding
comp31077_c1_seq1.p1				
comp31077_c1_seq4.p1				
comp31078_c0_seq2.p1	sp|Q54HS3|SET1_DICDI_Histone-lysine_N-methyltransferase_set1_OS=Dictyostelium_discoideum_GN=set1_PE=1_SV=1	7.00E-41	GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0008168,GO:0016568,GO:0016571,GO:0016740,GO:0018024,GO:0031152,GO:0032259,GO:0034968,GO:0040029,GO:0042800,GO:0051568	nucleus,nucleus,nucleus,chromosome,chromosome,methyltransferase activity,chromatin modification,histone methylation,transferase activity,histone-lysine N-methyltransferase activity,aggregation involved in sorocarp development,methylation,histone lysine methylation,regulation of gene expression, epigenetic,histone methyltransferase activity (H3-K4 specific),histone H3-K4 methylation
comp31079_c0_seq1.p1				
comp31079_c0_seq1.p2	sp|Q54LB8|VP13A_DICDI_Putative_vacuolar_protein_sorting-associated_protein_13A_OS=Dictyostelium_discoideum_GN=vps13A_PE=2_SV=1	2.00E-43	GO:0005622,GO:0005794,GO:0005794,GO:0006623,GO:0006810,GO:0015031,GO:0019898,GO:0044351,GO:0045053	intracellular,Golgi apparatus,Golgi apparatus,protein targeting to vacuole,transport,protein transport,extrinsic component of membrane,macropinocytosis,protein retention in Golgi apparatus

comp31188_c1_seq3.p1				
comp31189_c0_seq1.p1				
comp31189_c0_seq1.p2				
comp31189_c0_seq3.p1				
comp31189_c0_seq5.p1				
comp31189_c0_seq6.p3				
comp31190_c0_seq2.p3				
comp31191_c0_seq3.p1	sp|P11275|KCC2A_RAT_Calcium/calmodulin-dependent_protein_kinase_type_II_subunit_alpha_OS=Rattus_norvegicus_GN=Camk2a_PE=1_SV=1	1.00E-66	GO:0000082,GO:0000166,GO:0002931,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004674,GO:0004683,GO:0004683,GO:0004683,GO:0004683,GO:0004683,GO:0004683,GO:0004683,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005516,GO:0005516,GO:0005524,GO:0005524,GO:0005739,GO:0005886,GO:0006468,GO:0006468,GO:0006468,GO:0006468,GO:0006816,GO:0010666,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0018105,GO:0030054,GO:0030425,GO:0032794,GO:0032839,GO:0035235,GO:0035254,GO:0042734,GO:0045202,GO:0045202,GO:0046777,GO:0046777,GO:0046928,GO:0048168,GO:0051928,GO:1902108	G1/S transition of mitotic cell cycle,nucleotide binding,response to ischemia,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,calmodulin-dependent protein kinase activity,calmodulin-dependent protein kinase activity,calmodulin-dependent protein kinase activity,calmodulin-dependent protein kinase activity,calmodulin-dependent protein kinase activity,calmodulin-dependent protein kinase activity,calmodulin-dependent protein kinase activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,calmodulin binding,calmodulin binding,ATP binding,ATP binding,mitochondrion,plasma membrane,protein phosphorylation,protein phosphorylation,protein phosphorylation,protein phosphorylation,calcium ion transport,positive regulation of cardiac muscle cell apoptotic process,membrane,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-serine phosphorylation,cell junction,dendrite,GTPase activating protein binding,dendrite cytoplasm,ionotropic glutamate receptor signaling pathway,glutamate receptor binding,presynaptic membrane,synapse,synapse,protein autophosphorylation,protein autophosphorylation,regulation of neurotransmitter secretion,regulation of neuronal synaptic plasticity,positive regulation of calcium ion transport,regulation of mitochondrial membrane permeability involved in apoptotic process
comp31192_c0_seq5.p1				
comp31192_c0_seq7.p1				
comp31192_c0_seq8.p1				
comp31192_c0_seq9.p1				
comp31193_c0_seq2.p1	sp|Q9SR00|PP213_ARATH_Pentatricopeptide_repeat-containing_protein_At3g04760,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g04760_PE=2_SV=1	1.00E-39	GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0010103	chloroplast,chloroplast,chloroplast,plastid,stomatal complex morphogenesis
comp31193_c0_seq5.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	7.00E-47		
comp31193_c0_seq5.p2	sp|Q4KL94|NT1AA_XENLA_Alpha_N-terminal_protein_methyltransferase_1A-A_OS=Xenopus_laevis_GN=mettl11a-a_PE=2_SV=1	7.00E-55	GO:0005634,GO:0005634,GO:0005634,GO:0007051,GO:0007059,GO:0008168,GO:0008168,GO:0008276,GO:0016740,GO:0018016,GO:0032259,GO:0035572,GO:0035573	nucleus,nucleus,nucleus,spindle organization,chromosome segregation,methyltransferase activity,methyltransferase activity,protein methyltransferase activity,transferase activity,N-terminal peptidyl-proline dimethylation,methylation,N-terminal peptidyl-serine dimethylation,N-terminal peptidyl-serine trimethylation
comp31193_c0_seq5.p4				
comp31193_c0_seq7.p1	sp|Q9SR00|PP213_ARATH_Pentatricopeptide_repeat-containing_protein_At3g04760,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g04760_PE=2_SV=1	1.00E-39	GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0010103	chloroplast,chloroplast,chloroplast,plastid,stomatal complex morphogenesis
comp31193_c0_seq7.p2	sp|Q4KL94|NT1AA_XENLA_Alpha_N-terminal_protein_methyltransferase_1A-A_OS=Xenopus_laevis_GN=mettl11a-a_PE=2_SV=1	3.00E-45	GO:0005634,GO:0005634,GO:0005634,GO:0007051,GO:0007059,GO:0008168,GO:0008168,GO:0008276,GO:0016740,GO:0018016,GO:0032259,GO:0035572,GO:0035573	nucleus,nucleus,nucleus,spindle organization,chromosome segregation,methyltransferase activity,methyltransferase activity,protein methyltransferase activity,transferase activity,N-terminal peptidyl-proline dimethylation,methylation,N-terminal peptidyl-serine dimethylation,N-terminal peptidyl-serine trimethylation
comp31193_c0_seq7.p4				
comp31195_c0_seq2.p1				
comp31195_c0_seq2.p2				
comp31195_c0_seq3.p1				
comp31195_c0_seq5.p1				
comp31196_c0_seq1.p2				
comp31197_c0_seq2.p1	sp|O94296|YOOC_SCHPO_Probable_phospholipid-transporting_ATPase_C887.12_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC887.12_PE=2_SV=1	2.00E-104	GO:0000166,GO:0000166,GO:0000287,GO:0004012,GO:0004012,GO:0004012,GO:0005524,GO:0005524,GO:0005783,GO:0005783,GO:0005789,GO:0005794,GO:0005794,GO:0005802,GO:0006812,GO:0006892,GO:0008152,GO:0015914,GO:0016020,GO:0016021,GO:0016021,GO:0016787,GO:0019829,GO:0045332,GO:0045332,GO:0045332,GO:0046872,GO:0098655	nucleotide binding,nucleotide binding,magnesium ion binding,phospholipid-translocating ATPase activity,phospholipid-translocating ATPase activity,phospholipid-translocating ATPase activity,ATP binding,ATP binding,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,Golgi apparatus,Golgi apparatus,trans-Golgi network,cation transport,post-Golgi vesicle-mediated transport,metabolic process,phospholipid transport,membrane,integral component of membrane,integral component of membrane,hydrolase activity,cation-transporting ATPase activity,phospholipid translocation,phospholipid translocation,phospholipid translocation,metal ion binding,cation transmembrane transport
comp31197_c0_seq3.p1				
comp31197_c0_seq3.p2				
comp31198_c0_seq2.p1	sp|Q9LPV5|NRT25_ARATH_High_affinity_nitrate_transporter_2.5_OS=Arabidopsis_thaliana_GN=NRT2.5_PE=2_SV=1	7.00E-70	GO:0005886,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0042128,GO:0055085	plasma membrane,membrane,membrane,integral component of membrane,integral component of membrane,nitrate assimilation,transmembrane transport
comp31198_c0_seq3.p1	sp|P22152|CRNA_EMENI_Nitrate_transporter_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=crnA_PE=2_SV=2	4.00E-22	GO:0003674,GO:0005215,GO:0006810,GO:0006810,GO:0015112,GO:0015112,GO:0015112,GO:0015112,GO:0015112,GO:0015112,GO:0015113,GO:0015513,GO:0015706,GO:0015706,GO:0015706,GO:0015706,GO:0015706,GO:0015706,GO:0015706,GO:0015707,GO:0015707,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0022832,GO:0042128,GO:0051049,GO:0055085	molecular_function,transporter activity,transport,transport,nitrate transmembrane transporter activity,nitrate transmembrane transporter activity,nitrate transmembrane transporter activity,nitrate transmembrane transporter activity,nitrate transmembrane transporter activity,nitrate transmembrane transporter activity,nitrite transmembrane transporter activity,nitrite uptake transmembrane transporter activity,nitrate transport,nitrate transport,nitrate transport,nitrate transport,nitrate transport,nitrate transport,nitrate transport,nitrite transport,nitrite transport,membrane,membrane,integral component of membrane,integral component of membrane,voltage-gated channel activity,nitrate assimilation,regulation of transport,transmembrane transport
comp31198_c0_seq4.p1	sp|Q9LPV5|NRT25_ARATH_High_affinity_nitrate_transporter_2.5_OS=Arabidopsis_thaliana_GN=NRT2.5_PE=2_SV=1	2.00E-59	GO:0005886,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0042128,GO:0055085	plasma membrane,membrane,membrane,integral component of membrane,integral component of membrane,nitrate assimilation,transmembrane transport
comp31200_c0_seq1.p1				
comp31201_c0_seq1.p2				
comp31202_c0_seq2.p2				
comp31202_c0_seq3.p1				
comp31202_c0_seq6.p2				
comp31202_c1_seq2.p1				
comp31202_c1_seq3.p1				
comp31202_c1_seq5.p1				
comp31203_c0_seq2.p1	sp|P02576|ACTA_PHYPO_Actin,_plasmodial_isoform_OS=Physarum_polycephalum_GN=ARDA_PE=1_SV=2	6.00E-142	GO:0000166,GO:0005524,GO:0005737,GO:0005856,GO:0005856	nucleotide binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton
comp31203_c0_seq3.p1	sp|P18603|ACT4_ARTSX_Actin,_clone_403_OS=Artemia_sp._PE=2_SV=1	1.00E-133	GO:0000166,GO:0005524,GO:0005737,GO:0005856,GO:0005856	nucleotide binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton
comp31203_c0_seq4.p1	sp|P18603|ACT4_ARTSX_Actin,_clone_403_OS=Artemia_sp._PE=2_SV=1	2.00E-144	GO:0000166,GO:0005524,GO:0005737,GO:0005856,GO:0005856	nucleotide binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton
comp31204_c0_seq3.p1				
comp31204_c0_seq4.p1				
comp31204_c0_seq5.p1				
comp31205_c1_seq1.p1				
comp31205_c1_seq1.p2				
comp31205_c1_seq4.p1				
comp31206_c0_seq1.p1				
comp31207_c0_seq3.p1	sp|Q5QQ50|XYLT2_CANFA_Xylosyltransferase_2_OS=Canis_familiaris_GN=XYLT2_PE=2_SV=1	3.00E-18	GO:0000139,GO:0005783,GO:0005789,GO:0005794,GO:0006024,GO:0006024,GO:0008375,GO:0015012,GO:0016020,GO:0016020,GO:0016021,GO:0016740,GO:0016757,GO:0030158,GO:0030158,GO:0030166,GO:0030206,GO:0030210	Golgi membrane,endoplasmic reticulum,endoplasmic reticulum membrane,Golgi apparatus,glycosaminoglycan biosynthetic process,glycosaminoglycan biosynthetic process,acetylglucosaminyltransferase activity,heparan sulfate proteoglycan biosynthetic process,membrane,membrane,integral component of membrane,transferase activity,transferase activity, transferring glycosyl groups,protein xylosyltransferase activity,protein xylosyltransferase activity,proteoglycan biosynthetic process,chondroitin sulfate biosynthetic process,heparin biosynthetic process
comp31207_c0_seq3.p2	sp|P50872|TRPE_AZOBR_Anthranilate_synthase_OS=Azospirillum_brasilense_GN=trpE(G)_PE=4_SV=1	2.00E-125	GO:0000162,GO:0000162,GO:0000162,GO:0004049,GO:0004049,GO:0006541,GO:0008152,GO:0008652,GO:0009058,GO:0009073,GO:0016829,GO:0016833	tryptophan biosynthetic process,tryptophan biosynthetic process,tryptophan biosynthetic process,anthranilate synthase activity,anthranilate synthase activity,glutamine metabolic process,metabolic process,cellular amino acid biosynthetic process,biosynthetic process,aromatic amino acid family biosynthetic process,lyase activity,oxo-acid-lyase activity
comp31207_c0_seq5.p1	sp|P15395|TRPE_RHIME_Anthranilate_synthase_OS=Rhizobium_meliloti_(strain_1021)_GN=trpE(G)_PE=4_SV=1	4.00E-109	GO:0000162,GO:0000162,GO:0000162,GO:0004049,GO:0004049,GO:0006541,GO:0008152,GO:0008652,GO:0009058,GO:0009073,GO:0016829,GO:0016833	tryptophan biosynthetic process,tryptophan biosynthetic process,tryptophan biosynthetic process,anthranilate synthase activity,anthranilate synthase activity,glutamine metabolic process,metabolic process,cellular amino acid biosynthetic process,biosynthetic process,aromatic amino acid family biosynthetic process,lyase activity,oxo-acid-lyase activity
comp31207_c0_seq6.p1				
comp31208_c0_seq3.p1	sp|O48709|PI5K3_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_3_OS=Arabidopsis_thaliana_GN=PIP5K3_PE=2_SV=1	4.00E-25	GO:0000166,GO:0005524,GO:0005524,GO:0005737,GO:0005886,GO:0016301,GO:0016307,GO:0016308,GO:0016308,GO:0016308,GO:0016310,GO:0016324,GO:0016740,GO:0046488,GO:0046854,GO:0046854,GO:0046854,GO:0046854,GO:0048765,GO:0048767,GO:0048767,GO:0048768	nucleotide binding,ATP binding,ATP binding,cytoplasm,plasma membrane,kinase activity,phosphatidylinositol phosphate kinase activity,1-phosphatidylinositol-4-phosphate 5-kinase activity,1-phosphatidylinositol-4-phosphate 5-kinase activity,1-phosphatidylinositol-4-phosphate 5-kinase activity,phosphorylation,apical plasma membrane,transferase activity,phosphatidylinositol metabolic process,phosphatidylinositol phosphorylation,phosphatidylinositol phosphorylation,phosphatidylinositol phosphorylation,phosphatidylinositol phosphorylation,root hair cell differentiation,root hair elongation,root hair elongation,root hair cell tip growth
comp31209_c1_seq1.p1				
comp31209_c2_seq11.p1				
comp31209_c2_seq3.p1	sp|Q9BV94|EDEM2_HUMAN_ER_degradation-enhancing_alpha-mannosidase-like_2_OS=Homo_sapiens_GN=EDEM2_PE=1_SV=2	5.00E-74	GO:0005509,GO:0005576,GO:0005576,GO:0005783,GO:0005788,GO:0005789,GO:0006457,GO:0006986,GO:0016020,GO:0018279,GO:0043687,GO:0044267,GO:0004571	calcium ion binding,extracellular region,extracellular region,endoplasmic reticulum,endoplasmic reticulum lumen,endoplasmic reticulum membrane,protein folding,response to unfolded protein,membrane,protein N-linked glycosylation via asparagine,post-translational protein modification,cellular protein metabolic process,mannosyl-oligosaccharide 1,2-alpha-mannosidase activity
comp31209_c2_seq4.p1	sp|Q2HXL6|EDEM3_MOUSE_ER_degradation-enhancing_alpha-mannosidase-like_3_OS=Mus_musculus_GN=Edem3_PE=1_SV=2	7.00E-31	GO:0004569,GO:0004571,GO:0004571,GO:0005509,GO:0005783,GO:0005788,GO:0005788,GO:0006516,GO:0006986,GO:0016020,GO:0016787,GO:0043161	glycoprotein endo-alpha-1,2-mannosidase activity,mannosyl-oligosaccharide 1,2-alpha-mannosidase activity,mannosyl-oligosaccharide 1,2-alpha-mannosidase activity,calcium ion binding,endoplasmic reticulum,endoplasmic reticulum lumen,endoplasmic reticulum lumen,glycoprotein catabolic process,response to unfolded protein,membrane,hydrolase activity,proteasome-mediated ubiquitin-dependent protein catabolic process
comp31209_c2_seq6.p1	sp|Q9BV94|EDEM2_HUMAN_ER_degradation-enhancing_alpha-mannosidase-like_2_OS=Homo_sapiens_GN=EDEM2_PE=1_SV=2	5.00E-36	GO:0005509,GO:0005576,GO:0005576,GO:0005783,GO:0005788,GO:0005789,GO:0006457,GO:0006986,GO:0016020,GO:0018279,GO:0043687,GO:0044267,GO:0004571	calcium ion binding,extracellular region,extracellular region,endoplasmic reticulum,endoplasmic reticulum lumen,endoplasmic reticulum membrane,protein folding,response to unfolded protein,membrane,protein N-linked glycosylation via asparagine,post-translational protein modification,cellular protein metabolic process,mannosyl-oligosaccharide 1,2-alpha-mannosidase activity
comp31209_c2_seq7.p1	sp|Q9ZU38|RPIA_ARATH_Probable_ribose-5-phosphate_isomerase_OS=Arabidopsis_thaliana_GN=At2g01290_PE=2_SV=1	4.00E-80	GO:0004751,GO:0004751,GO:0004751,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006098,GO:0008219,GO:0009052,GO:0010228,GO:0016853	ribose-5-phosphate isomerase activity,ribose-5-phosphate isomerase activity,ribose-5-phosphate isomerase activity,cytoplasm,cytoplasm,cytoplasm,cytoplasm,pentose-phosphate shunt,cell death,pentose-phosphate shunt, non-oxidative branch,vegetative to reproductive phase transition of meristem,isomerase activity
comp31211_c0_seq2.p1	sp|Q2UEA0|NUF2_ASPOR_Probable_kinetochore_protein_nuf2_OS=Aspergillus_oryzae_(strain_ATCC_42149_/_RIB_40)_GN=nuf2_PE=3_SV=1	4.00E-25	GO:0000775,GO:0000775,GO:0000776,GO:0000777,GO:0005634,GO:0005634,GO:0005694,GO:0007049,GO:0007067,GO:0007067,GO:0051301	chromosome, centromeric region,chromosome, centromeric region,kinetochore,condensed chromosome kinetochore,nucleus,nucleus,chromosome,cell cycle,mitotic nuclear division,mitotic nuclear division,cell division
comp31211_c0_seq2.p3	sp|P40112|PSB3_RAT_Proteasome_subunit_beta_type-3_OS=Rattus_norvegicus_GN=Psmb3_PE=1_SV=1	4.00E-35	GO:0000502,GO:0004175,GO:0004298,GO:0004298,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005839,GO:0005839,GO:0006508,GO:0008233,GO:0016787,GO:0051603	proteasome complex,endopeptidase activity,threonine-type endopeptidase activity,threonine-type endopeptidase activity,nucleus,nucleus,cytoplasm,cytoplasm,proteasome core complex,proteasome core complex,proteolysis,peptidase activity,hydrolase activity,proteolysis involved in cellular protein catabolic process
comp31211_c0_seq5.p1	sp|Q7S9H0|NUF2_NEUCR_Probable_kinetochore_protein_nuf-2_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=nuf-2_PE=3_SV=1	9.00E-20	GO:0000775,GO:0000775,GO:0000776,GO:0000777,GO:0005634,GO:0005634,GO:0005694,GO:0007049,GO:0007067,GO:0007067,GO:0051301	chromosome, centromeric region,chromosome, centromeric region,kinetochore,condensed chromosome kinetochore,nucleus,nucleus,chromosome,cell cycle,mitotic nuclear division,mitotic nuclear division,cell division
comp31211_c0_seq7.p1	sp|Q2UEA0|NUF2_ASPOR_Probable_kinetochore_protein_nuf2_OS=Aspergillus_oryzae_(strain_ATCC_42149_/_RIB_40)_GN=nuf2_PE=3_SV=1	4.00E-25	GO:0000775,GO:0000775,GO:0000776,GO:0000777,GO:0005634,GO:0005634,GO:0005694,GO:0007049,GO:0007067,GO:0007067,GO:0051301	chromosome, centromeric region,chromosome, centromeric region,kinetochore,condensed chromosome kinetochore,nucleus,nucleus,chromosome,cell cycle,mitotic nuclear division,mitotic nuclear division,cell division
comp31211_c0_seq9.p1				
comp31212_c0_seq1.p1				
comp31212_c0_seq1.p5				
comp31212_c0_seq2.p1	sp|Q9IA79|BI1_PAROL_Probable_Bax_inhibitor_1_OS=Paralichthys_olivaceus_GN=tmbim6_PE=2_SV=1	8.00E-41	GO:0005783,GO:0005789,GO:0006915,GO:0006986,GO:0016020,GO:0016021,GO:0016021,GO:0043066	endoplasmic reticulum,endoplasmic reticulum membrane,apoptotic process,response to unfolded protein,membrane,integral component of membrane,integral component of membrane,negative regulation of apoptotic process
comp31212_c0_seq3.p1				
comp31212_c0_seq4.p1				
comp31213_c0_seq2.p1	sp|Q54X82|AP1B_DICDI_AP-1_complex_subunit_beta_OS=Dictyostelium_discoideum_GN=ap1b1_PE=3_SV=1	4.00E-20	GO:0000281,GO:0005515,GO:0005515,GO:0005515,GO:0005794,GO:0005794,GO:0006810,GO:0006886,GO:0006971,GO:0008565,GO:0015031,GO:0015031,GO:0016020,GO:0016192,GO:0030117,GO:0030121,GO:0030122,GO:0030122,GO:0030131,GO:0030132,GO:0030665,GO:0031152,GO:0031410,GO:0033298,GO:0044351	mitotic cytokinesis,protein binding,protein binding,protein binding,Golgi apparatus,Golgi apparatus,transport,intracellular protein transport,hypotonic response,protein transporter activity,protein transport,protein transport,membrane,vesicle-mediated transport,membrane coat,AP-1 adaptor complex,AP-2 adaptor complex,AP-2 adaptor complex,clathrin adaptor complex,clathrin coat of coated pit,clathrin-coated vesicle membrane,aggregation involved in sorocarp development,cytoplasmic vesicle,contractile vacuole organization,macropinocytosis
comp31213_c0_seq4.p1	sp|Q9FNI6|SM3L2_ARATH_Putative_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A_member_3-like_2_OS=Arabidopsis_thaliana_GN=At5g22750_PE=2_SV=1	4.00E-67	GO:0000166,GO:0000724,GO:0000724,GO:0003676,GO:0003677,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006261,GO:0006281,GO:0006974,GO:0008270,GO:0009294,GO:0016568,GO:0016787,GO:0016818,GO:0045003,GO:0046872,GO:0046872	nucleotide binding,double-strand break repair via homologous recombination,double-strand break repair via homologous recombination,nucleic acid binding,DNA binding,helicase activity,ATP binding,ATP binding,nucleus,nucleus,DNA-dependent DNA replication,DNA repair,cellular response to DNA damage stimulus,zinc ion binding,DNA mediated transformation,chromatin modification,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,double-strand break repair via synthesis-dependent strand annealing,metal ion binding,metal ion binding
comp31213_c0_seq4.p2	sp|Q9LDK9|APBLA_ARATH_Beta-adaptin-like_protein_A_OS=Arabidopsis_thaliana_GN=BETAA-AD_PE=1_SV=1	3.00E-157	GO:0005794,GO:0005794,GO:0006810,GO:0006886,GO:0008565,GO:0015031,GO:0015031,GO:0016020,GO:0016192,GO:0030117,GO:0030131,GO:0030665,GO:0031410,GO:0043424	Golgi apparatus,Golgi apparatus,transport,intracellular protein transport,protein transporter activity,protein transport,protein transport,membrane,vesicle-mediated transport,membrane coat,clathrin adaptor complex,clathrin-coated vesicle membrane,cytoplasmic vesicle,protein histidine kinase binding
comp31213_c0_seq4.p3				
comp31214_c1_seq1.p1	sp|Q9XYL0|CTDS_DICDI_Probable_C-terminal_domain_small_phosphatase_OS=Dictyostelium_discoideum_GN=fcpA_PE=3_SV=1	3.00E-29	GO:0003674,GO:0004721,GO:0004721,GO:0005575,GO:0005634,GO:0005634,GO:0006972,GO:0008152,GO:0016311,GO:0016311,GO:0016311,GO:0016787,GO:0016791,GO:0044351,GO:0046872	molecular_function,phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,cellular_component,nucleus,nucleus,hyperosmotic response,metabolic process,dephosphorylation,dephosphorylation,dephosphorylation,hydrolase activity,phosphatase activity,macropinocytosis,metal ion binding
comp31215_c0_seq2.p1				
comp31215_c0_seq2.p6				
comp31215_c0_seq4.p1				
comp31215_c0_seq4.p2				
comp31216_c1_seq1.p1				
comp31216_c1_seq4.p1	sp|Q96V64|EXG_BLUGR_Glucan_1,3-beta-glucosidase_OS=Blumeria_graminis_PE=3_SV=1	2.00E-55	GO:0004338,GO:0004553,GO:0005576,GO:0005576,GO:0005975,GO:0008152,GO:0016787,GO:0016798,GO:0071555	glucan exo-1,3-beta-glucosidase activity,hydrolase activity, hydrolyzing O-glycosyl compounds,extracellular region,extracellular region,carbohydrate metabolic process,metabolic process,hydrolase activity,hydrolase activity, acting on glycosyl bonds,cell wall organization
comp31218_c0_seq5.p1				
comp31218_c0_seq9.p1				
comp31219_c1_seq1.p1				
comp31219_c2_seq1.p1	sp|Q640S2|CRBN_XENTR_Protein_cereblon_OS=Xenopus_tropicalis_GN=crbn_PE=2_SV=1	5.00E-26	GO:0004176,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0006200,GO:0006508,GO:0016567,GO:0016567,GO:0031464,GO:0043161	ATP-dependent peptidase activity,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,ATP catabolic process,proteolysis,protein ubiquitination,protein ubiquitination,Cul4A-RING E3 ubiquitin ligase complex,proteasome-mediated ubiquitin-dependent protein catabolic process
comp31219_c2_seq2.p1				
comp31220_c0_seq2.p1				
comp31220_c0_seq4.p1	sp|P49852|HMP_BACSU_Flavohemoprotein_OS=Bacillus_subtilis_GN=hmp_PE=2_SV=1	8.00E-11	GO:0005344,GO:0005344,GO:0005506,GO:0006810,GO:0008941,GO:0008941,GO:0008941,GO:0009636,GO:0015671,GO:0015671,GO:0015671,GO:0016491,GO:0016491,GO:0019825,GO:0020037,GO:0046872,GO:0051409,GO:0055114,GO:0055114,GO:0071949	oxygen transporter activity,oxygen transporter activity,iron ion binding,transport,nitric oxide dioxygenase activity,nitric oxide dioxygenase activity,nitric oxide dioxygenase activity,response to toxic substance,oxygen transport,oxygen transport,oxygen transport,oxidoreductase activity,oxidoreductase activity,oxygen binding,heme binding,metal ion binding,response to nitrosative stress,oxidation-reduction process,oxidation-reduction process,FAD binding
comp31221_c0_seq2.p1	sp|Q3EAQ5|PTR36_ARATH_Probable_peptide/nitrate_transporter_At3g43790_OS=Arabidopsis_thaliana_GN=ZIFL2_PE=2_SV=2	1.00E-22	GO:0006810,GO:0009624,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0055085	transport,response to nematode,membrane,membrane,integral component of membrane,integral component of membrane,transmembrane transport
comp31221_c0_seq2.p3				
comp31221_c0_seq4.p1	sp|Q8RWN2|ZIF1_ARATH_Protein_ZINC_INDUCED_FACILITATOR_1_OS=Arabidopsis_thaliana_GN=ZIF1_PE=1_SV=2	9.00E-13	GO:0005215,GO:0005773,GO:0005774,GO:0005886,GO:0006810,GO:0009624,GO:0009705,GO:0010043,GO:0016020,GO:0016021,GO:0016021,GO:0055069,GO:0055085	transporter activity,vacuole,vacuolar membrane,plasma membrane,transport,response to nematode,plant-type vacuole membrane,response to zinc ion,membrane,integral component of membrane,integral component of membrane,zinc ion homeostasis,transmembrane transport
comp31221_c0_seq4.p2	sp|Q3EAQ5|PTR36_ARATH_Probable_peptide/nitrate_transporter_At3g43790_OS=Arabidopsis_thaliana_GN=ZIFL2_PE=2_SV=2	1.00E-24	GO:0006810,GO:0009624,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0055085	transport,response to nematode,membrane,membrane,integral component of membrane,integral component of membrane,transmembrane transport
comp31221_c0_seq4.p4				
comp31222_c0_seq2.p1				
comp31222_c0_seq2.p2				
comp31222_c0_seq4.p1				
comp31222_c0_seq4.p2				
comp31222_c0_seq7.p1				
comp31222_c0_seq7.p2				
comp31223_c0_seq1.p1				
comp31223_c1_seq1.p1				
comp31224_c0_seq1.p2				
comp31224_c0_seq2.p1				
comp31224_c0_seq21.p1				
comp31224_c0_seq4.p1				
comp31225_c0_seq1.p1	sp|Q9FNU2|AB25B_ORYSJ_ABC_transporter_B_family_member_25_OS=Oryza_sativa_subsp._japonica_GN=OsABCB25_PE=2_SV=1	2.00E-120	GO:0000166,GO:0000166,GO:0000325,GO:0005215,GO:0005524,GO:0005524,GO:0005524,GO:0005773,GO:0005773,GO:0005774,GO:0005774,GO:0006200,GO:0006200,GO:0006810,GO:0006810,GO:0006810,GO:0008152,GO:0010044,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016021,GO:0016887,GO:0016887,GO:0017111,GO:0042626,GO:0042626,GO:0042626,GO:0055085,GO:0055085,GO:0055085	nucleotide binding,nucleotide binding,plant-type vacuole,transporter activity,ATP binding,ATP binding,ATP binding,vacuole,vacuole,vacuolar membrane,vacuolar membrane,ATP catabolic process,ATP catabolic process,transport,transport,transport,metabolic process,response to aluminum ion,membrane,membrane,integral component of membrane,integral component of membrane,integral component of membrane,integral component of membrane,ATPase activity,ATPase activity,nucleoside-triphosphatase activity,ATPase activity, coupled to transmembrane movement of substances,ATPase activity, coupled to transmembrane movement of substances,ATPase activity, coupled to transmembrane movement of substances,transmembrane transport,transmembrane transport,transmembrane transport
comp31226_c1_seq4.p1				
comp31226_c1_seq9.p1				
comp31227_c0_seq2.p1				
comp31228_c0_seq1.p1	sp|Q3EDF8|PPR28_ARATH_Pentatricopeptide_repeat-containing_protein_At1g09900_OS=Arabidopsis_thaliana_GN=At1g09900_PE=2_SV=1	4.00E-35	GO:0003674,GO:0016020	molecular_function,membrane
comp31229_c0_seq1.p1	sp|Q9C0C7|AMRA1_HUMAN_Activating_molecule_in_BECN1-regulated_autophagy_protein_1_OS=Homo_sapiens_GN=AMBRA1_PE=1_SV=2	3.00E-22	GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005776,GO:0005829,GO:0005930,GO:0005930,GO:0006914,GO:0006914,GO:0006914,GO:0007275,GO:0007399,GO:0008285,GO:0021915,GO:0030154,GO:0031410,GO:0031625,GO:0043231,GO:0043524,GO:0043552,GO:0045335,GO:1903599,GO:1903599,GO:1903599,GO:1903599,GO:1903599,GO:2000785,GO:0005739,GO:0005739	protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,cytoplasm,autophagic vacuole,cytosol,axoneme,axoneme,autophagy,autophagy,autophagy,multicellular organismal development,nervous system development,negative regulation of cell proliferation,neural tube development,cell differentiation,cytoplasmic vesicle,ubiquitin protein ligase binding,intracellular membrane-bounded organelle,negative regulation of neuron apoptotic process,positive regulation of phosphatidylinositol 3-kinase activity,phagocytic vesicle,positive regulation of mitochondrion degradation,positive regulation of mitochondrion degradation,positive regulation of mitochondrion degradation,positive regulation of mitochondrion degradation,positive regulation of mitochondrion degradation,regulation of autophagic vacuole assembly,mitochondrion,mitochondrion
comp31229_c0_seq8.p1	sp|P97779|HMMR_RAT_Hyaluronan-mediated_motility_receptor_OS=Rattus_norvegicus_GN=Hmmr_PE=2_SV=1	7.00E-11	GO:0005540,GO:0005540,GO:0005540,GO:0005737,GO:0005737,GO:0007010,GO:0007267,GO:0009986	hyaluronic acid binding,hyaluronic acid binding,hyaluronic acid binding,cytoplasm,cytoplasm,cytoskeleton organization,cell-cell signaling,cell surface
comp31229_c1_seq3.p1				
comp3123_c0_seq1.p1	sp|P08331|CPDB_ECOLI_2',3'-cyclic-nucleotide_2'-phosphodiesterase/3'-nucleotidase_OS=Escherichia_coli_(strain_K12)_GN=cpdB_PE=1_SV=2	4.00E-77	GO:0000166,GO:0000166,GO:0003824,GO:0006974,GO:0008152,GO:0008254,GO:0008254,GO:0008254,GO:0008663,GO:0008663,GO:0008663,GO:0008663,GO:0009117,GO:0009166,GO:0009166,GO:0016311,GO:0016311,GO:0016787,GO:0016787,GO:0016788,GO:0042597,GO:0042597,GO:0042597,GO:0046872,GO:0046872	nucleotide binding,nucleotide binding,catalytic activity,cellular response to DNA damage stimulus,metabolic process,3'-nucleotidase activity,3'-nucleotidase activity,3'-nucleotidase activity,2',3'-cyclic-nucleotide 2'-phosphodiesterase activity,2',3'-cyclic-nucleotide 2'-phosphodiesterase activity,2',3'-cyclic-nucleotide 2'-phosphodiesterase activity,2',3'-cyclic-nucleotide 2'-phosphodiesterase activity,nucleotide metabolic process,nucleotide catabolic process,nucleotide catabolic process,dephosphorylation,dephosphorylation,hydrolase activity,hydrolase activity,hydrolase activity, acting on ester bonds,periplasmic space,periplasmic space,periplasmic space,metal ion binding,metal ion binding
comp31230_c0_seq1.p2				
comp31230_c0_seq2.p2				
comp31230_c0_seq3.p1				
comp31231_c0_seq1.p1	sp|Q54ZR7|SRPR_DICDI_Signal_recognition_particle_receptor_subunit_alpha_OS=Dictyostelium_discoideum_GN=srpr_PE=3_SV=1	4.00E-126	GO:0000166,GO:0003924,GO:0005047,GO:0005047,GO:0005047,GO:0005525,GO:0005525,GO:0005783,GO:0005785,GO:0005789,GO:0005789,GO:0006184,GO:0006614,GO:0006810,GO:0006886,GO:0016020,GO:0044351,GO:0045047	nucleotide binding,GTPase activity,signal recognition particle binding,signal recognition particle binding,signal recognition particle binding,GTP binding,GTP binding,endoplasmic reticulum,signal recognition particle receptor complex,endoplasmic reticulum membrane,endoplasmic reticulum membrane,GTP catabolic process,SRP-dependent cotranslational protein targeting to membrane,transport,intracellular protein transport,membrane,macropinocytosis,protein targeting to ER
comp31231_c0_seq1.p2	sp|Q99383|HRP1_YEAST_Nuclear_polyadenylated_RNA-binding_protein_4_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=HRP1_PE=1_SV=1	1.00E-41	GO:0000166,GO:0000184,GO:0003676,GO:0003723,GO:0003723,GO:0003729,GO:0003729,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005849,GO:0006378,GO:0006378,GO:0006379,GO:0006397,GO:0010494,GO:0072423	nucleotide binding,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nucleic acid binding,RNA binding,RNA binding,mRNA binding,mRNA binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,mRNA cleavage factor complex,mRNA polyadenylation,mRNA polyadenylation,mRNA cleavage,mRNA processing,cytoplasmic stress granule,response to DNA damage checkpoint signaling
comp31231_c0_seq3.p1	sp|Q54ZR7|SRPR_DICDI_Signal_recognition_particle_receptor_subunit_alpha_OS=Dictyostelium_discoideum_GN=srpr_PE=3_SV=1	4.00E-126	GO:0000166,GO:0003924,GO:0005047,GO:0005047,GO:0005047,GO:0005525,GO:0005525,GO:0005783,GO:0005785,GO:0005789,GO:0005789,GO:0006184,GO:0006614,GO:0006810,GO:0006886,GO:0016020,GO:0044351,GO:0045047	nucleotide binding,GTPase activity,signal recognition particle binding,signal recognition particle binding,signal recognition particle binding,GTP binding,GTP binding,endoplasmic reticulum,signal recognition particle receptor complex,endoplasmic reticulum membrane,endoplasmic reticulum membrane,GTP catabolic process,SRP-dependent cotranslational protein targeting to membrane,transport,intracellular protein transport,membrane,macropinocytosis,protein targeting to ER
comp31231_c0_seq3.p2	sp|Q99383|HRP1_YEAST_Nuclear_polyadenylated_RNA-binding_protein_4_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=HRP1_PE=1_SV=1	1.00E-42	GO:0000166,GO:0000184,GO:0003676,GO:0003723,GO:0003723,GO:0003729,GO:0003729,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005849,GO:0006378,GO:0006378,GO:0006379,GO:0006397,GO:0010494,GO:0072423	nucleotide binding,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nucleic acid binding,RNA binding,RNA binding,mRNA binding,mRNA binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,mRNA cleavage factor complex,mRNA polyadenylation,mRNA polyadenylation,mRNA cleavage,mRNA processing,cytoplasmic stress granule,response to DNA damage checkpoint signaling
comp31231_c0_seq5.p1	sp|Q54ZR7|SRPR_DICDI_Signal_recognition_particle_receptor_subunit_alpha_OS=Dictyostelium_discoideum_GN=srpr_PE=3_SV=1	4.00E-126	GO:0000166,GO:0003924,GO:0005047,GO:0005047,GO:0005047,GO:0005525,GO:0005525,GO:0005783,GO:0005785,GO:0005789,GO:0005789,GO:0006184,GO:0006614,GO:0006810,GO:0006886,GO:0016020,GO:0044351,GO:0045047	nucleotide binding,GTPase activity,signal recognition particle binding,signal recognition particle binding,signal recognition particle binding,GTP binding,GTP binding,endoplasmic reticulum,signal recognition particle receptor complex,endoplasmic reticulum membrane,endoplasmic reticulum membrane,GTP catabolic process,SRP-dependent cotranslational protein targeting to membrane,transport,intracellular protein transport,membrane,macropinocytosis,protein targeting to ER
comp31231_c0_seq5.p2	sp|Q99383|HRP1_YEAST_Nuclear_polyadenylated_RNA-binding_protein_4_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=HRP1_PE=1_SV=1	3.00E-42	GO:0000166,GO:0000184,GO:0003676,GO:0003723,GO:0003723,GO:0003729,GO:0003729,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005849,GO:0006378,GO:0006378,GO:0006379,GO:0006397,GO:0010494,GO:0072423	nucleotide binding,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nucleic acid binding,RNA binding,RNA binding,mRNA binding,mRNA binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,mRNA cleavage factor complex,mRNA polyadenylation,mRNA polyadenylation,mRNA cleavage,mRNA processing,cytoplasmic stress granule,response to DNA damage checkpoint signaling
comp31231_c0_seq7.p1	sp|Q54ZR7|SRPR_DICDI_Signal_recognition_particle_receptor_subunit_alpha_OS=Dictyostelium_discoideum_GN=srpr_PE=3_SV=1	4.00E-126	GO:0000166,GO:0003924,GO:0005047,GO:0005047,GO:0005047,GO:0005525,GO:0005525,GO:0005783,GO:0005785,GO:0005789,GO:0005789,GO:0006184,GO:0006614,GO:0006810,GO:0006886,GO:0016020,GO:0044351,GO:0045047	nucleotide binding,GTPase activity,signal recognition particle binding,signal recognition particle binding,signal recognition particle binding,GTP binding,GTP binding,endoplasmic reticulum,signal recognition particle receptor complex,endoplasmic reticulum membrane,endoplasmic reticulum membrane,GTP catabolic process,SRP-dependent cotranslational protein targeting to membrane,transport,intracellular protein transport,membrane,macropinocytosis,protein targeting to ER
comp31231_c0_seq7.p2	sp|Q99383|HRP1_YEAST_Nuclear_polyadenylated_RNA-binding_protein_4_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=HRP1_PE=1_SV=1	2.00E-42	GO:0000166,GO:0000184,GO:0003676,GO:0003723,GO:0003723,GO:0003729,GO:0003729,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005849,GO:0006378,GO:0006378,GO:0006379,GO:0006397,GO:0010494,GO:0072423	nucleotide binding,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nucleic acid binding,RNA binding,RNA binding,mRNA binding,mRNA binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,mRNA cleavage factor complex,mRNA polyadenylation,mRNA polyadenylation,mRNA cleavage,mRNA processing,cytoplasmic stress granule,response to DNA damage checkpoint signaling
comp31231_c0_seq8.p1	sp|Q54ZR7|SRPR_DICDI_Signal_recognition_particle_receptor_subunit_alpha_OS=Dictyostelium_discoideum_GN=srpr_PE=3_SV=1	4.00E-126	GO:0000166,GO:0003924,GO:0005047,GO:0005047,GO:0005047,GO:0005525,GO:0005525,GO:0005783,GO:0005785,GO:0005789,GO:0005789,GO:0006184,GO:0006614,GO:0006810,GO:0006886,GO:0016020,GO:0044351,GO:0045047	nucleotide binding,GTPase activity,signal recognition particle binding,signal recognition particle binding,signal recognition particle binding,GTP binding,GTP binding,endoplasmic reticulum,signal recognition particle receptor complex,endoplasmic reticulum membrane,endoplasmic reticulum membrane,GTP catabolic process,SRP-dependent cotranslational protein targeting to membrane,transport,intracellular protein transport,membrane,macropinocytosis,protein targeting to ER
comp31231_c0_seq8.p2	sp|Q99383|HRP1_YEAST_Nuclear_polyadenylated_RNA-binding_protein_4_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=HRP1_PE=1_SV=1	1.00E-41	GO:0000166,GO:0000184,GO:0003676,GO:0003723,GO:0003723,GO:0003729,GO:0003729,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005849,GO:0006378,GO:0006378,GO:0006379,GO:0006397,GO:0010494,GO:0072423	nucleotide binding,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nucleic acid binding,RNA binding,RNA binding,mRNA binding,mRNA binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,mRNA cleavage factor complex,mRNA polyadenylation,mRNA polyadenylation,mRNA cleavage,mRNA processing,cytoplasmic stress granule,response to DNA damage checkpoint signaling
comp31231_c0_seq9.p1	sp|Q54ZR7|SRPR_DICDI_Signal_recognition_particle_receptor_subunit_alpha_OS=Dictyostelium_discoideum_GN=srpr_PE=3_SV=1	4.00E-126	GO:0000166,GO:0003924,GO:0005047,GO:0005047,GO:0005047,GO:0005525,GO:0005525,GO:0005783,GO:0005785,GO:0005789,GO:0005789,GO:0006184,GO:0006614,GO:0006810,GO:0006886,GO:0016020,GO:0044351,GO:0045047	nucleotide binding,GTPase activity,signal recognition particle binding,signal recognition particle binding,signal recognition particle binding,GTP binding,GTP binding,endoplasmic reticulum,signal recognition particle receptor complex,endoplasmic reticulum membrane,endoplasmic reticulum membrane,GTP catabolic process,SRP-dependent cotranslational protein targeting to membrane,transport,intracellular protein transport,membrane,macropinocytosis,protein targeting to ER
comp31231_c0_seq9.p2	sp|Q99383|HRP1_YEAST_Nuclear_polyadenylated_RNA-binding_protein_4_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=HRP1_PE=1_SV=1	8.00E-42	GO:0000166,GO:0000184,GO:0003676,GO:0003723,GO:0003723,GO:0003729,GO:0003729,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005849,GO:0006378,GO:0006378,GO:0006379,GO:0006397,GO:0010494,GO:0072423	nucleotide binding,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nucleic acid binding,RNA binding,RNA binding,mRNA binding,mRNA binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,mRNA cleavage factor complex,mRNA polyadenylation,mRNA polyadenylation,mRNA cleavage,mRNA processing,cytoplasmic stress granule,response to DNA damage checkpoint signaling
comp31232_c0_seq4.p1				
comp31233_c0_seq2.p1				
comp31233_c0_seq4.p1	sp|Q16720|AT2B3_HUMAN_Plasma_membrane_calcium-transporting_ATPase_3_OS=Homo_sapiens_GN=ATP2B3_PE=1_SV=3	0	GO:0000166,GO:0000166,GO:0005388,GO:0005388,GO:0005388,GO:0005516,GO:0005524,GO:0005524,GO:0005794,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006810,GO:0006811,GO:0006812,GO:0006816,GO:0007596,GO:0008152,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016787,GO:0019829,GO:0031982,GO:0034220,GO:0034220,GO:0046872,GO:0046872,GO:0055085,GO:0070588	nucleotide binding,nucleotide binding,calcium-transporting ATPase activity,calcium-transporting ATPase activity,calcium-transporting ATPase activity,calmodulin binding,ATP binding,ATP binding,Golgi apparatus,plasma membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,transport,transport,ion transport,cation transport,calcium ion transport,blood coagulation,metabolic process,membrane,membrane,integral component of membrane,integral component of membrane,hydrolase activity,cation-transporting ATPase activity,vesicle,ion transmembrane transport,ion transmembrane transport,metal ion binding,metal ion binding,transmembrane transport,calcium ion transmembrane transport
comp31233_c0_seq4.p2	sp|Q8GUI6|JMJ14_ARATH_Probable_lysine-specific_demethylase_JMJ14_OS=Arabidopsis_thaliana_GN=JMJ14_PE=1_SV=1	5.00E-81	GO:0003700,GO:0005634,GO:0005634,GO:0005654,GO:0006351,GO:0006355,GO:0006355,GO:0006355,GO:0009910,GO:0010216,GO:0016491,GO:0016568,GO:0032453,GO:0032453,GO:0034720,GO:0043687,GO:0045893,GO:0046872,GO:0048573,GO:0051213,GO:0055114	sequence-specific DNA binding transcription factor activity,nucleus,nucleus,nucleoplasm,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,negative regulation of flower development,maintenance of DNA methylation,oxidoreductase activity,chromatin modification,histone demethylase activity (H3-K4 specific),histone demethylase activity (H3-K4 specific),histone H3-K4 demethylation,post-translational protein modification,positive regulation of transcription, DNA-templated,metal ion binding,photoperiodism, flowering,dioxygenase activity,oxidation-reduction process
comp31233_c0_seq5.p1				
comp31233_c0_seq6.p2				
comp31234_c0_seq1.p2				
comp31236_c0_seq1.p1				
comp31237_c0_seq1.p2				
comp31237_c0_seq3.p1	sp|Q99MT2|MSH4_MOUSE_MutS_protein_homolog_4_OS=Mus_musculus_GN=Msh4_PE=2_SV=1	6.00E-53	GO:0000166,GO:0000793,GO:0000794,GO:0000794,GO:0000794,GO:0000795,GO:0000795,GO:0000795,GO:0001541,GO:0003677,GO:0005524,GO:0005524,GO:0005634,GO:0005654,GO:0005654,GO:0006200,GO:0006298,GO:0007126,GO:0007126,GO:0007129,GO:0007129,GO:0007131,GO:0007283,GO:0007292,GO:0008094,GO:0030983,GO:0030983,GO:0045143,GO:0051026,GO:0051321,GO:0000710,GO:0003684,GO:0032300	nucleotide binding,condensed chromosome,condensed nuclear chromosome,condensed nuclear chromosome,condensed nuclear chromosome,synaptonemal complex,synaptonemal complex,synaptonemal complex,ovarian follicle development,DNA binding,ATP binding,ATP binding,nucleus,nucleoplasm,nucleoplasm,ATP catabolic process,mismatch repair,meiotic nuclear division,meiotic nuclear division,synapsis,synapsis,reciprocal meiotic recombination,spermatogenesis,female gamete generation,DNA-dependent ATPase activity,mismatched DNA binding,mismatched DNA binding,homologous chromosome segregation,chiasma assembly,meiotic cell cycle,meiotic mismatch repair,damaged DNA binding,mismatch repair complex
comp31237_c0_seq3.p2	sp|O15457|MSH4_HUMAN_MutS_protein_homolog_4_OS=Homo_sapiens_GN=MSH4_PE=2_SV=2	1.00E-37	GO:0000166,GO:0000793,GO:0000794,GO:0000795,GO:0000795,GO:0001541,GO:0003677,GO:0003677,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006200,GO:0006298,GO:0007126,GO:0007129,GO:0007131,GO:0007131,GO:0007283,GO:0007292,GO:0008094,GO:0030983,GO:0030983,GO:0045143,GO:0051026,GO:0051321,GO:0000710,GO:0003684,GO:0032300	nucleotide binding,condensed chromosome,condensed nuclear chromosome,synaptonemal complex,synaptonemal complex,ovarian follicle development,DNA binding,DNA binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,nucleus,nucleus,ATP catabolic process,mismatch repair,meiotic nuclear division,synapsis,reciprocal meiotic recombination,reciprocal meiotic recombination,spermatogenesis,female gamete generation,DNA-dependent ATPase activity,mismatched DNA binding,mismatched DNA binding,homologous chromosome segregation,chiasma assembly,meiotic cell cycle,meiotic mismatch repair,damaged DNA binding,mismatch repair complex
comp31237_c0_seq3.p4				
comp31237_c0_seq4.p1	sp|O15457|MSH4_HUMAN_MutS_protein_homolog_4_OS=Homo_sapiens_GN=MSH4_PE=2_SV=2	5.00E-36	GO:0000166,GO:0000793,GO:0000794,GO:0000795,GO:0000795,GO:0001541,GO:0003677,GO:0003677,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006200,GO:0006298,GO:0007126,GO:0007129,GO:0007131,GO:0007131,GO:0007283,GO:0007292,GO:0008094,GO:0030983,GO:0030983,GO:0045143,GO:0051026,GO:0051321,GO:0000710,GO:0003684,GO:0032300	nucleotide binding,condensed chromosome,condensed nuclear chromosome,synaptonemal complex,synaptonemal complex,ovarian follicle development,DNA binding,DNA binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,nucleus,nucleus,ATP catabolic process,mismatch repair,meiotic nuclear division,synapsis,reciprocal meiotic recombination,reciprocal meiotic recombination,spermatogenesis,female gamete generation,DNA-dependent ATPase activity,mismatched DNA binding,mismatched DNA binding,homologous chromosome segregation,chiasma assembly,meiotic cell cycle,meiotic mismatch repair,damaged DNA binding,mismatch repair complex
comp31237_c0_seq4.p2	sp|O15457|MSH4_HUMAN_MutS_protein_homolog_4_OS=Homo_sapiens_GN=MSH4_PE=2_SV=2	1.00E-37	GO:0000166,GO:0000793,GO:0000794,GO:0000795,GO:0000795,GO:0001541,GO:0003677,GO:0003677,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006200,GO:0006298,GO:0007126,GO:0007129,GO:0007131,GO:0007131,GO:0007283,GO:0007292,GO:0008094,GO:0030983,GO:0030983,GO:0045143,GO:0051026,GO:0051321,GO:0000710,GO:0003684,GO:0032300	nucleotide binding,condensed chromosome,condensed nuclear chromosome,synaptonemal complex,synaptonemal complex,ovarian follicle development,DNA binding,DNA binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,nucleus,nucleus,ATP catabolic process,mismatch repair,meiotic nuclear division,synapsis,reciprocal meiotic recombination,reciprocal meiotic recombination,spermatogenesis,female gamete generation,DNA-dependent ATPase activity,mismatched DNA binding,mismatched DNA binding,homologous chromosome segregation,chiasma assembly,meiotic cell cycle,meiotic mismatch repair,damaged DNA binding,mismatch repair complex
comp31237_c0_seq4.p4				
comp31237_c0_seq5.p2	sp|Q24X61|MUTS_DESHY_DNA_mismatch_repair_protein_MutS_OS=Desulfitobacterium_hafniense_(strain_Y51)_GN=mutS_PE=3_SV=1	1.00E-17	GO:0000166,GO:0003677,GO:0003684,GO:0005524,GO:0005524,GO:0005524,GO:0006281,GO:0006298,GO:0006298,GO:0006974,GO:0030983	nucleotide binding,DNA binding,damaged DNA binding,ATP binding,ATP binding,ATP binding,DNA repair,mismatch repair,mismatch repair,cellular response to DNA damage stimulus,mismatched DNA binding
comp31239_c0_seq1.p1	sp|Q7ZWM3|CEL3B_XENLA_CUGBP_Elav-like_family_member_3-B_OS=Xenopus_laevis_GN=tnrc4-b_PE=2_SV=1	7.00E-25	GO:0000166,GO:0003676,GO:0003723,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006397,GO:0048026	nucleotide binding,nucleic acid binding,RNA binding,nucleus,nucleus,cytoplasm,cytoplasm,mRNA processing,positive regulation of mRNA splicing, via spliceosome
comp31239_c0_seq2.p1	sp|Q7ZWM3|CEL3B_XENLA_CUGBP_Elav-like_family_member_3-B_OS=Xenopus_laevis_GN=tnrc4-b_PE=2_SV=1	2.00E-24	GO:0000166,GO:0003676,GO:0003723,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006397,GO:0048026	nucleotide binding,nucleic acid binding,RNA binding,nucleus,nucleus,cytoplasm,cytoplasm,mRNA processing,positive regulation of mRNA splicing, via spliceosome
comp31240_c0_seq5.p1				
comp31240_c0_seq8.p1				
comp31241_c0_seq2.p1	sp|Q5ZIL9|KBP_CHICK_KIF1-binding_protein_homolog_OS=Gallus_gallus_GN=kbp_PE=2_SV=1	6.00E-20	GO:0005737,GO:0005739,GO:0005739,GO:0005739,GO:0005856,GO:0005856,GO:0006839,GO:0006839,GO:0006839,GO:0007275,GO:0007399,GO:0007399,GO:0019894,GO:0019894,GO:0030154	cytoplasm,mitochondrion,mitochondrion,mitochondrion,cytoskeleton,cytoskeleton,mitochondrial transport,mitochondrial transport,mitochondrial transport,multicellular organismal development,nervous system development,nervous system development,kinesin binding,kinesin binding,cell differentiation
comp31241_c0_seq2.p2				
comp31241_c0_seq2.p4				
comp31241_c0_seq3.p1				
comp31241_c0_seq7.p1	sp|Q5ZIL9|KBP_CHICK_KIF1-binding_protein_homolog_OS=Gallus_gallus_GN=kbp_PE=2_SV=1	1.00E-19	GO:0005737,GO:0005739,GO:0005739,GO:0005739,GO:0005856,GO:0005856,GO:0006839,GO:0006839,GO:0006839,GO:0007275,GO:0007399,GO:0007399,GO:0019894,GO:0019894,GO:0030154	cytoplasm,mitochondrion,mitochondrion,mitochondrion,cytoskeleton,cytoskeleton,mitochondrial transport,mitochondrial transport,mitochondrial transport,multicellular organismal development,nervous system development,nervous system development,kinesin binding,kinesin binding,cell differentiation
comp31241_c0_seq7.p2				
comp31243_c0_seq12.p1	sp|Q54JR2|ABCC3_DICDI_ABC_transporter_C_family_member_3_OS=Dictyostelium_discoideum_GN=abcC3_PE=3_SV=1	0	GO:0000166,GO:0005215,GO:0005524,GO:0005524,GO:0006200,GO:0006810,GO:0006810,GO:0006810,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016887,GO:0031154,GO:0042626,GO:0042626,GO:0044351,GO:0055085	nucleotide binding,transporter activity,ATP binding,ATP binding,ATP catabolic process,transport,transport,transport,membrane,membrane,integral component of membrane,integral component of membrane,ATPase activity,culmination involved in sorocarp development,ATPase activity, coupled to transmembrane movement of substances,ATPase activity, coupled to transmembrane movement of substances,macropinocytosis,transmembrane transport
comp31244_c1_seq1.p1	sp|A9A8T5|DHQS_METM6_3-dehydroquinate_synthase_OS=Methanococcus_maripaludis_(strain_C6_/_ATCC_BAA-1332)_GN=MmarC6_0943_PE=3_SV=1	3.00E-41	GO:0003856,GO:0008652,GO:0009073,GO:0009073,GO:0009073,GO:0016491,GO:0016491,GO:0016639,GO:0051287,GO:0055114,GO:0055114	3-dehydroquinate synthase activity,cellular amino acid biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp31244_c1_seq10.p1	sp|Q58646|DHQS_METJA_3-dehydroquinate_synthase_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ1249_PE=1_SV=1	4.00E-40	GO:0003856,GO:0008652,GO:0009073,GO:0009073,GO:0009073,GO:0016491,GO:0016491,GO:0016639,GO:0051287,GO:0055114,GO:0055114	3-dehydroquinate synthase activity,cellular amino acid biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp31244_c1_seq10.p2				
comp31244_c1_seq11.p1	sp|Q2NI00|DHQS_METST_3-dehydroquinate_synthase_OS=Methanosphaera_stadtmanae_(strain_DSM_3091)_GN=Msp_0090_PE=3_SV=1	4.00E-41	GO:0003856,GO:0008652,GO:0009073,GO:0009073,GO:0009073,GO:0016491,GO:0016491,GO:0016639,GO:0051287,GO:0055114,GO:0055114	3-dehydroquinate synthase activity,cellular amino acid biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp31244_c1_seq14.p1	sp|A0B6K6|DHQS_METTP_3-dehydroquinate_synthase_OS=Methanosaeta_thermophila_(strain_DSM_6194_/_PT)_GN=Mthe_0539_PE=3_SV=2	1.00E-14	GO:0003856,GO:0008652,GO:0009073,GO:0009073,GO:0009073,GO:0016491,GO:0016491,GO:0016639,GO:0051287,GO:0055114,GO:0055114	3-dehydroquinate synthase activity,cellular amino acid biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp31244_c1_seq17.p1	sp|A0B6K6|DHQS_METTP_3-dehydroquinate_synthase_OS=Methanosaeta_thermophila_(strain_DSM_6194_/_PT)_GN=Mthe_0539_PE=3_SV=2	2.00E-14	GO:0003856,GO:0008652,GO:0009073,GO:0009073,GO:0009073,GO:0016491,GO:0016491,GO:0016639,GO:0051287,GO:0055114,GO:0055114	3-dehydroquinate synthase activity,cellular amino acid biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp31244_c1_seq2.p1	sp|A9A8T5|DHQS_METM6_3-dehydroquinate_synthase_OS=Methanococcus_maripaludis_(strain_C6_/_ATCC_BAA-1332)_GN=MmarC6_0943_PE=3_SV=1	2.00E-46	GO:0003856,GO:0008652,GO:0009073,GO:0009073,GO:0009073,GO:0016491,GO:0016491,GO:0016639,GO:0051287,GO:0055114,GO:0055114	3-dehydroquinate synthase activity,cellular amino acid biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp31244_c1_seq20.p1	sp|A7I8L5|DHQS_METB6_3-dehydroquinate_synthase_OS=Methanoregula_boonei_(strain_6A8)_GN=Mboo_1559_PE=3_SV=1	3.00E-42	GO:0003856,GO:0008652,GO:0009073,GO:0009073,GO:0009073,GO:0016491,GO:0016491,GO:0016639,GO:0051287,GO:0055114,GO:0055114	3-dehydroquinate synthase activity,cellular amino acid biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp31244_c1_seq21.p1	sp|A7I8L5|DHQS_METB6_3-dehydroquinate_synthase_OS=Methanoregula_boonei_(strain_6A8)_GN=Mboo_1559_PE=3_SV=1	6.00E-47	GO:0003856,GO:0008652,GO:0009073,GO:0009073,GO:0009073,GO:0016491,GO:0016491,GO:0016639,GO:0051287,GO:0055114,GO:0055114	3-dehydroquinate synthase activity,cellular amino acid biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp31244_c1_seq5.p1	sp|Q58646|DHQS_METJA_3-dehydroquinate_synthase_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ1249_PE=1_SV=1	2.00E-35	GO:0003856,GO:0008652,GO:0009073,GO:0009073,GO:0009073,GO:0016491,GO:0016491,GO:0016639,GO:0051287,GO:0055114,GO:0055114	3-dehydroquinate synthase activity,cellular amino acid biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp31244_c1_seq5.p2				
comp31244_c1_seq6.p1	sp|Q58646|DHQS_METJA_3-dehydroquinate_synthase_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ1249_PE=1_SV=1	2.00E-28	GO:0003856,GO:0008652,GO:0009073,GO:0009073,GO:0009073,GO:0016491,GO:0016491,GO:0016639,GO:0051287,GO:0055114,GO:0055114	3-dehydroquinate synthase activity,cellular amino acid biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,aromatic amino acid family biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp31244_c1_seq9.p1				
comp31244_c1_seq9.p3				
comp31246_c0_seq1.p1	sp|Q54LB8|VP13A_DICDI_Putative_vacuolar_protein_sorting-associated_protein_13A_OS=Dictyostelium_discoideum_GN=vps13A_PE=2_SV=1	9.00E-28	GO:0005622,GO:0005794,GO:0005794,GO:0006623,GO:0006810,GO:0015031,GO:0019898,GO:0044351,GO:0045053	intracellular,Golgi apparatus,Golgi apparatus,protein targeting to vacuole,transport,protein transport,extrinsic component of membrane,macropinocytosis,protein retention in Golgi apparatus
comp31246_c0_seq2.p1				
comp31246_c0_seq4.p1				
comp31247_c0_seq1.p1	sp|Q651D5|PIP27_ORYSJ_Probable_aquaporin_PIP2-7_OS=Oryza_sativa_subsp._japonica_GN=PIP2-7_PE=2_SV=2	3.00E-45	GO:0005215,GO:0005886,GO:0005886,GO:0006810,GO:0006810,GO:0016020,GO:0016020,GO:0016021	transporter activity,plasma membrane,plasma membrane,transport,transport,membrane,membrane,integral component of membrane
comp31248_c0_seq3.p1	sp|Q6IP59|CTL2_XENLA_Choline_transporter-like_protein_2_OS=Xenopus_laevis_GN=slc44a2_PE=2_SV=1	3.00E-52	GO:0006810,GO:0016020,GO:0016020,GO:0016021	transport,membrane,membrane,integral component of membrane
comp31249_c0_seq1.p1				
comp31249_c0_seq11.p2				
comp31249_c0_seq12.p1				
comp31249_c0_seq13.p1				
comp31249_c0_seq14.p1				
comp31249_c0_seq16.p1				
comp31249_c0_seq16.p2				
comp31249_c0_seq17.p1				
comp31249_c0_seq2.p1				
comp31249_c0_seq3.p2				
comp31249_c0_seq3.p3				
comp31249_c0_seq4.p1				
comp31249_c0_seq4.p5				
comp31249_c0_seq8.p1				
comp31250_c0_seq3.p1	sp|O75417|DPOLQ_HUMAN_DNA_polymerase_theta_OS=Homo_sapiens_GN=POLQ_PE=1_SV=2	3.00E-40	GO:0000166,GO:0003676,GO:0003677,GO:0003684,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0005524,GO:0005524,GO:0005654,GO:0006200,GO:0006260,GO:0006261,GO:0006281,GO:0006281,GO:0006281,GO:0006974,GO:0016740,GO:0016779,GO:0043142,GO:0071897,GO:0071897,GO:0071897,GO:0071897,GO:0071897	nucleotide binding,nucleic acid binding,DNA binding,damaged DNA binding,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,ATP binding,ATP binding,nucleoplasm,ATP catabolic process,DNA replication,DNA-dependent DNA replication,DNA repair,DNA repair,DNA repair,cellular response to DNA damage stimulus,transferase activity,nucleotidyltransferase activity,single-stranded DNA-dependent ATPase activity,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process
comp31250_c0_seq4.p1	sp|O75417|DPOLQ_HUMAN_DNA_polymerase_theta_OS=Homo_sapiens_GN=POLQ_PE=1_SV=2	4.00E-40	GO:0000166,GO:0003676,GO:0003677,GO:0003684,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0005524,GO:0005524,GO:0005654,GO:0006200,GO:0006260,GO:0006261,GO:0006281,GO:0006281,GO:0006281,GO:0006974,GO:0016740,GO:0016779,GO:0043142,GO:0071897,GO:0071897,GO:0071897,GO:0071897,GO:0071897	nucleotide binding,nucleic acid binding,DNA binding,damaged DNA binding,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,ATP binding,ATP binding,nucleoplasm,ATP catabolic process,DNA replication,DNA-dependent DNA replication,DNA repair,DNA repair,DNA repair,cellular response to DNA damage stimulus,transferase activity,nucleotidyltransferase activity,single-stranded DNA-dependent ATPase activity,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process
comp31250_c0_seq5.p1	sp|O75417|DPOLQ_HUMAN_DNA_polymerase_theta_OS=Homo_sapiens_GN=POLQ_PE=1_SV=2	2.00E-41	GO:0000166,GO:0003676,GO:0003677,GO:0003684,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0005524,GO:0005524,GO:0005654,GO:0006200,GO:0006260,GO:0006261,GO:0006281,GO:0006281,GO:0006281,GO:0006974,GO:0016740,GO:0016779,GO:0043142,GO:0071897,GO:0071897,GO:0071897,GO:0071897,GO:0071897	nucleotide binding,nucleic acid binding,DNA binding,damaged DNA binding,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,ATP binding,ATP binding,nucleoplasm,ATP catabolic process,DNA replication,DNA-dependent DNA replication,DNA repair,DNA repair,DNA repair,cellular response to DNA damage stimulus,transferase activity,nucleotidyltransferase activity,single-stranded DNA-dependent ATPase activity,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process
comp31251_c0_seq1.p1				
comp31251_c0_seq1.p2				
comp31252_c0_seq1.p1				
comp31253_c0_seq2.p1				
comp31253_c0_seq4.p1				
comp31253_c0_seq9.p1				
comp31254_c2_seq1.p1				
comp31254_c2_seq1.p2				
comp31254_c2_seq3.p2				
comp31254_c2_seq4.p1				
comp31254_c2_seq4.p2				
comp31255_c0_seq1.p1	sp|Q7TNH6|NPHP3_MOUSE_Nephrocystin-3_OS=Mus_musculus_GN=Nphp3_PE=1_SV=2	7.00E-38	GO:0003674,GO:0005929,GO:0005929,GO:0005929,GO:0006629,GO:0007163,GO:0007368,GO:0016055,GO:0030198,GO:0030814,GO:0042995,GO:0048496,GO:0060271,GO:0060271,GO:0060271,GO:0060993,GO:0072372,GO:0090090,GO:0097543,GO:0097546,GO:2000095	molecular_function,cilium,cilium,cilium,lipid metabolic process,establishment or maintenance of cell polarity,determination of left/right symmetry,Wnt signaling pathway,extracellular matrix organization,regulation of cAMP metabolic process,cell projection,maintenance of organ identity,cilium morphogenesis,cilium morphogenesis,cilium morphogenesis,kidney morphogenesis,primary cilium,negative regulation of canonical Wnt signaling pathway,ciliary inversin compartment,ciliary base,regulation of Wnt signaling pathway, planar cell polarity pathway
comp31255_c0_seq2.p1	sp|Q7TNH6|NPHP3_MOUSE_Nephrocystin-3_OS=Mus_musculus_GN=Nphp3_PE=1_SV=2	9.00E-38	GO:0003674,GO:0005929,GO:0005929,GO:0005929,GO:0006629,GO:0007163,GO:0007368,GO:0016055,GO:0030198,GO:0030814,GO:0042995,GO:0048496,GO:0060271,GO:0060271,GO:0060271,GO:0060993,GO:0072372,GO:0090090,GO:0097543,GO:0097546,GO:2000095	molecular_function,cilium,cilium,cilium,lipid metabolic process,establishment or maintenance of cell polarity,determination of left/right symmetry,Wnt signaling pathway,extracellular matrix organization,regulation of cAMP metabolic process,cell projection,maintenance of organ identity,cilium morphogenesis,cilium morphogenesis,cilium morphogenesis,kidney morphogenesis,primary cilium,negative regulation of canonical Wnt signaling pathway,ciliary inversin compartment,ciliary base,regulation of Wnt signaling pathway, planar cell polarity pathway
comp31256_c0_seq1.p1				
comp31256_c0_seq1.p7				
comp31256_c0_seq4.p1				
comp31257_c0_seq1.p1				
comp31257_c0_seq1.p11				
comp31257_c0_seq1.p13				
comp31257_c0_seq1.p3				
comp31257_c0_seq2.p1				
comp31257_c0_seq2.p11				
comp31258_c0_seq10.p1				
comp31258_c0_seq4.p1				
comp31258_c0_seq8.p1				
comp31260_c0_seq10.p1				
comp31260_c0_seq2.p1				
comp31260_c0_seq6.p1				
comp31260_c0_seq6.p3				
comp31260_c0_seq9.p1				
comp31261_c0_seq12.p1				
comp31261_c0_seq3.p1				
comp31261_c0_seq4.p1	sp|Q2U002|EIF3G_ASPOR_Eukaryotic_translation_initiation_factor_3_subunit_G_OS=Aspergillus_oryzae_(strain_ATCC_42149_/_RIB_40)_GN=tif35_PE=3_SV=1	5.00E-13	GO:0000166,GO:0001731,GO:0003676,GO:0003723,GO:0003723,GO:0003743,GO:0003743,GO:0003743,GO:0005575,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005852,GO:0005852,GO:0006412,GO:0006413,GO:0006413,GO:0006446,GO:0008150,GO:0016282,GO:0033290	nucleotide binding,formation of translation preinitiation complex,nucleic acid binding,RNA binding,RNA binding,translation initiation factor activity,translation initiation factor activity,translation initiation factor activity,cellular_component,cytoplasm,cytoplasm,cytoplasm,cytoplasm,eukaryotic translation initiation factor 3 complex,eukaryotic translation initiation factor 3 complex,translation,translational initiation,translational initiation,regulation of translational initiation,biological_process,eukaryotic 43S preinitiation complex,eukaryotic 48S preinitiation complex
comp31261_c0_seq7.p1	sp|Q99NH0|ANR17_MOUSE_Ankyrin_repeat_domain-containing_protein_17_OS=Mus_musculus_GN=Ankrd17_PE=1_SV=2	2.00E-35	GO:0000785,GO:0001955,GO:0003682,GO:0003723,GO:0003723,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006275,GO:0007492,GO:0016020,GO:0042742,GO:0043123,GO:0044822,GO:0045787,GO:0051151,GO:1900087,GO:1900245,GO:1900246	chromatin,blood vessel maturation,chromatin binding,RNA binding,RNA binding,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,cytoplasm,regulation of DNA replication,endoderm development,membrane,defense response to bacterium,positive regulation of I-kappaB kinase/NF-kappaB signaling,poly(A) RNA binding,positive regulation of cell cycle,negative regulation of smooth muscle cell differentiation,positive regulation of G1/S transition of mitotic cell cycle,positive regulation of MDA-5 signaling pathway,positive regulation of RIG-I signaling pathway
comp31261_c0_seq7.p3	sp|Q2U002|EIF3G_ASPOR_Eukaryotic_translation_initiation_factor_3_subunit_G_OS=Aspergillus_oryzae_(strain_ATCC_42149_/_RIB_40)_GN=tif35_PE=3_SV=1	2.00E-31	GO:0000166,GO:0001731,GO:0003676,GO:0003723,GO:0003723,GO:0003743,GO:0003743,GO:0003743,GO:0005575,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005852,GO:0005852,GO:0006412,GO:0006413,GO:0006413,GO:0006446,GO:0008150,GO:0016282,GO:0033290	nucleotide binding,formation of translation preinitiation complex,nucleic acid binding,RNA binding,RNA binding,translation initiation factor activity,translation initiation factor activity,translation initiation factor activity,cellular_component,cytoplasm,cytoplasm,cytoplasm,cytoplasm,eukaryotic translation initiation factor 3 complex,eukaryotic translation initiation factor 3 complex,translation,translational initiation,translational initiation,regulation of translational initiation,biological_process,eukaryotic 43S preinitiation complex,eukaryotic 48S preinitiation complex
comp31261_c0_seq8.p1				
comp31262_c0_seq1.p2				
comp31264_c0_seq1.p1				
comp31264_c0_seq2.p1				
comp31265_c0_seq2.p1				
comp31265_c0_seq4.p1				
comp31265_c0_seq5.p1				
comp31265_c0_seq5.p5				
comp31266_c0_seq2.p3				
comp31266_c0_seq3.p1				
comp31266_c0_seq9.p1				
comp31267_c0_seq1.p1				
comp31267_c0_seq3.p1				
comp31269_c0_seq1.p2				
comp31269_c0_seq2.p1				
comp31269_c0_seq4.p1	sp|Q54Q40|D1039_DICDI_Probable_ubiquitin_thioesterase_DG1039_OS=Dictyostelium_discoideum_GN=DG1039_PE=3_SV=1	2.00E-53	GO:0003674,GO:0005575,GO:0006508,GO:0008150,GO:0008233,GO:0008237,GO:0016787,GO:0046872	molecular_function,cellular_component,proteolysis,biological_process,peptidase activity,metallopeptidase activity,hydrolase activity,metal ion binding
comp31270_c0_seq1.p1	sp|Q09690|POM1_SCHPO_Dual_specificity_protein_kinase_pom1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=pom1_PE=1_SV=1	4.00E-53	GO:0000166,GO:0000753,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004674,GO:0004674,GO:0004712,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0006468,GO:0007165,GO:0008361,GO:0008361,GO:0010972,GO:0010972,GO:0010972,GO:0010972,GO:0010972,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0030427,GO:0030428,GO:0032153,GO:0032153,GO:0032153,GO:0034613,GO:0034613,GO:0035839,GO:0051285,GO:0051286,GO:0051286,GO:0051286,GO:0051286,GO:0051519,GO:0070650,GO:0071343,GO:0071574,GO:1903486,GO:2000769	nucleotide binding,cell morphogenesis involved in conjugation with cellular fusion,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine/tyrosine kinase activity,protein binding,protein binding,ATP binding,ATP binding,protein phosphorylation,signal transduction,regulation of cell size,regulation of cell size,negative regulation of G2/M transition of mitotic cell cycle,negative regulation of G2/M transition of mitotic cell cycle,negative regulation of G2/M transition of mitotic cell cycle,negative regulation of G2/M transition of mitotic cell cycle,negative regulation of G2/M transition of mitotic cell cycle,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,site of polarized growth,cell septum,cell division site,cell division site,cell division site,cellular protein localization,cellular protein localization,non-growing cell tip,cell cortex of cell tip,cell tip,cell tip,cell tip,cell tip,activation of bipolar cell growth,actin filament bundle distribution,negative regulation of establishment of actomyosin contractile ring localization,protein localization to medial cortex,establishment of mitotic actomyosin contractile ring localization,regulation of establishment or maintenance of cell polarity regulating cell shape
comp31271_c0_seq2.p1				
comp31271_c0_seq2.p2				
comp31272_c0_seq1.p1	sp|Q54YZ9|DHKJ_DICDI_Hybrid_signal_transduction_histidine_kinase_J_OS=Dictyostelium_discoideum_GN=dhkJ_PE=3_SV=2	2.00E-22	GO:0000155,GO:0000155,GO:0000156,GO:0000160,GO:0000160,GO:0000166,GO:0004673,GO:0004871,GO:0004871,GO:0005524,GO:0005615,GO:0007165,GO:0007165,GO:0007234,GO:0009927,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0018106,GO:0023014,GO:0023014	phosphorelay sensor kinase activity,phosphorelay sensor kinase activity,phosphorelay response regulator activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,protein histidine kinase activity,signal transducer activity,signal transducer activity,ATP binding,extracellular space,signal transduction,signal transduction,osmosensory signaling via phosphorelay pathway,histidine phosphotransfer kinase activity,membrane,integral component of membrane,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-histidine phosphorylation,signal transduction by phosphorylation,signal transduction by phosphorylation
comp31273_c0_seq2.p1	sp|P51892|DNLI1_XENLA_DNA_ligase_1_OS=Xenopus_laevis_GN=lig1_PE=2_SV=1	3.00E-179	GO:0000166,GO:0003677,GO:0003909,GO:0003910,GO:0003910,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006260,GO:0006281,GO:0006281,GO:0006310,GO:0006310,GO:0006974,GO:0007049,GO:0016874,GO:0046872,GO:0051103,GO:0051301,GO:0071897	nucleotide binding,DNA binding,DNA ligase activity,DNA ligase (ATP) activity,DNA ligase (ATP) activity,ATP binding,ATP binding,nucleus,nucleus,DNA replication,DNA repair,DNA repair,DNA recombination,DNA recombination,cellular response to DNA damage stimulus,cell cycle,ligase activity,metal ion binding,DNA ligation involved in DNA repair,cell division,DNA biosynthetic process
comp31273_c0_seq2.p2				
comp31274_c0_seq1.p1				
comp31275_c1_seq1.p1				
comp31275_c1_seq2.p1				
comp31275_c1_seq4.p2				
comp31276_c0_seq1.p2				
comp31276_c0_seq4.p1	sp|Q6PFM0|JMJD6_DANRE_Bifunctional_arginine_demethylase_and_lysyl-hydroxylase_JMJD6_OS=Danio_rerio_GN=jmjd6_PE=2_SV=2	7.00E-33	GO:0002040,GO:0003723,GO:0003727,GO:0005634,GO:0005634,GO:0005654,GO:0005654,GO:0005730,GO:0005730,GO:0006351,GO:0006355,GO:0006397,GO:0006909,GO:0007275,GO:0008380,GO:0016491,GO:0016568,GO:0018395,GO:0030154,GO:0033746,GO:0033749,GO:0046872,GO:0048024,GO:0051213,GO:0055114,GO:0070078,GO:0070079,GO:0070815	sprouting angiogenesis,RNA binding,single-stranded RNA binding,nucleus,nucleus,nucleoplasm,nucleoplasm,nucleolus,nucleolus,transcription, DNA-templated,regulation of transcription, DNA-templated,mRNA processing,phagocytosis,multicellular organismal development,RNA splicing,oxidoreductase activity,chromatin modification,peptidyl-lysine hydroxylation to 5-hydroxy-L-lysine,cell differentiation,histone demethylase activity (H3-R2 specific),histone demethylase activity (H4-R3 specific),metal ion binding,regulation of mRNA splicing, via spliceosome,dioxygenase activity,oxidation-reduction process,histone H3-R2 demethylation,histone H4-R3 demethylation,peptidyl-lysine 5-dioxygenase activity
comp31276_c0_seq5.p1	sp|Q6PFM0|JMJD6_DANRE_Bifunctional_arginine_demethylase_and_lysyl-hydroxylase_JMJD6_OS=Danio_rerio_GN=jmjd6_PE=2_SV=2	5.00E-48	GO:0002040,GO:0003723,GO:0003727,GO:0005634,GO:0005634,GO:0005654,GO:0005654,GO:0005730,GO:0005730,GO:0006351,GO:0006355,GO:0006397,GO:0006909,GO:0007275,GO:0008380,GO:0016491,GO:0016568,GO:0018395,GO:0030154,GO:0033746,GO:0033749,GO:0046872,GO:0048024,GO:0051213,GO:0055114,GO:0070078,GO:0070079,GO:0070815	sprouting angiogenesis,RNA binding,single-stranded RNA binding,nucleus,nucleus,nucleoplasm,nucleoplasm,nucleolus,nucleolus,transcription, DNA-templated,regulation of transcription, DNA-templated,mRNA processing,phagocytosis,multicellular organismal development,RNA splicing,oxidoreductase activity,chromatin modification,peptidyl-lysine hydroxylation to 5-hydroxy-L-lysine,cell differentiation,histone demethylase activity (H3-R2 specific),histone demethylase activity (H4-R3 specific),metal ion binding,regulation of mRNA splicing, via spliceosome,dioxygenase activity,oxidation-reduction process,histone H3-R2 demethylation,histone H4-R3 demethylation,peptidyl-lysine 5-dioxygenase activity
comp31276_c0_seq6.p3				
comp31277_c1_seq1.p1	sp|O34580|PCRA_BACSU_ATP-dependent_DNA_helicase_pcrA_OS=Bacillus_subtilis_GN=pcrA_PE=1_SV=1	8.00E-14	GO:0000166,GO:0003677,GO:0003677,GO:0004003,GO:0004386,GO:0005524,GO:0005524,GO:0005737,GO:0006268,GO:0006281,GO:0006974,GO:0016787,GO:0016787	nucleotide binding,DNA binding,DNA binding,ATP-dependent DNA helicase activity,helicase activity,ATP binding,ATP binding,cytoplasm,DNA unwinding involved in DNA replication,DNA repair,cellular response to DNA damage stimulus,hydrolase activity,hydrolase activity
comp31277_c1_seq1.p2				
comp31277_c1_seq3.p1	sp|Q02322|UVRD_HAEIN_DNA_helicase_II_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=uvrD_PE=1_SV=2	2.00E-15	GO:0000166,GO:0003677,GO:0003677,GO:0004003,GO:0004386,GO:0005524,GO:0005524,GO:0005737,GO:0006260,GO:0006268,GO:0006281,GO:0006974,GO:0016787,GO:0016787,GO:0042802	nucleotide binding,DNA binding,DNA binding,ATP-dependent DNA helicase activity,helicase activity,ATP binding,ATP binding,cytoplasm,DNA replication,DNA unwinding involved in DNA replication,DNA repair,cellular response to DNA damage stimulus,hydrolase activity,hydrolase activity,identical protein binding
comp31277_c1_seq3.p2				
comp31277_c1_seq6.p1	sp|O34580|PCRA_BACSU_ATP-dependent_DNA_helicase_pcrA_OS=Bacillus_subtilis_GN=pcrA_PE=1_SV=1	8.00E-14	GO:0000166,GO:0003677,GO:0003677,GO:0004003,GO:0004386,GO:0005524,GO:0005524,GO:0005737,GO:0006268,GO:0006281,GO:0006974,GO:0016787,GO:0016787	nucleotide binding,DNA binding,DNA binding,ATP-dependent DNA helicase activity,helicase activity,ATP binding,ATP binding,cytoplasm,DNA unwinding involved in DNA replication,DNA repair,cellular response to DNA damage stimulus,hydrolase activity,hydrolase activity
comp31277_c1_seq8.p1	sp|Q02322|UVRD_HAEIN_DNA_helicase_II_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=uvrD_PE=1_SV=2	2.00E-15	GO:0000166,GO:0003677,GO:0003677,GO:0004003,GO:0004386,GO:0005524,GO:0005524,GO:0005737,GO:0006260,GO:0006268,GO:0006281,GO:0006974,GO:0016787,GO:0016787,GO:0042802	nucleotide binding,DNA binding,DNA binding,ATP-dependent DNA helicase activity,helicase activity,ATP binding,ATP binding,cytoplasm,DNA replication,DNA unwinding involved in DNA replication,DNA repair,cellular response to DNA damage stimulus,hydrolase activity,hydrolase activity,identical protein binding
comp31278_c0_seq5.p1				
comp31278_c0_seq5.p2				
comp31278_c0_seq7.p1				
comp31278_c0_seq8.p1				
comp31278_c0_seq8.p2				
comp31278_c0_seq9.p1				
comp31278_c0_seq9.p2				
comp31278_c0_seq9.p4				
comp31279_c0_seq3.p2				
comp31279_c0_seq4.p1				
comp31280_c0_seq1.p1				
comp31280_c0_seq2.p1				
comp31280_c0_seq4.p1				
comp31280_c0_seq6.p1				
comp31281_c0_seq1.p1				
comp31282_c0_seq5.p2				
comp31282_c0_seq6.p1				
comp31283_c0_seq2.p1				
comp31283_c0_seq3.p1				
comp31284_c0_seq2.p1				
comp31284_c0_seq2.p2				
comp31284_c0_seq7.p1				
comp31284_c0_seq7.p2				
comp31284_c0_seq7.p3				
comp31285_c0_seq1.p1	sp|Q54BT3|ABCB2_DICDI_ABC_transporter_B_family_member_2_OS=Dictyostelium_discoideum_GN=abcB2_PE=3_SV=1	0	GO:0000166,GO:0005215,GO:0005524,GO:0005524,GO:0006200,GO:0006810,GO:0006810,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016887,GO:0042626,GO:0042626,GO:0042626,GO:0055085,GO:0055085	nucleotide binding,transporter activity,ATP binding,ATP binding,ATP catabolic process,transport,transport,membrane,membrane,integral component of membrane,integral component of membrane,integral component of membrane,ATPase activity,ATPase activity, coupled to transmembrane movement of substances,ATPase activity, coupled to transmembrane movement of substances,ATPase activity, coupled to transmembrane movement of substances,transmembrane transport,transmembrane transport
comp31285_c0_seq3.p1	sp|B2HMK0|FAA32_MYCMM_Long-chain-fatty-acid--AMP_ligase_FadD32_OS=Mycobacterium_marinum_(strain_ATCC_BAA-535_/_M)_GN=fadD32_PE=3_SV=1	3.00E-79	GO:0000166,GO:0003824,GO:0005524,GO:0006629,GO:0006631,GO:0006633,GO:0008152,GO:0016874	nucleotide binding,catalytic activity,ATP binding,lipid metabolic process,fatty acid metabolic process,fatty acid biosynthetic process,metabolic process,ligase activity
comp31287_c0_seq2.p1	sp|P00275|THIO1_CORNE_Thioredoxin_C-1_OS=Corynebacterium_nephridii_PE=1_SV=1	5.00E-18	GO:0006662,GO:0015035,GO:0045454,GO:0055114	glycerol ether metabolic process,protein disulfide oxidoreductase activity,cell redox homeostasis,oxidation-reduction process
comp31287_c0_seq3.p1				
comp31288_c0_seq2.p1	sp|B2GUZ1|UBP4_RAT_Ubiquitin_carboxyl-terminal_hydrolase_4_OS=Rattus_norvegicus_GN=Usp4_PE=1_SV=1	4.00E-74	GO:0000244,GO:0004197,GO:0004221,GO:0004221,GO:0004221,GO:0004843,GO:0004843,GO:0004843,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005886,GO:0006508,GO:0006511,GO:0008233,GO:0008234,GO:0016579,GO:0016579,GO:0016579,GO:0016579,GO:0016787,GO:0031397,GO:0031397,GO:0031647,GO:0031647,GO:0031685,GO:0034394,GO:0034394,GO:0036459,GO:0042802,GO:0043161,GO:0046872,GO:0061136	spliceosomal tri-snRNP complex assembly,cysteine-type endopeptidase activity,ubiquitin thiolesterase activity,ubiquitin thiolesterase activity,ubiquitin thiolesterase activity,ubiquitin-specific protease activity,ubiquitin-specific protease activity,ubiquitin-specific protease activity,nucleus,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,cytoplasm,plasma membrane,proteolysis,ubiquitin-dependent protein catabolic process,peptidase activity,cysteine-type peptidase activity,protein deubiquitination,protein deubiquitination,protein deubiquitination,protein deubiquitination,hydrolase activity,negative regulation of protein ubiquitination,negative regulation of protein ubiquitination,regulation of protein stability,regulation of protein stability,adenosine receptor binding,protein localization to cell surface,protein localization to cell surface,ubiquitinyl hydrolase activity,identical protein binding,proteasome-mediated ubiquitin-dependent protein catabolic process,metal ion binding,regulation of proteasomal protein catabolic process
comp31289_c0_seq1.p1				
comp31289_c0_seq3.p1				
comp31289_c0_seq4.p1				
comp31290_c0_seq2.p2				
comp31291_c0_seq1.p1	sp|Q9M5K3|DLDH1_ARATH_Dihydrolipoyl_dehydrogenase_1,_mitochondrial_OS=Arabidopsis_thaliana_GN=LPD1_PE=1_SV=2	0	GO:0004148,GO:0004148,GO:0005507,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005747,GO:0005759,GO:0008270,GO:0016491,GO:0016491,GO:0016668,GO:0042744,GO:0045454,GO:0046686,GO:0046686,GO:0046686,GO:0048046,GO:0050660,GO:0050897,GO:0055114,GO:0055114,GO:0005794	dihydrolipoyl dehydrogenase activity,dihydrolipoyl dehydrogenase activity,copper ion binding,ATP binding,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrial respiratory chain complex I,mitochondrial matrix,zinc ion binding,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor,hydrogen peroxide catabolic process,cell redox homeostasis,response to cadmium ion,response to cadmium ion,response to cadmium ion,apoplast,flavin adenine dinucleotide binding,cobalt ion binding,oxidation-reduction process,oxidation-reduction process,Golgi apparatus
comp31291_c0_seq1.p2	sp|Q7RTR2|NLRC3_HUMAN_Protein_NLRC3_OS=Homo_sapiens_GN=NLRC3_PE=2_SV=2	1.00E-15	GO:0000166,GO:0003674,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0007249,GO:0031396,GO:0032088,GO:0032496,GO:0042110,GO:0043124,GO:0043124	nucleotide binding,molecular_function,ATP binding,cytoplasm,cytoplasm,cytoplasm,I-kappaB kinase/NF-kappaB signaling,regulation of protein ubiquitination,negative regulation of NF-kappaB transcription factor activity,response to lipopolysaccharide,T cell activation,negative regulation of I-kappaB kinase/NF-kappaB signaling,negative regulation of I-kappaB kinase/NF-kappaB signaling
comp31291_c0_seq13.p1	sp|Q9CR42|ANKR1_MOUSE_Ankyrin_repeat_domain-containing_protein_1_OS=Mus_musculus_GN=Ankrd1_PE=2_SV=1	1.00E-17	GO:0000122,GO:0001085,GO:0001105,GO:0002039,GO:0003677,GO:0003714,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005667,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0006357,GO:0008134,GO:0010976,GO:0030016,GO:0031432,GO:0031432,GO:0031674,GO:0031674,GO:0031674,GO:0035690,GO:0035914,GO:0035994,GO:0042692,GO:0042826,GO:0043065,GO:0043517,GO:0045944,GO:0050714,GO:0055008,GO:0070412,GO:0071222,GO:0071222,GO:0071260,GO:0071347,GO:0071356,GO:0071407,GO:0071456,GO:0071560,GO:2000279	negative regulation of transcription from RNA polymerase II promoter,RNA polymerase II transcription factor binding,RNA polymerase II transcription coactivator activity,p53 binding,DNA binding,transcription corepressor activity,protein binding,nucleus,nucleus,nucleus,nucleus,nucleus,transcription factor complex,cytoplasm,cytoplasm,cytoplasm,cytosol,regulation of transcription from RNA polymerase II promoter,transcription factor binding,positive regulation of neuron projection development,myofibril,titin binding,titin binding,I band,I band,I band,cellular response to drug,skeletal muscle cell differentiation,response to muscle stretch,muscle cell differentiation,histone deacetylase binding,positive regulation of apoptotic process,positive regulation of DNA damage response, signal transduction by p53 class mediator,positive regulation of transcription from RNA polymerase II promoter,positive regulation of protein secretion,cardiac muscle tissue morphogenesis,R-SMAD binding,cellular response to lipopolysaccharide,cellular response to lipopolysaccharide,cellular response to mechanical stimulus,cellular response to interleukin-1,cellular response to tumor necrosis factor,cellular response to organic cyclic compound,cellular response to hypoxia,cellular response to transforming growth factor beta stimulus,negative regulation of DNA biosynthetic process
comp31291_c0_seq7.p1	sp|Q9M5K3|DLDH1_ARATH_Dihydrolipoyl_dehydrogenase_1,_mitochondrial_OS=Arabidopsis_thaliana_GN=LPD1_PE=1_SV=2	0	GO:0004148,GO:0004148,GO:0005507,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005747,GO:0005759,GO:0008270,GO:0016491,GO:0016491,GO:0016668,GO:0042744,GO:0045454,GO:0046686,GO:0046686,GO:0046686,GO:0048046,GO:0050660,GO:0050897,GO:0055114,GO:0055114,GO:0005794	dihydrolipoyl dehydrogenase activity,dihydrolipoyl dehydrogenase activity,copper ion binding,ATP binding,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrial respiratory chain complex I,mitochondrial matrix,zinc ion binding,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor,hydrogen peroxide catabolic process,cell redox homeostasis,response to cadmium ion,response to cadmium ion,response to cadmium ion,apoplast,flavin adenine dinucleotide binding,cobalt ion binding,oxidation-reduction process,oxidation-reduction process,Golgi apparatus
comp31292_c0_seq1.p1				
comp31292_c0_seq2.p1	sp|Q9C585|UBP8_ARATH_Ubiquitin_carboxyl-terminal_hydrolase_8_OS=Arabidopsis_thaliana_GN=UBP8_PE=2_SV=1	2.00E-61	GO:0006508,GO:0006511,GO:0008233,GO:0008234,GO:0016787,GO:0036459	proteolysis,ubiquitin-dependent protein catabolic process,peptidase activity,cysteine-type peptidase activity,hydrolase activity,ubiquitinyl hydrolase activity
comp31292_c0_seq3.p1				
comp31294_c0_seq1.p1				
comp31294_c0_seq3.p1	sp|Q2KHI9|MCM9_MOUSE_DNA_replication_licensing_factor_MCM9_OS=Mus_musculus_GN=Mcm9_PE=2_SV=2	3.00E-174	GO:0000166,GO:0000724,GO:0000724,GO:0003677,GO:0003677,GO:0004386,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006281,GO:0006974,GO:0006974,GO:0006974,GO:0007276,GO:0007292,GO:0016787,GO:0097362,GO:0097362,GO:0006260	nucleotide binding,double-strand break repair via homologous recombination,double-strand break repair via homologous recombination,DNA binding,DNA binding,helicase activity,protein binding,ATP binding,ATP binding,nucleus,nucleus,DNA repair,cellular response to DNA damage stimulus,cellular response to DNA damage stimulus,cellular response to DNA damage stimulus,gamete generation,female gamete generation,hydrolase activity,MCM8-MCM9 complex,MCM8-MCM9 complex,DNA replication
comp31294_c0_seq3.p6				
comp31294_c0_seq5.p1	sp|Q2KHI9|MCM9_MOUSE_DNA_replication_licensing_factor_MCM9_OS=Mus_musculus_GN=Mcm9_PE=2_SV=2	2.00E-136	GO:0000166,GO:0000724,GO:0000724,GO:0003677,GO:0003677,GO:0004386,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006281,GO:0006974,GO:0006974,GO:0006974,GO:0007276,GO:0007292,GO:0016787,GO:0097362,GO:0097362,GO:0006260	nucleotide binding,double-strand break repair via homologous recombination,double-strand break repair via homologous recombination,DNA binding,DNA binding,helicase activity,protein binding,ATP binding,ATP binding,nucleus,nucleus,DNA repair,cellular response to DNA damage stimulus,cellular response to DNA damage stimulus,cellular response to DNA damage stimulus,gamete generation,female gamete generation,hydrolase activity,MCM8-MCM9 complex,MCM8-MCM9 complex,DNA replication
comp31294_c0_seq6.p1				
comp31294_c0_seq6.p2				
comp31295_c0_seq10.p1	sp|Q05609|CTR1_ARATH_Serine/threonine-protein_kinase_CTR1_OS=Arabidopsis_thaliana_GN=CTR1_PE=1_SV=1	6.00E-29	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004674,GO:0004712,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005789,GO:0006468,GO:0009686,GO:0009723,GO:0009744,GO:0009750,GO:0009873,GO:0010105,GO:0010105,GO:0010105,GO:0010105,GO:0010182,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0046777,GO:0048510,GO:0071281,GO:2000035,GO:2000069	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine/tyrosine kinase activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,endoplasmic reticulum membrane,protein phosphorylation,gibberellin biosynthetic process,response to ethylene,response to sucrose,response to fructose,ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,sugar mediated signaling pathway,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,protein autophosphorylation,regulation of timing of transition from vegetative to reproductive phase,cellular response to iron ion,regulation of stem cell division,regulation of post-embryonic root development
comp31295_c0_seq4.p1	sp|Q15034|HERC3_HUMAN_Probable_E3_ubiquitin-protein_ligase_HERC3_OS=Homo_sapiens_GN=HERC3_PE=1_SV=1	2.00E-20	GO:0004842,GO:0004842,GO:0005634,GO:0005737,GO:0005737,GO:0016023,GO:0016567,GO:0016874,GO:0031410,GO:0042787	ubiquitin-protein transferase activity,ubiquitin-protein transferase activity,nucleus,cytoplasm,cytoplasm,cytoplasmic membrane-bounded vesicle,protein ubiquitination,ligase activity,cytoplasmic vesicle,protein ubiquitination involved in ubiquitin-dependent protein catabolic process
comp31295_c0_seq4.p2	sp|Q05609|CTR1_ARATH_Serine/threonine-protein_kinase_CTR1_OS=Arabidopsis_thaliana_GN=CTR1_PE=1_SV=1	2.00E-30	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004674,GO:0004712,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005789,GO:0006468,GO:0009686,GO:0009723,GO:0009744,GO:0009750,GO:0009873,GO:0010105,GO:0010105,GO:0010105,GO:0010105,GO:0010182,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0046777,GO:0048510,GO:0071281,GO:2000035,GO:2000069	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine/tyrosine kinase activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,endoplasmic reticulum membrane,protein phosphorylation,gibberellin biosynthetic process,response to ethylene,response to sucrose,response to fructose,ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,sugar mediated signaling pathway,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,protein autophosphorylation,regulation of timing of transition from vegetative to reproductive phase,cellular response to iron ion,regulation of stem cell division,regulation of post-embryonic root development
comp31295_c0_seq7.p1	sp|Q15034|HERC3_HUMAN_Probable_E3_ubiquitin-protein_ligase_HERC3_OS=Homo_sapiens_GN=HERC3_PE=1_SV=1	2.00E-20	GO:0004842,GO:0004842,GO:0005634,GO:0005737,GO:0005737,GO:0016023,GO:0016567,GO:0016874,GO:0031410,GO:0042787	ubiquitin-protein transferase activity,ubiquitin-protein transferase activity,nucleus,cytoplasm,cytoplasm,cytoplasmic membrane-bounded vesicle,protein ubiquitination,ligase activity,cytoplasmic vesicle,protein ubiquitination involved in ubiquitin-dependent protein catabolic process
comp31295_c0_seq7.p2				
comp31295_c0_seq7.p3				
comp31295_c0_seq8.p1	sp|Q15034|HERC3_HUMAN_Probable_E3_ubiquitin-protein_ligase_HERC3_OS=Homo_sapiens_GN=HERC3_PE=1_SV=1	4.00E-20	GO:0004842,GO:0004842,GO:0005634,GO:0005737,GO:0005737,GO:0016023,GO:0016567,GO:0016874,GO:0031410,GO:0042787	ubiquitin-protein transferase activity,ubiquitin-protein transferase activity,nucleus,cytoplasm,cytoplasm,cytoplasmic membrane-bounded vesicle,protein ubiquitination,ligase activity,cytoplasmic vesicle,protein ubiquitination involved in ubiquitin-dependent protein catabolic process
comp31295_c0_seq8.p2				
comp31296_c0_seq1.p1	sp|Q8IWG1|WDR63_HUMAN_WD_repeat-containing_protein_63_OS=Homo_sapiens_GN=WDR63_PE=2_SV=1	6.00E-82		
comp31296_c0_seq1.p2	sp|P0C872|JMJD7_MOUSE_JmjC_domain-containing_protein_7_OS=Mus_musculus_GN=Jmjd7_PE=2_SV=1	8.00E-11	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp31296_c0_seq1.p5				
comp31296_c0_seq15.p1	sp|Q8IWG1|WDR63_HUMAN_WD_repeat-containing_protein_63_OS=Homo_sapiens_GN=WDR63_PE=2_SV=1	7.00E-62		
comp31296_c0_seq15.p2	sp|P0C872|JMJD7_MOUSE_JmjC_domain-containing_protein_7_OS=Mus_musculus_GN=Jmjd7_PE=2_SV=1	8.00E-11	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp31296_c0_seq15.p4				
comp31296_c0_seq15.p5				
comp31296_c0_seq18.p1	sp|Q16960|DYI3_ANTCR_Dynein_intermediate_chain_3,_ciliary_OS=Anthocidaris_crassispina_PE=2_SV=1	6.00E-21	GO:0003774,GO:0005737,GO:0005856,GO:0005874,GO:0005929,GO:0008152,GO:0030286,GO:0042995	motor activity,cytoplasm,cytoskeleton,microtubule,cilium,metabolic process,dynein complex,cell projection
comp31296_c0_seq26.p1	sp|Q16960|DYI3_ANTCR_Dynein_intermediate_chain_3,_ciliary_OS=Anthocidaris_crassispina_PE=2_SV=1	3.00E-17	GO:0003774,GO:0005737,GO:0005856,GO:0005874,GO:0005929,GO:0008152,GO:0030286,GO:0042995	motor activity,cytoplasm,cytoskeleton,microtubule,cilium,metabolic process,dynein complex,cell projection
comp31296_c0_seq26.p2				
comp31297_c0_seq1.p1				
comp31298_c0_seq1.p1	sp|Q2V4F9|SPXM1_ARATH_SPX_domain-containing_membrane_protein_At1g63010_OS=Arabidopsis_thaliana_GN=At1g63010_PE=1_SV=1	5.00E-36	GO:0005773,GO:0005774,GO:0016020,GO:0016021,GO:0016021,GO:0055085	vacuole,vacuolar membrane,membrane,integral component of membrane,integral component of membrane,transmembrane transport
comp31298_c0_seq1.p3				
comp31298_c0_seq10.p2				
comp31298_c0_seq13.p1				
comp31298_c0_seq3.p1	sp|Q6EPQ3|SPXM1_ORYSJ_SPX_domain-containing_membrane_protein_Os02g45520_OS=Oryza_sativa_subsp._japonica_GN=Os02g0678200_PE=2_SV=1	9.00E-39	GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0055085	membrane,membrane,integral component of membrane,integral component of membrane,transmembrane transport
comp31298_c0_seq4.p1				
comp31298_c0_seq5.p1				

comp31299_c0_seq2.p1				
comp31299_c0_seq3.p1				
comp31300_c0_seq1.p1				
comp31300_c0_seq2.p1				
comp31302_c0_seq7.p1	sp|Q8T9W1|TAGD_DICDI_Serine_protease/ABC_transporter_B_family_protein_tagD_OS=Dictyostelium_discoideum_GN=tagD_PE=3_SV=1	4.00E-48	GO:0000166,GO:0004252,GO:0005524,GO:0005524,GO:0006200,GO:0006508,GO:0006508,GO:0006810,GO:0006810,GO:0006810,GO:0008233,GO:0008236,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016787,GO:0016887,GO:0042626,GO:0042626,GO:0055085	nucleotide binding,serine-type endopeptidase activity,ATP binding,ATP binding,ATP catabolic process,proteolysis,proteolysis,transport,transport,transport,peptidase activity,serine-type peptidase activity,membrane,membrane,integral component of membrane,integral component of membrane,integral component of membrane,hydrolase activity,ATPase activity,ATPase activity, coupled to transmembrane movement of substances,ATPase activity, coupled to transmembrane movement of substances,transmembrane transport
comp31302_c0_seq7.p2	sp|B1LJ30|RLMI_ECOSM_Ribosomal_RNA_large_subunit_methyltransferase_I_OS=Escherichia_coli_(strain_SMS-3-5_/_SECEC)_GN=rlmI_PE=3_SV=1	3.00E-27	GO:0003723,GO:0003723,GO:0005737,GO:0005737,GO:0005737,GO:0006364,GO:0008168,GO:0008168,GO:0008649,GO:0016434,GO:0016740,GO:0031167,GO:0032259	RNA binding,RNA binding,cytoplasm,cytoplasm,cytoplasm,rRNA processing,methyltransferase activity,methyltransferase activity,rRNA methyltransferase activity,rRNA (cytosine) methyltransferase activity,transferase activity,rRNA methylation,methylation
comp31302_c0_seq8.p1	sp|Q8T9W1|TAGD_DICDI_Serine_protease/ABC_transporter_B_family_protein_tagD_OS=Dictyostelium_discoideum_GN=tagD_PE=3_SV=1	4.00E-48	GO:0000166,GO:0004252,GO:0005524,GO:0005524,GO:0006200,GO:0006508,GO:0006508,GO:0006810,GO:0006810,GO:0006810,GO:0008233,GO:0008236,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016787,GO:0016887,GO:0042626,GO:0042626,GO:0055085	nucleotide binding,serine-type endopeptidase activity,ATP binding,ATP binding,ATP catabolic process,proteolysis,proteolysis,transport,transport,transport,peptidase activity,serine-type peptidase activity,membrane,membrane,integral component of membrane,integral component of membrane,integral component of membrane,hydrolase activity,ATPase activity,ATPase activity, coupled to transmembrane movement of substances,ATPase activity, coupled to transmembrane movement of substances,transmembrane transport
comp31302_c0_seq8.p2	sp|B1LJ30|RLMI_ECOSM_Ribosomal_RNA_large_subunit_methyltransferase_I_OS=Escherichia_coli_(strain_SMS-3-5_/_SECEC)_GN=rlmI_PE=3_SV=1	3.00E-27	GO:0003723,GO:0003723,GO:0005737,GO:0005737,GO:0005737,GO:0006364,GO:0008168,GO:0008168,GO:0008649,GO:0016434,GO:0016740,GO:0031167,GO:0032259	RNA binding,RNA binding,cytoplasm,cytoplasm,cytoplasm,rRNA processing,methyltransferase activity,methyltransferase activity,rRNA methyltransferase activity,rRNA (cytosine) methyltransferase activity,transferase activity,rRNA methylation,methylation
comp31303_c0_seq4.p1				
comp31303_c0_seq5.p1				
comp31303_c0_seq7.p1				
comp31304_c0_seq5.p1	sp|Q5JSP0|FGD3_HUMAN_FYVE,_RhoGEF_and_PH_domain-containing_protein_3_OS=Homo_sapiens_GN=FGD3_PE=1_SV=1	4.00E-19	GO:0001726,GO:0005085,GO:0005085,GO:0005089,GO:0005737,GO:0005737,GO:0005737,GO:0005794,GO:0005829,GO:0005829,GO:0005829,GO:0005856,GO:0005856,GO:0007010,GO:0007264,GO:0008360,GO:0030027,GO:0030036,GO:0031267,GO:0032321,GO:0035023,GO:0043065,GO:0043088,GO:0043547,GO:0043547,GO:0046847,GO:0046872,GO:0046872,GO:0048011,GO:0048011,GO:0051056,GO:0097190	ruffle,guanyl-nucleotide exchange factor activity,guanyl-nucleotide exchange factor activity,Rho guanyl-nucleotide exchange factor activity,cytoplasm,cytoplasm,cytoplasm,Golgi apparatus,cytosol,cytosol,cytosol,cytoskeleton,cytoskeleton,cytoskeleton organization,small GTPase mediated signal transduction,regulation of cell shape,lamellipodium,actin cytoskeleton organization,small GTPase binding,positive regulation of Rho GTPase activity,regulation of Rho protein signal transduction,positive regulation of apoptotic process,regulation of Cdc42 GTPase activity,positive regulation of GTPase activity,positive regulation of GTPase activity,filopodium assembly,metal ion binding,metal ion binding,neurotrophin TRK receptor signaling pathway,neurotrophin TRK receptor signaling pathway,regulation of small GTPase mediated signal transduction,apoptotic signaling pathway
comp31304_c0_seq7.p1	sp|Q69ZL1|FGD6_MOUSE_FYVE,_RhoGEF_and_PH_domain-containing_protein_6_OS=Mus_musculus_GN=Fgd6_PE=1_SV=2	2.00E-25	GO:0003674,GO:0005085,GO:0005089,GO:0005575,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0008150,GO:0032321,GO:0035023,GO:0043547,GO:0046872,GO:0046872	molecular_function,guanyl-nucleotide exchange factor activity,Rho guanyl-nucleotide exchange factor activity,cellular_component,cytoplasm,cytoplasm,cytoskeleton,cytoskeleton,biological_process,positive regulation of Rho GTPase activity,regulation of Rho protein signal transduction,positive regulation of GTPase activity,metal ion binding,metal ion binding
comp31304_c0_seq7.p10				
comp31304_c0_seq8.p1				
comp31304_c0_seq9.p1	sp|Q69ZL1|FGD6_MOUSE_FYVE,_RhoGEF_and_PH_domain-containing_protein_6_OS=Mus_musculus_GN=Fgd6_PE=1_SV=2	5.00E-28	GO:0003674,GO:0005085,GO:0005089,GO:0005575,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0008150,GO:0032321,GO:0035023,GO:0043547,GO:0046872,GO:0046872	molecular_function,guanyl-nucleotide exchange factor activity,Rho guanyl-nucleotide exchange factor activity,cellular_component,cytoplasm,cytoplasm,cytoskeleton,cytoskeleton,biological_process,positive regulation of Rho GTPase activity,regulation of Rho protein signal transduction,positive regulation of GTPase activity,metal ion binding,metal ion binding
comp31304_c0_seq9.p9				
comp31305_c0_seq1.p1				
comp31305_c0_seq2.p1				
comp31306_c0_seq1.p1				
comp31307_c0_seq1.p1				
comp31307_c0_seq2.p2	sp|Q8R3A2|CV040_MOUSE_UPF0595_protein_C22orf40_homolog_OS=Mus_musculus_PE=2_SV=1	6.00E-15	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp31307_c0_seq4.p2				
comp31309_c0_seq3.p1				
comp31309_c0_seq7.p1				
comp31310_c0_seq1.p1				
comp31310_c0_seq1.p4				
comp31310_c0_seq3.p1				
comp31310_c0_seq4.p1				
comp31310_c0_seq4.p3				
comp31311_c0_seq3.p1				
comp31311_c0_seq4.p1				
comp31312_c0_seq1.p1				
comp31313_c0_seq2.p1				
comp31313_c0_seq2.p2				
comp31313_c0_seq4.p1				
comp31315_c0_seq1.p1				
comp31315_c0_seq1.p2				
comp31315_c0_seq5.p1				
comp31315_c0_seq5.p2				
comp31317_c0_seq1.p1	sp|Q9VAY3|MFRN_DROME_Mitoferrin_OS=Drosophila_melanogaster_GN=mfrn_PE=2_SV=1	8.00E-14	GO:0005381,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0006810,GO:0006811,GO:0016020,GO:0016021,GO:0034755,GO:0048250,GO:0048515,GO:0055072,GO:0055085	iron ion transmembrane transporter activity,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,transport,ion transport,membrane,integral component of membrane,iron ion transmembrane transport,mitochondrial iron ion transport,spermatid differentiation,iron ion homeostasis,transmembrane transport
comp31317_c0_seq10.p1				
comp31317_c0_seq3.p1	sp|Q9VAY3|MFRN_DROME_Mitoferrin_OS=Drosophila_melanogaster_GN=mfrn_PE=2_SV=1	7.00E-14	GO:0005381,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0006810,GO:0006811,GO:0016020,GO:0016021,GO:0034755,GO:0048250,GO:0048515,GO:0055072,GO:0055085	iron ion transmembrane transporter activity,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,transport,ion transport,membrane,integral component of membrane,iron ion transmembrane transport,mitochondrial iron ion transport,spermatid differentiation,iron ion homeostasis,transmembrane transport
comp31317_c0_seq5.p1				
comp31317_c0_seq6.p1				
comp31317_c0_seq7.p1				
comp31317_c0_seq8.p1	sp|O94480|YC6D_SCHPO_UPF0617_protein_C1919.13c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC1919.13c_PE=2_SV=1	6.00E-21	[illegible]	[illegible]
comp31318_c0_seq2.p2				
comp31318_c0_seq2.p4				
comp31318_c0_seq5.p1				
comp31320_c0_seq1.p1	sp|Q9LFQ3|SNL2_ARATH_Paired_amphipathic_helix_protein_Sin3-like_2_OS=Arabidopsis_thaliana_GN=SNL2_PE=1_SV=2	1.00E-64	[illegible]	[illegible]
comp31320_c0_seq1.p2	sp|Q5XGY1|TSR1_XENLA_Pre-rRNA-processing_protein_TSR1_homolog_OS=Xenopus_laevis_GN=tsr1_PE=2_SV=1	3.00E-114	[illegible]	[illegible]
comp31320_c0_seq3.p1	sp|Q5XGY1|TSR1_XENLA_Pre-rRNA-processing_protein_TSR1_homolog_OS=Xenopus_laevis_GN=tsr1_PE=2_SV=1	1.00E-67	[illegible]	[illegible]
comp31321_c0_seq1.p1	sp|P0CS40|JIP5_CRYNJ_WD_repeat-containing_protein_JIP5_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=JIP5_PE=3_SV=1	7.00E-45	GO:0005634,GO:0005730	[illegible]
comp31321_c0_seq1.p6				
comp31321_c0_seq11.p1	sp|Q54SA5|WDR55_DICDI_WD_repeat-containing_protein_55_homolog_OS=Dictyostelium_discoideum_GN=wdr55_PE=3_SV=1	4.00E-62	[illegible]	[illegible]
comp31321_c0_seq5.p4				
comp31321_c0_seq6.p4				
comp31321_c0_seq8.p1	sp|B4QTL6|WDR55_DROSI_WD_repeat-containing_protein_55_homolog_OS=Drosophila_simulans_GN=GD18783_PE=3_SV=1	3.00E-30	[illegible]	[illegible]
comp31322_c0_seq3.p1				
comp31322_c0_seq5.p1	sp|Q3TZI6|CCNJ_MOUSE_Cyclin-J_OS=Mus_musculus_GN=Ccnj_PE=2_SV=2	9.00E-23	[illegible]	[illegible]
comp31323_c0_seq2.p1	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	3.00E-14	[illegible]	[illegible]
comp31323_c0_seq4.p1	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	3.00E-14	[illegible]	[illegible]
comp31326_c0_seq1.p1	sp|Q5XVJ4|FAN1_ARATH_Fanconi-associated_nuclease_1_homolog_OS=Arabidopsis_thaliana_GN=At1g48360_PE=2_SV=2	2.00E-27	[illegible]	[illegible]
comp31327_c0_seq3.p1				
comp31327_c0_seq3.p2				
comp31327_c0_seq4.p1	sp|Q9VR91|HERC2_DROME_Probable_E3_ubiquitin-protein_ligase_HERC2_OS=Drosophila_melanogaster_GN=HERC2_PE=1_SV=3	2.00E-39	[illegible]	[illegible]
comp31328_c1_seq1.p1				
comp31328_c1_seq1.p2	sp|Q4V9P6|ADAL_DANRE_Adenosine_deaminase-like_protein_OS=Danio_rerio_GN=adal_PE=2_SV=1	4.00E-47	[illegible]	[illegible]
comp31329_c0_seq3.p1	sp|Q9WV87|NOX1_RAT_NADPH_oxidase_1_OS=Rattus_norvegicus_GN=Nox1_PE=2_SV=1	6.00E-13	[illegible]	[illegible]
comp31330_c0_seq1.p1				
comp31331_c0_seq2.p1				
comp31331_c0_seq3.p1				
comp31331_c0_seq6.p1				
comp31332_c0_seq1.p1				
comp31332_c0_seq12.p1				
comp31332_c0_seq5.p1				
comp31332_c0_seq7.p1				
comp31332_c0_seq9.p1				
comp31333_c0_seq2.p1				
comp31333_c0_seq4.p1				
comp31333_c0_seq5.p1				
comp31333_c0_seq5.p2	sp|Q6ZSG1|RN165_HUMAN_RING_finger_protein_165_OS=Homo_sapiens_GN=RNF165_PE=1_SV=1	1.00E-11	GO:0008270,GO:0046872	[illegible]
comp31333_c0_seq6.p1	sp|Q6ZSG1|RN165_HUMAN_RING_finger_protein_165_OS=Homo_sapiens_GN=RNF165_PE=1_SV=1	6.00E-11	GO:0008270,GO:0046872	[illegible]
comp31334_c0_seq1.p1				
comp31335_c0_seq4.p1				
comp31335_c0_seq4.p3				
comp31336_c0_seq4.p1				
comp31336_c0_seq6.p1				
comp31336_c0_seq7.p1				
comp31338_c0_seq10.p1				
comp31338_c0_seq10.p3	sp|P49620|DGKG_RAT_Diacylglycerol_kinase_gamma_OS=Rattus_norvegicus_GN=Dgkg_PE=2_SV=1	1.00E-25	[illegible]	[illegible]
comp31338_c0_seq10.p4	sp|P49620|DGKG_RAT_Diacylglycerol_kinase_gamma_OS=Rattus_norvegicus_GN=Dgkg_PE=2_SV=1	2.00E-27	[illegible]	[illegible]
comp31338_c0_seq12.p1				
comp31338_c0_seq27.p1				
comp31338_c0_seq29.p1				
comp31338_c0_seq29.p3	sp|P49620|DGKG_RAT_Diacylglycerol_kinase_gamma_OS=Rattus_norvegicus_GN=Dgkg_PE=2_SV=1	1.00E-25	[illegible]	[illegible]
comp31338_c0_seq29.p4	sp|P49620|DGKG_RAT_Diacylglycerol_kinase_gamma_OS=Rattus_norvegicus_GN=Dgkg_PE=2_SV=1	2.00E-27	[illegible]	[illegible]
comp31338_c0_seq33.p1				
comp31338_c0_seq33.p3				
comp31338_c0_seq34.p1				
comp31338_c0_seq34.p3	sp|Q54Q72|RDCII_DICDI_PH_domain-containing_rcdII_OS=Dictyostelium_discoideum_GN=rcdII_PE=2_SV=1	3.00E-13	[illegible]	[illegible]
comp31338_c0_seq51.p1				
comp31339_c0_seq1.p1				
comp31339_c0_seq11.p1	sp|Q08AW4|PKHM3_XENLA_Pleckstrin_homology_domain-containing_family_M_member_3_OS=Xenopus_laevis_GN=plekhm3_PE=2_SV=1	4.00E-18	[illegible]	[illegible]
comp31339_c0_seq11.p2				
comp31339_c0_seq11.p3				
comp31339_c0_seq15.p1				
comp31339_c0_seq18.p1	sp|Q08AW4|PKHM3_XENLA_Pleckstrin_homology_domain-containing_family_M_member_3_OS=Xenopus_laevis_GN=plekhm3_PE=2_SV=1	4.00E-18	[illegible]	[illegible]
comp31339_c0_seq18.p2				
comp31339_c0_seq18.p3				
comp31339_c0_seq2.p1	sp|Q08AW4|PKHM3_XENLA_Pleckstrin_homology_domain-containing_family_M_member_3_OS=Xenopus_laevis_GN=plekhm3_PE=2_SV=1	4.00E-18	[illegible]	[illegible]
comp31339_c0_seq2.p2				
comp31339_c0_seq2.p3				
comp31339_c0_seq5.p1	sp|Q08AW4|PKHM3_XENLA_Pleckstrin_homology_domain-containing_family_M_member_3_OS=Xenopus_laevis_GN=plekhm3_PE=2_SV=1	4.00E-18	[illegible]	[illegible]
comp31339_c0_seq5.p2				
comp31339_c0_seq5.p3				
comp31340_c0_seq2.p1	sp|P35251|RFC1_HUMAN_Replication_factor_C_subunit_1_OS=Homo_sapiens_GN=RFC1_PE=1_SV=4	4.00E-112	[illegible]	[illegible]
comp31342_c0_seq1.p1				
comp31342_c1_seq1.p1	sp|Q502K3|ANR52_DANRE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_C_OS=Danio_rerio_GN=ankrd52_PE=2_SV=1	1.00E-12	[illegible]	[illegible]
comp31342_c1_seq5.p1				
comp31342_c1_seq7.p1				
comp31342_c2_seq2.p2				
comp31342_c3_seq1.p1	sp|Q8CFK6|DEN1C_MOUSE_DENN_domain-containing_protein_1C_OS=Mus_musculus_GN=Dennd1c_PE=2_SV=1	3.00E-27	[illegible]	[illegible]
comp31342_c3_seq1.p2				
comp31343_c0_seq10.p1				
comp31343_c0_seq12.p1	sp|Q5RCE6|RL1D1_PONAB_Ribosomal_L1_domain-containing_protein_1_OS=Pongo_abelii_GN=RSL1D1_PE=2_SV=2	6.00E-19	[illegible]	[illegible]
comp31343_c0_seq7.p1				
comp31343_c0_seq8.p1				
comp31344_c0_seq1.p1	sp|Q6P158|DHX57_HUMAN_Putative_ATP-dependent_RNA_helicase_DHX57_OS=Homo_sapiens_GN=DHX57_PE=1_SV=2	1.00E-104	[illegible]	[illegible]
comp31344_c0_seq2.p1				
comp31344_c0_seq3.p1	sp|Q6P158|DHX57_HUMAN_Putative_ATP-dependent_RNA_helicase_DHX57_OS=Homo_sapiens_GN=DHX57_PE=1_SV=2	1.00E-49	[illegible]	[illegible]
comp31344_c1_seq1.p1				
comp31344_c1_seq1.p5				
comp31344_c1_seq2.p1				
comp31345_c0_seq1.p1				
comp31345_c0_seq1.p2				
comp31345_c0_seq1.p4				
comp31346_c0_seq3.p1	sp|Q9HZP7|ETFA_PSEAE_Electron_transfer_flavoprotein_subunit_alpha_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=etfA_PE=3_SV=1	7.00E-113	[illegible]	[illegible]
comp31346_c0_seq5.p1				
comp31346_c0_seq7.p1				
comp31347_c0_seq11.p1				
comp31347_c0_seq11.p11				
comp31347_c0_seq11.p5				
comp31347_c0_seq11.p6				
comp31347_c0_seq13.p1				
comp31347_c0_seq19.p2				
comp31347_c0_seq22.p1				
comp31347_c0_seq22.p4				
comp31347_c0_seq24.p2				
comp31347_c0_seq3.p1				
comp31347_c0_seq4.p4				
comp31347_c0_seq5.p1				
comp31347_c0_seq5.p5				
comp31347_c0_seq8.p1				
comp31347_c0_seq9.p1				
comp31349_c0_seq1.p1	sp|Q9DBT4|ENTP4_MOUSE_Ectonucleoside_triphosphate_diphosphohydrolase_4_OS=Mus_musculus_GN=Entpd4_PE=2_SV=1	9.00E-31	[illegible]	[illegible]
comp31349_c0_seq2.p1	sp|O93295|ENTP8_CHICK_Ectonucleoside_triphosphate_diphosphohydrolase_8_OS=Gallus_gallus_GN=ENTPD8_PE=1_SV=1	8.00E-11	[illegible]	[illegible]
comp31349_c1_seq1.p1	sp|Q8GW20|Y5390_ARATH_Uncharacterized_protein_At5g03900,_chloroplastic_OS=Arabidopsis_thaliana_GN=At5g03900_PE=1_SV=2	1.00E-52	[illegible]	[illegible]
comp31350_c0_seq10.p1	sp|Q8L3Z8|FZR2_ARATH_Protein_FIZZY-RELATED_2_OS=Arabidopsis_thaliana_GN=FZR2_PE=1_SV=1	2.00E-178	[illegible]	[illegible]
comp31350_c0_seq10.p2				
comp31350_c0_seq3.p1	sp|Q8L3Z8|FZR2_ARATH_Protein_FIZZY-RELATED_2_OS=Arabidopsis_thaliana_GN=FZR2_PE=1_SV=1	2.00E-124	[illegible]	[illegible]
comp31350_c0_seq4.p1	sp|Q8L3Z8|FZR2_ARATH_Protein_FIZZY-RELATED_2_OS=Arabidopsis_thaliana_GN=FZR2_PE=1_SV=1	4.00E-90	[illegible]	[illegible]
comp31350_c0_seq8.p1				
comp31350_c0_seq8.p2	sp|Q8L3Z8|FZR2_ARATH_Protein_FIZZY-RELATED_2_OS=Arabidopsis_thaliana_GN=FZR2_PE=1_SV=1	8.00E-144	[illegible]	[illegible]
comp31350_c0_seq8.p4	sp|Q9R1K5|FZR_MOUSE_Fizzy-related_protein_homolog_OS=Mus_musculus_GN=Fzr1_PE=1_SV=1	1.00E-28	[illegible]	[illegible]
comp31351_c0_seq2.p1				
comp31351_c0_seq2.p2				
comp31351_c0_seq3.p1				
comp31352_c1_seq1.p1	sp|Q6ZUT9|DEN5B_HUMAN_DENN_domain-containing_protein_5B_OS=Homo_sapiens_GN=DENND5B_PE=1_SV=2	3.00E-30	[illegible]	[illegible]
comp31353_c0_seq1.p1				
comp31353_c0_seq2.p1				
comp31354_c1_seq2.p1				
comp31355_c0_seq2.p1				
comp31355_c0_seq4.p1				
comp31356_c0_seq1.p1	sp|Q50KB1|SEP2_EMIHU_Protein_disulfide-isomerase-like_protein_EhSep2_OS=Emiliania_huxleyi_GN=SEP2_PE=1_SV=2	3.00E-38	[illegible]	[illegible]
comp31356_c0_seq2.p1	sp|Q50KB1|SEP2_EMIHU_Protein_disulfide-isomerase-like_protein_EhSep2_OS=Emiliania_huxleyi_GN=SEP2_PE=1_SV=2	4.00E-30	[illegible]	[illegible]
comp31357_c0_seq15.p1				
comp31357_c0_seq2.p1				
comp31357_c0_seq4.p1				
comp31357_c0_seq5.p1				
comp31357_c0_seq9.p1				
comp31358_c0_seq2.p1				
comp31360_c0_seq2.p2				
comp31360_c0_seq7.p1				
comp31360_c0_seq8.p1				
comp31361_c0_seq5.p1				
comp31362_c0_seq1.p1				
comp31363_c0_seq3.p1	sp|A7HVV8|DNLJ_PARL1_DNA_ligase_OS=Parvibaculum_lavamentivorans_(strain_DS-1_/_DSM_13023_/_NCIMB_13966)_GN=ligA_PE=3_SV=1	8.00E-116	[illegible]	[illegible]
comp31363_c0_seq4.p2				
comp31363_c0_seq5.p1				
comp31366_c0_seq2.p1	sp|Q7Z4L5|TT21B_HUMAN_Tetratricopeptide_repeat_protein_21B_OS=Homo_sapiens_GN=TTC21B_PE=1_SV=2	2.00E-146	[illegible]	[illegible]
comp31367_c0_seq1.p1				
comp31367_c0_seq4.p1				
comp31367_c1_seq1.p1				
comp31368_c0_seq3.p1				
comp31368_c0_seq4.p1				
comp31370_c0_seq1.p1	sp|O13728|AIN1_SCHPO_Alpha-actinin-like_protein_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ain1_PE=2_SV=1	9.00E-27	[illegible]	[illegible]
comp31370_c0_seq1.p3				
comp31371_c0_seq1.p1				
comp31371_c0_seq2.p1				
comp31371_c0_seq4.p1				
comp31371_c0_seq5.p1				
comp31371_c0_seq8.p1				
comp31372_c0_seq10.p1				
comp31372_c0_seq11.p1				
comp31372_c0_seq3.p1				
comp31372_c0_seq5.p1				
comp31372_c0_seq6.p1				
comp31372_c0_seq9.p2	sp|Q54JC2|Y2881_DICDI_Uncharacterized_protein_DDB_G0288155_OS=Dictyostelium_discoideum_GN=DDB_G0288155_PE=1_SV=1	1.00E-22	GO:0044351	[illegible]
comp31373_c0_seq2.p2	sp|O13959|RBX1_SCHPO_RING-box_protein_pip1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=pip1_PE=1_SV=2	1.00E-34	[illegible]	[illegible]
comp31375_c0_seq11.p1				
comp31375_c0_seq12.p1	sp|Q5TZA2|CROCC_HUMAN_Rootletin_OS=Homo_sapiens_GN=CROCC_PE=1_SV=1	7.00E-12	[illegible]	[illegible]
comp31375_c0_seq12.p4				
comp31375_c0_seq14.p1	sp|Q9HHM7|SPH1_HALSA_Smc-like_protein_Sph1_OS=Halobacterium_salinarium_(strain_ATCC_700922_/_JCM_11081_/_NRC-1)_GN=sph1_PE=3_SV=1	2.00E-11	GO:0005737,GO:0005737	[illegible]
comp31375_c0_seq14.p2				
comp31375_c0_seq8.p1	sp|Q5TZA2|CROCC_HUMAN_Rootletin_OS=Homo_sapiens_GN=CROCC_PE=1_SV=1	1.00E-11	[illegible]	[illegible]
comp31375_c0_seq9.p1				
comp31375_c0_seq9.p2	sp|Q9HHM7|SPH1_HALSA_Smc-like_protein_Sph1_OS=Halobacterium_salinarium_(strain_ATCC_700922_/_JCM_11081_/_NRC-1)_GN=sph1_PE=3_SV=1	1.00E-12	GO:0005737,GO:0005737	[illegible]
comp31375_c0_seq9.p4				
comp31376_c0_seq2.p2				
comp31377_c0_seq2.p1	sp|Q9Y6F1|PARP3_HUMAN_Poly_[ADP-ribose]_polymerase_3_OS=Homo_sapiens_GN=PARP3_PE=1_SV=3	4.00E-141	[illegible]	[illegible]
comp31377_c1_seq2.p1	sp|Q6ERS0|CIPKR_ORYSJ_Putative_CBL-interacting_protein_kinase_27_OS=Oryza_sativa_subsp._japonica_GN=CIPK27_PE=3_SV=1	2.00E-22	[illegible]	[illegible]
comp31377_c1_seq3.p1	sp|Q6ERS0|CIPKR_ORYSJ_Putative_CBL-interacting_protein_kinase_27_OS=Oryza_sativa_subsp._japonica_GN=CIPK27_PE=3_SV=1	2.00E-22	[illegible]	[illegible]
comp31377_c1_seq4.p1				
comp31378_c0_seq1.p1				
comp31378_c0_seq2.p1				
comp31378_c0_seq4.p1				
comp31379_c0_seq14.p1	sp|Q9D9B4|CJ011_MOUSE_Leucine-rich_repeat-containing_protein_C10orf11_homolog_OS=Mus_musculus_PE=2_SV=1	6.00E-28	[illegible]	[illegible]
comp31379_c0_seq2.p1	sp|O95149|SPN1_HUMAN_Snurportin-1_OS=Homo_sapiens_GN=SNUPN_PE=1_SV=1	2.00E-39	[illegible]	[illegible]
comp31380_c1_seq1.p2				
comp31380_c1_seq1.p3				
comp31380_c1_seq1.p4				
comp31380_c1_seq2.p1	sp|Q96321|IMA1_ARATH_Importin_subunit_alpha-1_OS=Arabidopsis_thaliana_GN=KAP1_PE=1_SV=2	2.00E-82	[illegible]	[illegible]
comp31380_c2_seq1.p1	sp|Q8K0V4|CNOT3_MOUSE_CCR4-NOT_transcription_complex_subunit_3_OS=Mus_musculus_GN=Cnot3_PE=1_SV=1	2.00E-47	[illegible]	[illegible]
comp31381_c0_seq1.p1	sp|Q5BQN8|CENPJ_PANTR_Centromere_protein_J_OS=Pan_troglodytes_GN=CENPJ_PE=2_SV=1	2.00E-20	[illegible]	[illegible]
comp31381_c0_seq2.p1				
comp31381_c0_seq4.p1				
comp31381_c0_seq5.p1	sp|Q5BQN8|CENPJ_PANTR_Centromere_protein_J_OS=Pan_troglodytes_GN=CENPJ_PE=2_SV=1	2.00E-20	[illegible]	[illegible]
comp31382_c0_seq14.p1				
comp31382_c0_seq5.p1	sp|P28367|RF2_BACSU_Peptide_chain_release_factor_2_OS=Bacillus_subtilis_GN=prfB_PE=3_SV=2	1.00E-91	[illegible]	[illegible]
comp31382_c0_seq9.p1	sp|P28367|RF2_BACSU_Peptide_chain_release_factor_2_OS=Bacillus_subtilis_GN=prfB_PE=3_SV=2	1.00E-91	[illegible]	[illegible]
comp31382_c0_seq9.p3				
comp31383_c0_seq1.p2				
comp31383_c0_seq3.p1				
comp31383_c0_seq6.p1				
comp31384_c0_seq1.p1	sp|Q04942|AFSQ1_STRCO_Transcriptional_regulatory_protein_AfsQ1_OS=Streptomyces_coelicolor_GN=afsQ1_PE=1_SV=2	8.00E-14	[illegible]	[illegible]
comp31384_c0_seq2.p1	sp|Q04942|AFSQ1_STRCO_Transcriptional_regulatory_protein_AfsQ1_OS=Streptomyces_coelicolor_GN=afsQ1_PE=1_SV=2	8.00E-14	[illegible]	[illegible]
comp31384_c1_seq1.p1				
comp31384_c1_seq2.p1				
comp31385_c0_seq1.p1	sp|Q9CYX7|RRP15_MOUSE_RRP15-like_protein_OS=Mus_musculus_GN=Rrp15_PE=2_SV=2	1.00E-11	[illegible]	[illegible]
comp31385_c0_seq2.p1				
comp31385_c0_seq3.p1				
comp31387_c0_seq14.p1	sp|Q9Z2Z6|MCAT_MOUSE_Mitochondrial_carnitine/acylcarnitine_carrier_protein_OS=Mus_musculus_GN=Slc25a20_PE=1_SV=1	7.00E-75	[illegible]	[illegible]
comp31387_c0_seq15.p2				
comp31387_c0_seq18.p1	sp|Q9Z2Z6|MCAT_MOUSE_Mitochondrial_carnitine/acylcarnitine_carrier_protein_OS=Mus_musculus_GN=Slc25a20_PE=1_SV=1	4.00E-14	[illegible]	[illegible]
comp31387_c0_seq3.p1	sp|Q9VQG4|COLT_DROME_Congested-like_trachea_protein_OS=Drosophila_melanogaster_GN=colt_PE=2_SV=1	3.00E-39	[illegible]	[illegible]
comp31387_c0_seq5.p1	sp|Q27257|DIF1_CAEEL_Protein_dif-1_OS=Caenorhabditis_elegans_GN=dif-1_PE=2_SV=1	3.00E-42	[illegible]	[illegible]
comp31387_c0_seq5.p2	sp|Q9Z2Z6|MCAT_MOUSE_Mitochondrial_carnitine/acylcarnitine_carrier_protein_OS=Mus_musculus_GN=Slc25a20_PE=1_SV=1	4.00E-14	[illegible]	[illegible]
comp31388_c0_seq2.p1				
comp31389_c0_seq1.p1				
comp31389_c0_seq3.p1				
comp31389_c0_seq5.p1				
comp31390_c0_seq2.p1				
comp31391_c0_seq1.p1				
comp31391_c0_seq2.p1				
comp31391_c0_seq3.p1				
comp31391_c0_seq4.p1				
comp31392_c0_seq3.p1	sp|Q8BW96|KCC1D_MOUSE_Calcium/calmodulin-dependent_protein_kinase_type_1D_OS=Mus_musculus_GN=Camk1d_PE=1_SV=2	2.00E-49	[illegible]	[illegible]
comp31392_c0_seq3.p2	sp|Q9T042|PDI54_ARATH_Protein_disulfide-isomerase_5-4_OS=Arabidopsis_thaliana_GN=PDIL5-4_PE=2_SV=1	4.00E-74	[illegible]	[illegible]
comp31393_c0_seq1.p1	sp|Q02357|ANK1_MOUSE_Ankyrin-1_OS=Mus_musculus_GN=Ank1_PE=1_SV=2	3.00E-32	[illegible]	[illegible]
comp31394_c0_seq4.p2				
comp31394_c0_seq4.p3				
comp31394_c0_seq5.p1				
comp31394_c0_seq6.p1	sp|Q9ZGE2|TILS_HELMO_tRNA(Ile)-lysidine_synthase_OS=Heliobacillus_mobilis_GN=tilS_PE=3_SV=1	3.00E-28	[illegible]	[illegible]
comp31395_c0_seq1.p1	sp|Q7Z401|MYCPP_HUMAN_C-myc_promoter-binding_protein_OS=Homo_sapiens_GN=DENND4A_PE=1_SV=2	3.00E-21	[illegible]	[illegible]
comp31395_c0_seq17.p1	sp|Q8RY89|PI5K8_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_8_OS=Arabidopsis_thaliana_GN=PIP5K8_PE=2_SV=1	5.00E-34	[illegible]	[illegible]
comp31395_c0_seq18.p1	sp|Q8RY89|PI5K8_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_8_OS=Arabidopsis_thaliana_GN=PIP5K8_PE=2_SV=1	5.00E-34	[illegible]	[illegible]
comp31396_c0_seq1.p1	sp|Q9FG38|SNX1_ARATH_Sorting_nexin_1_OS=Arabidopsis_thaliana_GN=SNX1_PE=1_SV=1	5.00E-38	[illegible]	[illegible]
comp31396_c0_seq10.p1	sp|Q9FG38|SNX1_ARATH_Sorting_nexin_1_OS=Arabidopsis_thaliana_GN=SNX1_PE=1_SV=1	2.00E-39	[illegible]	[illegible]
comp31396_c0_seq4.p1	sp|Q9FG38|SNX1_ARATH_Sorting_nexin_1_OS=Arabidopsis_thaliana_GN=SNX1_PE=1_SV=1	9.00E-32	[illegible]	[illegible]
comp31396_c0_seq4.p2				
comp31397_c0_seq2.p1				
comp31397_c0_seq3.p1				
comp31397_c0_seq6.p1				
comp31397_c1_seq1.p1	sp|Q9D8W5|PSD12_MOUSE_26S_proteasome_non-ATPase_regulatory_subunit_12_OS=Mus_musculus_GN=Psmd12_PE=2_SV=4	3.00E-113	[illegible]	[illegible]
comp31397_c4_seq1.p1	sp|P30124|HEM2_PEA_Delta-aminolevulinic_acid_dehydratase,_chloroplastic_(Fragment)_OS=Pisum_sativum_GN=HEMB_PE=1_SV=1	8.00E-129	[illegible]	[illegible]
comp31398_c0_seq1.p2				
comp31399_c0_seq1.p1	sp|Q9VX91|UBR1_DROME_E3_ubiquitin-protein_ligase_UBR1_OS=Drosophila_melanogaster_GN=UBR1_PE=2_SV=2	2.00E-17	[illegible]	[illegible]
comp31399_c0_seq3.p1				
comp31399_c0_seq3.p2	sp|Q9VX91|UBR1_DROME_E3_ubiquitin-protein_ligase_UBR1_OS=Drosophila_melanogaster_GN=UBR1_PE=2_SV=2	4.00E-18	[illegible]	[illegible]
comp31399_c1_seq1.p1				
comp31400_c0_seq1.p1				
comp31400_c1_seq1.p1				
comp31400_c1_seq5.p1	sp|Q99ME2|WDR6_MOUSE_WD_repeat-containing_protein_6_OS=Mus_musculus_GN=Wdr6_PE=2_SV=1	3.00E-13	[illegible]	[illegible]
comp31401_c0_seq1.p1				
comp31401_c0_seq6.p1				
comp31401_c0_seq6.p2				
comp31403_c0_seq2.p1				
comp31406_c1_seq2.p1				
comp31407_c0_seq1.p1	sp|O15905|SODF_BABBO_Superoxide_dismutase_[Fe]_OS=Babesia_bovis_GN=SODB_PE=2_SV=1	2.00E-73	[illegible]	[illegible]
comp31408_c0_seq1.p1				
comp31409_c1_seq12.p1	sp|Q69ZN7|MYOF_MOUSE_Myoferlin_OS=Mus_musculus_GN=Myof_PE=1_SV=2	1.00E-20	[illegible]	[illegible]
comp31409_c1_seq13.p1	sp|Q69ZN7|MYOF_MOUSE_Myoferlin_OS=Mus_musculus_GN=Myof_PE=1_SV=2	1.00E-20	[illegible]	[illegible]
comp31409_c1_seq15.p1	sp|Q9ESF1|OTOF_MOUSE_Otoferlin_OS=Mus_musculus_GN=Otof_PE=1_SV=1	3.00E-32	[illegible]	[illegible]
comp31409_c1_seq7.p1	sp|Q9ESF1|OTOF_MOUSE_Otoferlin_OS=Mus_musculus_GN=Otof_PE=1_SV=1	3.00E-32	[illegible]	[illegible]
comp31409_c1_seq9.p1	sp|Q5SPC5|OTOF_DANRE_Otoferlin_OS=Danio_rerio_GN=otof_PE=3_SV=1	3.00E-26	[illegible]	[illegible]
comp31409_c1_seq9.p2	sp|B3DLH6|MYOF_XENTR_Myoferlin_OS=Xenopus_tropicalis_GN=myof_PE=2_SV=1	2.00E-16	[illegible]	[illegible]
comp31410_c0_seq2.p1	sp|Q55909|Y305_SYNY3_TVP38/TMEM64_family_membrane_protein_slr0305_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0305_PE=3_SV=1	3.00E-36	[illegible]	[illegible]
comp31410_c0_seq3.p1	sp|Q55909|Y305_SYNY3_TVP38/TMEM64_family_membrane_protein_slr0305_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0305_PE=3_SV=1	4.00E-19	[illegible]	[illegible]
comp31413_c0_seq1.p1	sp|P42620|YQJG_ECOLI_Uncharacterized_protein_yqjG_OS=Escherichia_coli_(strain_K12)_GN=yqjG_PE=3_SV=1	1.00E-73	GO:0016491,GO:0055114	[illegible]
comp31413_c0_seq6.p1	sp|P42620|YQJG_ECOLI_Uncharacterized_protein_yqjG_OS=Escherichia_coli_(strain_K12)_GN=yqjG_PE=3_SV=1	4.00E-74	GO:0016491,GO:0055114	[illegible]
comp31413_c0_seq7.p1				
comp31414_c0_seq1.p1				
comp31415_c0_seq1.p1				
comp31415_c0_seq2.p1	sp|Q2KID2|NTHL1_BOVIN_Endonuclease_III-like_protein_1_OS=Bos_taurus_GN=NTHL1_PE=2_SV=1	3.00E-34	[illegible]	[illegible]
comp31415_c0_seq2.p3				
comp31415_c0_seq4.p1	sp|Q2KID2|NTHL1_BOVIN_Endonuclease_III-like_protein_1_OS=Bos_taurus_GN=NTHL1_PE=2_SV=1	3.00E-25	[illegible]	[illegible]
comp31415_c0_seq4.p4				
comp31416_c0_seq1.p1	sp|Q05609|CTR1_ARATH_Serine/threonine-protein_kinase_CTR1_OS=Arabidopsis_thaliana_GN=CTR1_PE=1_SV=1	1.00E-29	[illegible]	[illegible]
comp31416_c0_seq3.p1				
comp31417_c0_seq1.p1	sp|Q9XT50|ATP7B_SHEEP_Copper-transporting_ATPase_2_OS=Ovis_aries_GN=ATP7B_PE=2_SV=1	6.00E-15	[illegible]	[illegible]
comp31417_c0_seq12.p1	sp|Q9SH30|HMA5_ARATH_Putative_copper-transporting_ATPase_HMA5_OS=Arabidopsis_thaliana_GN=HMA5_PE=2_SV=2	3.00E-101	[illegible]	[illegible]
comp31417_c0_seq12.p3	sp|Q64430|ATP7A_MOUSE_Copper-transporting_ATPase_1_OS=Mus_musculus_GN=Atp7a_PE=1_SV=3	3.00E-35	[illegible]	[illegible]
comp31417_c0_seq14.p1				
comp31417_c0_seq3.p1	sp|P77894|CTPV_MYCTU_Probable_cation-transporting_ATPase_V_OS=Mycobacterium_tuberculosis_GN=ctpV_PE=3_SV=1	3.00E-29		
comp31417_c0_seq8.p1	sp|Q9SH30|HMA5_ARATH_Putative_copper-transporting_ATPase_HMA5_OS=Arabidopsis_thaliana_GN=HMA5_PE=2_SV=2	3.00E-171	[illegible]	[illegible]
comp31417_c0_seq8.p3				
comp31417_c0_seq9.p1				
comp31418_c1_seq2.p1				
comp31418_c1_seq4.p1				
comp31418_c1_seq5.p1				
comp31421_c0_seq1.p1	sp|O35969|GAMT_MOUSE_Guanidinoacetate_N-methyltransferase_OS=Mus_musculus_GN=Gamt_PE=1_SV=1	7.00E-14	[illegible]	[illegible]
comp31421_c0_seq1.p2				
comp31421_c0_seq6.p1				
comp31422_c0_seq1.p1				
comp31422_c0_seq3.p1				
comp31423_c0_seq3.p1				
comp31424_c0_seq1.p1				

comp31424_c0_seq4.p1		
comp31424_c0_seq4.p9		
comp31424_c0_seq6.p1		
comp31425_c0_seq3.p1		
comp31426_c1_seq11.p1	sp|P50027|DNAJH_SYNY3_DnaJ-like_protein_slr0093_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0093_PE=4_SV=1	2.00E-16
comp31426_c1_seq3.p1		
comp31426_c1_seq4.p1	sp|D7UQM5|AURK_ASTPE_Aurora_kinase_OS=Asterina_pectinifera_GN=aur_PE=1_SV=1	2.00E-85
comp31426_c1_seq7.p1		
comp31426_c1_seq8.p1		
comp31426_c1_seq9.p1		
comp31427_c0_seq4.p1		
comp31427_c0_seq4.p2		
comp31428_c0_seq2.p1	sp|P84104|SRSF3_MOUSE_Serine/arginine-rich_splicing_factor_3_OS=Mus_musculus_GN=Srsf3_PE=1_SV=1	6.00E-20
comp31428_c0_seq4.p1	sp|P84104|SRSF3_MOUSE_Serine/arginine-rich_splicing_factor_3_OS=Mus_musculus_GN=Srsf3_PE=1_SV=1	3.00E-19
comp31428_c0_seq6.p1	sp|P84104|SRSF3_MOUSE_Serine/arginine-rich_splicing_factor_3_OS=Mus_musculus_GN=Srsf3_PE=1_SV=1	6.00E-20
comp31428_c0_seq6.p2		
comp31429_c0_seq1.p1	sp|Q0WVM4|Y2239_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At2g23950_OS=Arabidopsis_thaliana_GN=At2g23950_PE=2_SV=1	2.00E-11
comp31429_c0_seq2.p1	sp|Q8VZG8|Y4885_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At4g08850_OS=Arabidopsis_thaliana_GN=At4g08850_PE=1_SV=3	1.00E-16
comp31429_c0_seq2.p2		
comp31429_c0_seq4.p1	sp|Q8VZG8|Y4885_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At4g08850_OS=Arabidopsis_thaliana_GN=At4g08850_PE=1_SV=3	1.00E-16
comp31429_c0_seq4.p2		
comp31429_c0_seq7.p1	sp|Q0WVM4|Y2239_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At2g23950_OS=Arabidopsis_thaliana_GN=At2g23950_PE=2_SV=1	2.00E-11
comp31429_c0_seq8.p1	sp|Q8VZG8|Y4885_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At4g08850_OS=Arabidopsis_thaliana_GN=At4g08850_PE=1_SV=3	1.00E-16
comp31429_c0_seq8.p2		
comp31429_c0_seq9.p1	sp|Q8VZG8|Y4885_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At4g08850_OS=Arabidopsis_thaliana_GN=At4g08850_PE=1_SV=3	1.00E-16
comp31429_c0_seq9.p2		
comp31430_c0_seq5.p1		
comp31431_c0_seq1.p1	sp|C0LGW6|ERL1_ARATH_LRR_receptor-like_serine/threonine-protein_kinase_ERL1_OS=Arabidopsis_thaliana_GN=ERL1_PE=2_SV=1	2.00E-26
comp31432_c0_seq2.p1		
comp31432_c0_seq2.p3		
comp31432_c0_seq3.p1		
comp31434_c0_seq3.p1		
comp31434_c0_seq3.p2		
comp31435_c0_seq2.p1		
comp31435_c0_seq2.p4		
comp31435_c0_seq4.p1	sp|A7SWH1|PESC_NEMVE_Pescadillo_homolog_OS=Nematostella_vectensis_GN=v1g194255_PE=3_SV=1	2.00E-78
comp31436_c0_seq2.p1		
comp31436_c0_seq3.p1		
comp31439_c0_seq2.p1	sp|Q7TSG1|CE120_MOUSE_Centrosomal_protein_of_120_kDa_OS=Mus_musculus_GN=Cep120_PE=1_SV=1	1.00E-20
comp31439_c0_seq3.p1	sp|Q51371|ALGG_PSEAE_Poly(beta-D-mannuronate)_C5_epimerase_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=algG_PE=1_SV=1	7.00E-16
comp31439_c0_seq4.p1		
comp31439_c0_seq6.p1	sp|Q63862|MYH11_RAT_Myosin-11_(Fragments)_OS=Rattus_norvegicus_GN=Myh11_PE=2_SV=3	2.00E-16
comp31440_c0_seq2.p1		
comp31440_c0_seq9.p1		
comp31441_c0_seq1.p1		
comp31441_c0_seq2.p1		
comp31441_c0_seq3.p1		
comp31441_c0_seq4.p1		
comp31442_c1_seq2.p1		
comp31442_c1_seq3.p1		
comp31443_c0_seq2.p1	sp|Q9ZAE9|ACBC_ACTS5_2-epi-5-epi-valiolone_synthase_OS=Actinoplanes_sp._(strain_ATCC_31044_/_CBS_674.73_/_SE50/110)_GN=acbC_PE=3_SV=3	4.00E-85
comp31444_c0_seq3.p1		
comp31444_c0_seq5.p1		
comp31444_c0_seq6.p1		
comp31446_c0_seq1.p1		
comp31447_c0_seq3.p3		
comp31448_c0_seq1.p1	sp|Q2U2J6|PRP5_ASPOR_Pre-mRNA-processing_ATP-dependent_RNA_helicase_prp5_OS=Aspergillus_oryzae_(strain_ATCC_42149_/_RIB_40)_GN=prp5_PE=3_SV=1	2.00E-11
comp31448_c0_seq1.p2	sp|Q84UQ1|RH42_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_42_OS=Oryza_sativa_subsp._japonica_GN=Os08g0159900_PE=2_SV=1	4.00E-180
comp31448_c0_seq1.p3		
comp31449_c0_seq1.p1		
comp31450_c0_seq10.p1		
comp31450_c0_seq10.p2	sp|Q56232|AAT_THET8_Aspartate_aminotransferase_OS=Thermus_thermophilus_(strain_HB8_/_ATCC_27634_/_DSM_579)_GN=aspC_PE=1_SV=1	1.00E-53
comp31450_c0_seq12.p1		
comp31450_c0_seq5.p1		
comp31450_c0_seq5.p2	sp|Q56232|AAT_THET8_Aspartate_aminotransferase_OS=Thermus_thermophilus_(strain_HB8_/_ATCC_27634_/_DSM_579)_GN=aspC_PE=1_SV=1	5.00E-48
comp31451_c0_seq1.p1		
comp31451_c0_seq2.p1		
comp31452_c0_seq1.p1	sp|Q55C58|VPS16_DICDI_Vacuolar_protein_sorting-associated_protein_16_homolog_OS=Dictyostelium_discoideum_GN=vps16_PE=3_SV=2	1.00E-121
comp31453_c0_seq11.p1	sp|P21885|SPEA_BACSU_Arginine_decarboxylase_OS=Bacillus_subtilis_GN=speA_PE=1_SV=2	3.00E-56
comp31453_c0_seq11.p2		
comp31453_c0_seq11.p3		
comp31453_c0_seq12.p1	sp|Q02357|ANK1_MOUSE_Ankyrin-1_OS=Mus_musculus_GN=Ank1_PE=1_SV=2	4.00E-11
comp31453_c0_seq2.p1		
comp31453_c0_seq5.p1		
comp31453_c0_seq5.p2	sp|P21885|SPEA_BACSU_Arginine_decarboxylase_OS=Bacillus_subtilis_GN=speA_PE=1_SV=2	3.00E-56
comp31453_c0_seq6.p1		
comp31455_c0_seq2.p1	sp|Q9SCW4|HFB2A_ARATH_Heat_stress_transcription_factor_B-2a_OS=Arabidopsis_thaliana_GN=HSFB2A_PE=2_SV=1	2.00E-14
comp31456_c0_seq1.p1	sp|P28912|YHHI_ECOLI_H_repeat-associated_protein_yhhI_OS=Escherichia_coli_(strain_K12)_GN=yhhI_PE=3_SV=1	0
comp31457_c0_seq2.p1	sp|Q02212|COX2_PHYME_Cytochrome_c_oxidase_subunit_2_OS=Phytophthora_megasperma_GN=COX2_PE=3_SV=1	3.00E-42
comp31457_c0_seq4.p1	sp|O23657|RABC1_ARATH_Ras-related_protein_RABC1_OS=Arabidopsis_thaliana_GN=RABC1_PE=2_SV=1	6.00E-68
comp31457_c0_seq5.p1	sp|P26856|COX1_MARPO_Cytochrome_c_oxidase_subunit_1_OS=Marchantia_polymorpha_GN=COX1_PE=3_SV=2	0
comp31458_c1_seq1.p2		
comp31458_c1_seq4.p1		
comp31458_c2_seq11.p2		
comp31458_c2_seq14.p1		
comp31458_c2_seq14.p4		
comp31458_c2_seq15.p1		
comp31458_c2_seq15.p2	sp|P0AD12|YEEZ_ECOLI_Protein_yeeZ_OS=Escherichia_coli_(strain_K12)_GN=yeeZ_PE=1_SV=1	3.00E-15
comp31458_c2_seq2.p1	sp|P00582|DPO1_ECOLI_DNA_polymerase_I_OS=Escherichia_coli_(strain_K12)_GN=polA_PE=1_SV=1	1.00E-39
comp31458_c2_seq3.p2		
comp31458_c2_seq4.p2		
comp31458_c2_seq5.p2		
comp31458_c2_seq8.p1		
comp31458_c3_seq1.p1		
comp31458_c3_seq3.p2		
comp31458_c3_seq4.p1		
comp31459_c0_seq2.p1		
comp31459_c0_seq3.p1		
comp31459_c0_seq4.p1		
comp31459_c1_seq2.p1		
comp31459_c1_seq8.p2		
comp31460_c0_seq4.p1	sp|Q9FJR0|RENT1_ARATH_Regulator_of_nonsense_transcripts_1_homolog_OS=Arabidopsis_thaliana_GN=UPF1_PE=1_SV=2	3.00E-42
comp31460_c1_seq1.p1		
comp31461_c0_seq1.p1		
comp31463_c0_seq1.p1		
comp31463_c0_seq2.p1		
comp31463_c0_seq3.p1		
comp31463_c0_seq3.p3		
comp31464_c0_seq2.p1	sp|O77676|KGP1_RABIT_cGMP-dependent_protein_kinase_1_OS=Oryctolagus_cuniculus_GN=PRKG1_PE=1_SV=3	2.00E-56
comp31465_c0_seq4.p1	sp|P87149|MRS2_SCHPO_Mitochondrial_inner_membrane_magnesium_transporter_mrs2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=mrs2_PE=2_SV=1	9.00E-15
comp31465_c0_seq4.p2		
comp31465_c0_seq4.p3	sp|Q7TML3|S35F2_MOUSE_Solute_carrier_family_35_member_F2_OS=Mus_musculus_GN=Slc35f2_PE=2_SV=2	1.00E-27
comp31466_c0_seq2.p1	sp|Q6AXL5|HBAP1_DANRE_HSPB1-associated_protein_1_homolog_OS=Danio_rerio_GN=hspbap1_PE=2_SV=2	1.00E-64
comp31466_c0_seq2.p2		
comp31468_c0_seq1.p1	sp|Q54E34|Y6398_DICDI_Probable_protein_kinase_DDB_G0291842_OS=Dictyostelium_discoideum_GN=DDB_G0291842_PE=3_SV=1	7.00E-47
comp31469_c0_seq11.p1	sp|Q9ASR4|BCAL2_ARATH_Branched-chain-amino-acid_aminotransferase-like_protein_2_OS=Arabidopsis_thaliana_GN=At5g27410_PE=2_SV=1	4.00E-157
comp31469_c0_seq12.p1	sp|Q9ASR4|BCAL2_ARATH_Branched-chain-amino-acid_aminotransferase-like_protein_2_OS=Arabidopsis_thaliana_GN=At5g27410_PE=2_SV=1	1.00E-131
comp31469_c0_seq14.p1	sp|Q9ASR4|BCAL2_ARATH_Branched-chain-amino-acid_aminotransferase-like_protein_2_OS=Arabidopsis_thaliana_GN=At5g27410_PE=2_SV=1	1.00E-127
comp31469_c0_seq17.p1	sp|Q9ASR4|BCAL2_ARATH_Branched-chain-amino-acid_aminotransferase-like_protein_2_OS=Arabidopsis_thaliana_GN=At5g27410_PE=2_SV=1	3.00E-161
comp31469_c0_seq18.p1	sp|B0JQT7|LEPA_MICAN_Elongation_factor_4_OS=Microcystis_aeruginosa_(strain_NIES-843)_GN=lepA_PE=3_SV=1	0
comp31469_c0_seq4.p1		
comp31469_c0_seq4.p2	sp|P51566|AFC1_ARATH_Serine/threonine-protein_kinase_AFC1_OS=Arabidopsis_thaliana_GN=AFC1_PE=2_SV=2	3.00E-13
comp31469_c0_seq8.p1	sp|Q9ASR4|BCAL2_ARATH_Branched-chain-amino-acid_aminotransferase-like_protein_2_OS=Arabidopsis_thaliana_GN=At5g27410_PE=2_SV=1	2.00E-15
comp31470_c0_seq1.p3		
comp31470_c0_seq4.p2		
comp31470_c0_seq7.p2		
comp31472_c0_seq1.p1		
comp31472_c0_seq2.p1		
comp31472_c0_seq3.p1		
comp31472_c1_seq1.p1		
comp31473_c0_seq1.p1		
comp31474_c0_seq1.p1	sp|Q9ERI6|RDH14_MOUSE_Retinol_dehydrogenase_14_OS=Mus_musculus_GN=Rdh14_PE=1_SV=1	7.00E-53
comp31474_c1_seq11.p1	sp|Q5RBU8|ROA2_PONAB_Heterogeneous_nuclear_ribonucleoproteins_A2/B1_OS=Pongo_abelii_GN=HNRNPA2B1_PE=2_SV=1	5.00E-38
comp31474_c1_seq11.p2	sp|Q50568|FDHC_METTF_Probable_formate_transporter_OS=Methanobacterium_thermoformicicum_GN=fdhC_PE=3_SV=1	3.00E-59
comp31474_c1_seq12.p1	sp|O15527|OGG1_HUMAN_N-glycosylase/DNA_lyase_OS=Homo_sapiens_GN=OGG1_PE=1_SV=2	2.00E-57
comp31474_c1_seq13.p1	sp|O15527|OGG1_HUMAN_N-glycosylase/DNA_lyase_OS=Homo_sapiens_GN=OGG1_PE=1_SV=2	4.00E-60
comp31474_c1_seq4.p1	sp|O15527|OGG1_HUMAN_N-glycosylase/DNA_lyase_OS=Homo_sapiens_GN=OGG1_PE=1_SV=2	3.00E-58
comp31474_c1_seq9.p1	sp|O15527|OGG1_HUMAN_N-glycosylase/DNA_lyase_OS=Homo_sapiens_GN=OGG1_PE=1_SV=2	3.00E-59
comp31475_c0_seq1.p1	sp|Q2S2V6|MEND_SALRD_2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate_synthase_OS=Salinibacter_ruber_(strain_DSM_13855_/_M31)_GN=menD_PE=3_SV=1	6.00E-37
comp31475_c1_seq1.p1	sp|Q1AS21|MEND_RUBXD_2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate_synthase_OS=Rubrobacter_xylanophilus_(strain_DSM_9941_/_NBRC_16129)_GN=menD_PE=3_SV=1	6.00E-30
comp31476_c0_seq1.p1	sp|Q9BXW9|FACD2_HUMAN_Fanconi_anemia_group_D2_protein_OS=Homo_sapiens_GN=FANCD2_PE=1_SV=1	5.00E-50
comp31476_c0_seq4.p1	sp|Q6IV68|FACD2_RAT_Fanconi_anemia_group_D2_protein_homolog_OS=Rattus_norvegicus_GN=Fancd2_PE=2_SV=2	4.00E-22
comp31476_c0_seq5.p1	sp|Q6IV68|FACD2_RAT_Fanconi_anemia_group_D2_protein_homolog_OS=Rattus_norvegicus_GN=Fancd2_PE=2_SV=2	3.00E-25
comp31476_c0_seq6.p1	sp|Q9BXW9|FACD2_HUMAN_Fanconi_anemia_group_D2_protein_OS=Homo_sapiens_GN=FANCD2_PE=1_SV=1	1.00E-41
comp31477_c0_seq5.p1	sp|P24821|TENA_HUMAN_Tenascin_OS=Homo_sapiens_GN=TNC_PE=1_SV=3	3.00E-15
comp31477_c0_seq6.p2	sp|P0CC00|NDUA5_PONPY_NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_5_OS=Pongo_pygmaeus_GN=NDUFA5_PE=3_SV=1	1.00E-18
comp31477_c0_seq8.p1	sp|P24821|TENA_HUMAN_Tenascin_OS=Homo_sapiens_GN=TNC_PE=1_SV=3	4.00E-15
comp31477_c0_seq8.p5	sp|P0CC00|NDUA5_PONPY_NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_5_OS=Pongo_pygmaeus_GN=NDUFA5_PE=3_SV=1	1.00E-18
comp31478_c0_seq1.p1		
comp31478_c0_seq1.p2		
comp31478_c0_seq5.p1		
comp31478_c1_seq2.p1		
comp31480_c0_seq1.p1		
comp31480_c0_seq1.p2		
comp31482_c0_seq2.p1		
comp31482_c0_seq4.p1	sp|Q91WC9|DGLB_MOUSE_Sn1-specific_diacylglycerol_lipase_beta_OS=Mus_musculus_GN=Daglb_PE=1_SV=2	2.00E-33
comp31483_c0_seq1.p1		
comp31484_c0_seq2.p1		
comp31484_c0_seq3.p1		
comp31485_c0_seq1.p1		
comp31485_c0_seq2.p1		
comp31486_c0_seq2.p1	sp|Q54PB2|MRD1_DICDI_Multiple_RNA-binding_domain-containing_protein_1_OS=Dictyostelium_discoideum_GN=mrd1_PE=3_SV=1	3.00E-102
comp31486_c0_seq3.p1		
comp31486_c0_seq3.p2	sp|Q54PB2|MRD1_DICDI_Multiple_RNA-binding_domain-containing_protein_1_OS=Dictyostelium_discoideum_GN=mrd1_PE=3_SV=1	9.00E-142
comp31486_c0_seq3.p3		
comp31486_c0_seq3.p4		
comp31486_c0_seq7.p1		
comp31486_c0_seq8.p1		
comp31487_c0_seq6.p1	sp|Q5UQZ7|YR901_MIMIV_Putative_ankyrin_repeat_protein_R901_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R901_PE=4_SV=1	1.00E-12
comp31489_c0_seq10.p1		
comp31489_c0_seq10.p2		
comp31490_c1_seq1.p1	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	5.00E-82
comp31491_c0_seq1.p3		
comp31491_c0_seq4.p1	sp|P22699|GUN6_DICDI_Endoglucanase_OS=Dictyostelium_discoideum_GN=celA_PE=2_SV=1	2.00E-12
comp31491_c0_seq6.p1	sp|P22699|GUN6_DICDI_Endoglucanase_OS=Dictyostelium_discoideum_GN=celA_PE=2_SV=1	2.00E-12
comp31492_c0_seq4.p1	sp|P54121|AIG2_ARATH_Protein_AIG2_OS=Arabidopsis_thaliana_GN=AIG2_PE=2_SV=1	8.00E-11
comp31492_c0_seq5.p1	sp|P54121|AIG2_ARATH_Protein_AIG2_OS=Arabidopsis_thaliana_GN=AIG2_PE=2_SV=1	8.00E-11
comp31493_c0_seq3.p1	sp|Q55GU0|Y9955_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0267514_OS=Dictyostelium_discoideum_GN=DDB_G0267514_PE=3_SV=1	1.00E-18
comp31494_c0_seq1.p1	sp|Q08759|MYB_XENLA_Transcriptional_activator_Myb_OS=Xenopus_laevis_GN=myb_PE=2_SV=1	3.00E-50
comp31494_c0_seq1.p2		
comp31494_c0_seq2.p1		
comp31494_c0_seq3.p1	sp|Q08759|MYB_XENLA_Transcriptional_activator_Myb_OS=Xenopus_laevis_GN=myb_PE=2_SV=1	4.00E-50
comp31494_c0_seq3.p2		
comp31494_c0_seq4.p2		
comp31494_c0_seq5.p1	sp|Q08759|MYB_XENLA_Transcriptional_activator_Myb_OS=Xenopus_laevis_GN=myb_PE=2_SV=1	3.00E-50
comp31494_c0_seq5.p2		
comp31494_c0_seq6.p1	sp|Q08759|MYB_XENLA_Transcriptional_activator_Myb_OS=Xenopus_laevis_GN=myb_PE=2_SV=1	4.00E-50
comp31494_c0_seq6.p2		
comp31494_c0_seq7.p1	sp|Q5ZLG9|WDR59_CHICK_WD_repeat-containing_protein_59_OS=Gallus_gallus_GN=WDR59_PE=2_SV=1	7.00E-24
comp31495_c0_seq2.p1		
comp31496_c0_seq4.p1		
comp31496_c0_seq6.p1		
comp31497_c0_seq1.p1		
comp31497_c1_seq4.p1	sp|Q8CH02|SUGP1_MOUSE_SURP_and_G-patch_domain-containing_protein_1_OS=Mus_musculus_GN=Sugp1_PE=1_SV=1	2.00E-13
comp31497_c1_seq9.p1	sp|Q6DI35|TFP11_DANRE_Tuftelin-interacting_protein_11_OS=Danio_rerio_GN=tfip11_PE=1_SV=1	1.00E-92
comp31497_c2_seq1.p1		
comp31497_c2_seq2.p1		
comp31497_c2_seq3.p1		
comp31497_c2_seq5.p2		
comp31497_c2_seq7.p1		
comp31497_c2_seq7.p2	sp|Q91ZN5|S35B2_MOUSE_Adenosine_3'-phospho_5'-phosphosulfate_transporter_1_OS=Mus_musculus_GN=Slc35b2_PE=2_SV=1	2.00E-79
comp31498_c0_seq2.p1	sp|Q01484|ANK2_HUMAN_Ankyrin-2_OS=Homo_sapiens_GN=ANK2_PE=1_SV=3	1.00E-68
comp31498_c0_seq3.p2		
comp31499_c0_seq1.p1		
comp31499_c0_seq3.p1		
comp31500_c0_seq2.p1	sp|Q54DA8|STIP1_DICDI_Protein_STIP1_homolog_OS=Dictyostelium_discoideum_GN=sti1_PE=3_SV=1	2.00E-15
comp31500_c0_seq3.p1		
comp31500_c0_seq4.p1	sp|Q84K71|MATE2_ARATH_MATE_efflux_family_protein_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=DTX44_PE=2_SV=1	1.00E-31
comp31500_c0_seq5.p1	sp|Q84K71|MATE2_ARATH_MATE_efflux_family_protein_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=DTX44_PE=2_SV=1	2.00E-39
comp31500_c0_seq5.p2		
comp31501_c0_seq2.p1	sp|P14685|PSMD3_MOUSE_26S_proteasome_non-ATPase_regulatory_subunit_3_OS=Mus_musculus_GN=Psmd3_PE=2_SV=3	6.00E-113
comp31501_c0_seq2.p3		
comp31501_c0_seq4.p2		
comp31501_c0_seq5.p1		
comp31502_c0_seq1.p1	sp|Q9P209|CEP72_HUMAN_Centrosomal_protein_of_72_kDa_OS=Homo_sapiens_GN=CEP72_PE=1_SV=2	9.00E-11
comp31503_c1_seq1.p1		
comp31503_c1_seq1.p2		
comp31504_c0_seq2.p1		
comp31504_c0_seq3.p1		
comp31504_c0_seq4.p1		
comp31505_c0_seq3.p1	sp|Q6S5H8|TPC1_HORVU_Two_pore_calcium_channel_protein_1_OS=Hordeum_vulgare_GN=TPC1_PE=2_SV=1	6.00E-16
comp31505_c0_seq3.p2	sp|Q6PBN4|CQ10X_DANRE_Coenzyme_Q-binding_protein_COQ10_homolog,_mitochondrial_OS=Danio_rerio_GN=zgc:73324_PE=2_SV=2	7.00E-28
comp31505_c0_seq5.p1	sp|Q9UPQ8|DOLK_HUMAN_Dolichol_kinase_OS=Homo_sapiens_GN=DOLK_PE=1_SV=1	9.00E-17
comp31505_c0_seq6.p1		
comp31505_c0_seq8.p1	sp|Q6S5H8|TPC1_HORVU_Two_pore_calcium_channel_protein_1_OS=Hordeum_vulgare_GN=TPC1_PE=2_SV=1	6.00E-16
comp31505_c0_seq8.p2	sp|Q6PBN4|CQ10X_DANRE_Coenzyme_Q-binding_protein_COQ10_homolog,_mitochondrial_OS=Danio_rerio_GN=zgc:73324_PE=2_SV=2	7.00E-28
comp31505_c0_seq9.p1	sp|Q9UPQ8|DOLK_HUMAN_Dolichol_kinase_OS=Homo_sapiens_GN=DOLK_PE=1_SV=1	2.00E-19
comp31505_c1_seq2.p1	sp|P19454|CSK22_YEAST_Casein_kinase_II_subunit_alpha'_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=CKA2_PE=1_SV=2	3.00E-23
comp31506_c1_seq2.p2		
comp31506_c1_seq4.p1		
comp31508_c0_seq1.p1	sp|O60447|EVI5_HUMAN_Ecotropic_viral_integration_site_5_protein_homolog_OS=Homo_sapiens_GN=EVI5_PE=1_SV=3	8.00E-31
comp31508_c0_seq1.p2	sp|Q84WU4|GOGC3_ARATH_Golgin_candidate_3_OS=Arabidopsis_thaliana_GN=GC3_PE=1_SV=1	2.00E-13
comp31508_c0_seq1.p3	sp|Q90593|GRP78_CHICK_78_kDa_glucose-regulated_protein_OS=Gallus_gallus_GN=HSPA5_PE=1_SV=1	1.00E-94
comp31508_c0_seq2.p1	sp|Q90593|GRP78_CHICK_78_kDa_glucose-regulated_protein_OS=Gallus_gallus_GN=HSPA5_PE=1_SV=1	1.00E-94
comp31508_c1_seq1.p1	sp|Q71U34|HSP7C_SAGOE_Heat_shock_cognate_71_kDa_protein_OS=Saguinus_oedipus_GN=HSPA8_PE=2_SV=1	1.00E-151
comp31509_c1_seq3.p1		
comp31509_c1_seq3.p6		
comp31511_c0_seq4.p1		
comp31514_c0_seq3.p1	sp|A6BM06|ACCO1_DICMU_1-aminocyclopropane-1-carboxylate_oxidase_OS=Dictyostelium_mucoroides_GN=aco_PE=3_SV=1	3.00E-36
comp31514_c0_seq4.p1	sp|Q39111|GAOX2_ARATH_Gibberellin_20_oxidase_2_OS=Arabidopsis_thaliana_GN=20ox2_PE=2_SV=1	4.00E-13
comp31515_c0_seq4.p1		
comp31517_c0_seq12.p1		
comp31517_c0_seq12.p4		
comp31519_c0_seq2.p1	sp|Q8IUH5|ZDH17_HUMAN_Palmitoyltransferase_ZDHHC17_OS=Homo_sapiens_GN=ZDHHC17_PE=1_SV=2	2.00E-19
comp31519_c1_seq1.p1	sp|Q505D1|ANR28_MOUSE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_A_OS=Mus_musculus_GN=Ankrd28_PE=1_SV=1	6.00E-21
comp31519_c1_seq3.p1	sp|Q8C8R3|ANK2_MOUSE_Ankyrin-2_OS=Mus_musculus_GN=Ank2_PE=1_SV=2	7.00E-37
comp31519_c2_seq1.p2		
comp31519_c2_seq3.p1		
comp31520_c0_seq1.p1	sp|Q7TNH6|NPHP3_MOUSE_Nephrocystin-3_OS=Mus_musculus_GN=Nphp3_PE=1_SV=2	1.00E-38
comp31520_c0_seq1.p2		
comp31521_c0_seq5.p1		
comp31521_c0_seq8.p1		
comp31521_c0_seq8.p4		
comp31523_c0_seq1.p1	sp|Q9BU89|DOHH_HUMAN_Deoxyhypusine_hydroxylase_OS=Homo_sapiens_GN=DOHH_PE=1_SV=1	2.00E-29
comp31523_c0_seq3.p1	sp|Q9BU89|DOHH_HUMAN_Deoxyhypusine_hydroxylase_OS=Homo_sapiens_GN=DOHH_PE=1_SV=1	1.00E-59
comp31524_c0_seq1.p2	sp|Q03265|ATPA_MOUSE_ATP_synthase_subunit_alpha,_mitochondrial_OS=Mus_musculus_GN=Atp5a1_PE=1_SV=1	0
comp31524_c1_seq2.p1	sp|P46686|TULP2_MOUSE_Tubby-related_protein_2_OS=Mus_musculus_GN=Tulp2_PE=2_SV=3	6.00E-58
comp31525_c0_seq5.p1	sp|P84675|PFM_CHAGB_Putative_fungistatic_metabolite_OS=Chaetomium_globosum_(strain_ATCC_6205_/_CBS_148.51_/_DSM_1962_/_NBRC_6347_/_NRRL_1970)_GN=CHGG_05463_PE=1_SV=2	9.00E-11
comp31526_c0_seq1.p2		
comp31526_c1_seq2.p1		
comp31528_c0_seq1.p1		
comp31528_c0_seq2.p1		
comp31528_c0_seq6.p1		
comp31528_c0_seq8.p1		
comp31528_c1_seq2.p1	sp|Q28811|PHR_POTTR_Deoxyribodipyrimidine_photo-lyase_OS=Potorous_tridactylus_GN=PHR_PE=2_SV=1	8.00E-39
comp31528_c1_seq4.p1	sp|Q28811|PHR_POTTR_Deoxyribodipyrimidine_photo-lyase_OS=Potorous_tridactylus_GN=PHR_PE=2_SV=1	9.00E-152
comp31528_c1_seq4.p2	sp|B1YVG1|PDXH_BURA4_Pyridoxine/pyridoxamine_5'-phosphate_oxidase_OS=Burkholderia_ambifaria_(strain_MC40-6)_GN=pdxH_PE=3_SV=1	6.00E-72
comp31529_c0_seq1.p3		
comp31529_c1_seq10.p1		
comp31529_c1_seq10.p3		
comp31529_c1_seq12.p1	sp|Q9M354|AGD6_ARATH_Probable_ADP-ribosylation_factor_GTPase-activating_protein_AGD6_OS=Arabidopsis_thaliana_GN=AGD6_PE=1_SV=1	1.00E-21
comp31529_c1_seq3.p1		
comp31529_c1_seq3.p3		
comp31529_c1_seq7.p2		
comp31530_c0_seq1.p1		
comp31530_c0_seq2.p1		
comp31530_c0_seq3.p1		
comp31530_c0_seq3.p2		
comp31530_c0_seq4.p1		
comp31530_c0_seq4.p3		
comp31530_c1_seq2.p1	sp|P54926|IMP1_SOLLC_Inositol_monophosphatase_1_OS=Solanum_lycopersicum_GN=IMP1_PE=2_SV=1	3.00E-65
comp31530_c1_seq2.p4		
comp31530_c2_seq2.p2		
comp31530_c2_seq3.p1		
comp31531_c0_seq2.p1		
comp31531_c0_seq2.p4		
comp31531_c0_seq3.p1		
comp31531_c1_seq9.p1	sp|Q54WS5|ROCO6_DICDI_Probable_serine/threonine-protein_kinase_roco6_OS=Dictyostelium_discoideum_GN=roco6_PE=3_SV=1	3.00E-14
comp31531_c2_seq1.p1	sp|Q5NDL9|AER61_CANFA_Uncharacterized_glycosyltransferase_AER61_OS=Canis_familiaris_GN=AER61_PE=2_SV=1	1.00E-20
comp31533_c0_seq1.p1		
comp31533_c0_seq2.p1		
comp31534_c0_seq1.p1	sp|Q5BCC5|CAN_EMENI_Carbonic_anhydrase_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=AN1805_PE=1_SV=2	9.00E-45
comp31534_c0_seq1.p3		
comp31534_c0_seq2.p1	sp|Q5BCC5|CAN_EMENI_Carbonic_anhydrase_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=AN1805_PE=1_SV=2	2.00E-60
comp31534_c0_seq3.p1	sp|Q5BCC5|CAN_EMENI_Carbonic_anhydrase_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=AN1805_PE=1_SV=2	6.00E-60
comp31534_c0_seq4.p1	sp|Q5BCC5|CAN_EMENI_Carbonic_anhydrase_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=AN1805_PE=1_SV=2	4.00E-45
comp31534_c0_seq4.p4		
comp31534_c0_seq5.p1	sp|P61518|CAN_SHIFL_Carbonic_anhydrase_2_OS=Shigella_flexneri_GN=can_PE=3_SV=1	7.00E-19

comp31536_c0_seq3.p1	sp|P36993|PPM1B_MOUSE_Protein_phosphatase_1B_OS=Mus_musculus_GN=Ppm1b_PE=2_SV=1	3.00E-30	[illegible]	[illegible]
comp31536_c0_seq3.p2				
comp31537_c0_seq2.p1	sp|O61125|STK4_DICDI_Serine/threonine-protein_kinase_4_homolog_A_OS=Dictyostelium_discoideum_GN=krsA_PE=1_SV=1	6.00E-81	[illegible]	[illegible]
comp31537_c0_seq4.p1	sp|O61125|STK4_DICDI_Serine/threonine-protein_kinase_4_homolog_A_OS=Dictyostelium_discoideum_GN=krsA_PE=1_SV=1	3.00E-81	[illegible]	[illegible]
comp31537_c0_seq6.p1	sp|Q6PBU5|GRT1A_DANRE_Growth_hormone-regulated_TBC_protein_1-A_OS=Danio_rerio_GN=grtp1a_PE=2_SV=1	6.00E-26	GO:0005096,GO:0005097,GO:0032313,GO:0032851,GO:0043547	[illegible]
comp31537_c0_seq8.p1	sp|Q6PBU5|GRT1A_DANRE_Growth_hormone-regulated_TBC_protein_1-A_OS=Danio_rerio_GN=grtp1a_PE=2_SV=1	6.00E-26	GO:0005096,GO:0005097,GO:0032313,GO:0032851,GO:0043547	[illegible]
comp31537_c0_seq9.p1	sp|Q6PBU5|GRT1A_DANRE_Growth_hormone-regulated_TBC_protein_1-A_OS=Danio_rerio_GN=grtp1a_PE=2_SV=1	6.00E-26	GO:0005096,GO:0005097,GO:0032313,GO:0032851,GO:0043547	[illegible]
comp31539_c0_seq1.p2				
comp31539_c0_seq2.p1				
comp31539_c0_seq3.p2				
comp31539_c0_seq3.p4				
comp31540_c0_seq11.p1	sp|O75665|OFD1_HUMAN_Oral-facial-digital_syndrome_1_protein_OS=Homo_sapiens_GN=OFD1_PE=1_SV=1	5.00E-18	[illegible]	[illegible]
comp31540_c0_seq8.p1				
comp31541_c0_seq1.p1	sp|Q96T88|UHRF1_HUMAN_E3_ubiquitin-protein_ligase_UHRF1_OS=Homo_sapiens_GN=UHRF1_PE=1_SV=1	1.00E-12	[illegible]	[illegible]
comp31542_c0_seq13.p1	sp|Q23K29|TTL3D_TETTS_Tubulin_glycylase_3D_OS=Tetrahymena_thermophila_(strain_SB210)_GN=TTLL3D_PE=3_SV=1	3.00E-43	[illegible]	[illegible]
comp31542_c0_seq13.p2	sp|Q9FL12|DEGP9_ARATH_Protease_Do-like_9_OS=Arabidopsis_thaliana_GN=DEGP9_PE=2_SV=1	3.00E-54	[illegible]	[illegible]
comp31542_c0_seq13.p3	sp|Q9FL12|DEGP9_ARATH_Protease_Do-like_9_OS=Arabidopsis_thaliana_GN=DEGP9_PE=2_SV=1	7.00E-69	[illegible]	[illegible]
comp31542_c0_seq2.p1	sp|Q9FL12|DEGP9_ARATH_Protease_Do-like_9_OS=Arabidopsis_thaliana_GN=DEGP9_PE=2_SV=1	2.00E-146	[illegible]	[illegible]
comp31542_c0_seq2.p2	sp|Q23K29|TTL3D_TETTS_Tubulin_glycylase_3D_OS=Tetrahymena_thermophila_(strain_SB210)_GN=TTLL3D_PE=3_SV=1	3.00E-43	[illegible]	[illegible]
comp31542_c0_seq6.p1	sp|Q9FL12|DEGP9_ARATH_Protease_Do-like_9_OS=Arabidopsis_thaliana_GN=DEGP9_PE=2_SV=1	2.00E-146	[illegible]	[illegible]
comp31542_c0_seq6.p2	sp|Q23K29|TTL3D_TETTS_Tubulin_glycylase_3D_OS=Tetrahymena_thermophila_(strain_SB210)_GN=TTLL3D_PE=3_SV=1	3.00E-43	[illegible]	[illegible]
comp31542_c0_seq9.p1	sp|Q23K29|TTL3D_TETTS_Tubulin_glycylase_3D_OS=Tetrahymena_thermophila_(strain_SB210)_GN=TTLL3D_PE=3_SV=1	3.00E-43	[illegible]	[illegible]
comp31542_c0_seq9.p2	sp|Q9FL12|DEGP9_ARATH_Protease_Do-like_9_OS=Arabidopsis_thaliana_GN=DEGP9_PE=2_SV=1	3.00E-54	[illegible]	[illegible]
comp31542_c0_seq9.p3	sp|Q9FL12|DEGP9_ARATH_Protease_Do-like_9_OS=Arabidopsis_thaliana_GN=DEGP9_PE=2_SV=1	7.00E-69	[illegible]	[illegible]
comp31544_c0_seq1.p1				
comp31544_c0_seq13.p1				
comp31544_c0_seq18.p1				
comp31544_c0_seq20.p1	sp|A8Z4K0|ARSC_STAAT_Protein_ArsC_OS=Staphylococcus_aureus_(strain_USA300_/_TCH1516)_GN=arsC_PE=3_SV=1	8.00E-27	[illegible]	[illegible]
comp31544_c0_seq4.p1				
comp31545_c0_seq2.p2	sp|Q9LEK8|PIN1_DIGLA_Peptidyl-prolyl_cis-trans_isomerase_Pin1_OS=Digitalis_lanata_GN=PARV12.8_PE=1_SV=1	1.00E-41	[illegible]	[illegible]
comp31545_c0_seq2.p3	sp|O94777|DPM2_HUMAN_Dolichol_phosphate-mannose_biosynthesis_regulatory_protein_OS=Homo_sapiens_GN=DPM2_PE=1_SV=3	4.00E-22	[illegible]	[illegible]
comp31545_c0_seq4.p1	sp|Q9FKT8|COX15_ARATH_Cytochrome_c_oxidase_assembly_protein_COX15_OS=Arabidopsis_thaliana_GN=COX15_PE=2_SV=1	3.00E-58	[illegible]	[illegible]
comp31545_c0_seq4.p2	sp|C6Y4D0|YCGV_SCHPO_Putative_transcription_factor_C16C4.22_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC16C4.22_PE=3_SV=1	3.00E-11	[illegible]	[illegible]
comp31547_c0_seq1.p1				
comp31549_c0_seq1.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	1.00E-28	[illegible]	[illegible]
comp31550_c0_seq33.p1	sp|Q93VD3|CIPKN_ARATH_CBL-interacting_serine/threonine-protein_kinase_23_OS=Arabidopsis_thaliana_GN=CIPK23_PE=1_SV=1	4.00E-26	[illegible]	[illegible]
comp31550_c0_seq33.p2				
comp31550_c0_seq38.p1	sp|Q93VD3|CIPKN_ARATH_CBL-interacting_serine/threonine-protein_kinase_23_OS=Arabidopsis_thaliana_GN=CIPK23_PE=1_SV=1	4.00E-26	[illegible]	[illegible]
comp31550_c0_seq38.p2				
comp31551_c0_seq1.p1	sp|Q80XC6|CN102_MOUSE_UPF0614_protein_C14orf102_homolog_OS=Mus_musculus_PE=2_SV=3	2.00E-21	[illegible]	[illegible]
comp31551_c0_seq1.p2				
comp31551_c0_seq2.p1				
comp31551_c0_seq3.p1	sp|Q80XC6|CN102_MOUSE_UPF0614_protein_C14orf102_homolog_OS=Mus_musculus_PE=2_SV=3	2.00E-21	[illegible]	[illegible]
comp31552_c0_seq7.p1				
comp31553_c0_seq1.p1				
comp31554_c0_seq1.p1				
comp31555_c0_seq11.p1	sp|Q9SF85|ADK1_ARATH_Adenosine_kinase_1_OS=Arabidopsis_thaliana_GN=ADK1_PE=1_SV=1	1.00E-104	[illegible]	[illegible]
comp31555_c0_seq13.p1	sp|Q9SF85|ADK1_ARATH_Adenosine_kinase_1_OS=Arabidopsis_thaliana_GN=ADK1_PE=1_SV=1	1.00E-128	[illegible]	[illegible]
comp31555_c0_seq13.p2				
comp31555_c0_seq17.p1	sp|Q3YRY1|RL27_EHRCJ_50S_ribosomal_protein_L27_OS=Ehrlichia_canis_(strain_Jake)_GN=rpmA_PE=3_SV=1	1.00E-29	[illegible]	[illegible]
comp31555_c0_seq17.p3				
comp31555_c0_seq4.p1	sp|Q9XUJ7|DKF1_CAEEL_Serine/threonine-protein_kinase_dkf-1_OS=Caenorhabditis_elegans_GN=dkf-1_PE=1_SV=1	2.00E-28	[illegible]	[illegible]
comp31555_c0_seq8.p2				
comp31556_c0_seq1.p1	sp|P34136|HMDH2_DICDI_3-hydroxy-3-methylglutaryl-coenzyme_A_reductase_2_OS=Dictyostelium_discoideum_GN=hmgB_PE=2_SV=2	6.00E-111	[illegible]	[illegible]
comp31556_c0_seq1.p2				
comp31556_c0_seq1.p7				
comp31556_c0_seq4.p1				
comp31557_c0_seq1.p2				
comp31557_c0_seq2.p1				
comp31558_c0_seq1.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	8.00E-38		
comp31559_c0_seq1.p1	sp|Q2MHE4|HT1_ARATH_Serine/threonine-protein_kinase_HT1_OS=Arabidopsis_thaliana_GN=HT1_PE=1_SV=1	5.00E-35	[illegible]	[illegible]
comp31559_c0_seq2.p1				
comp31559_c0_seq2.p2	sp|Q2MHE4|HT1_ARATH_Serine/threonine-protein_kinase_HT1_OS=Arabidopsis_thaliana_GN=HT1_PE=1_SV=1	1.00E-25	[illegible]	[illegible]
comp31559_c0_seq3.p1	sp|Q2MHE4|HT1_ARATH_Serine/threonine-protein_kinase_HT1_OS=Arabidopsis_thaliana_GN=HT1_PE=1_SV=1	2.00E-33	[illegible]	[illegible]
comp31560_c0_seq1.p1				
comp31560_c0_seq2.p1				
comp31560_c0_seq2.p2	sp|Q5UP57|P4H_MIMIV_Putative_prolyl_4-hydroxylase_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L593_PE=1_SV=1	6.00E-15	[illegible]	[illegible]
comp31560_c0_seq3.p1	sp|Q5UP57|P4H_MIMIV_Putative_prolyl_4-hydroxylase_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L593_PE=1_SV=1	7.00E-18	[illegible]	[illegible]
comp31561_c0_seq1.p1	sp|P48786|PRH_PETCR_Pathogenesis-related_homeodomain_protein_OS=Petroselinum_crispum_GN=PRH_PE=2_SV=1	3.00E-18	[illegible]	[illegible]
comp31561_c0_seq2.p1	sp|P46605|HOX1A_MAIZE_Homeobox_protein_HOX1A_OS=Zea_mays_GN=HOX1A_PE=2_SV=1	2.00E-30	[illegible]	[illegible]
comp31561_c0_seq3.p1				
comp31561_c0_seq4.p1				
comp31562_c0_seq1.p1	sp|Q80TR8|VPRBP_MOUSE_Protein_VPRBP_OS=Mus_musculus_GN=Vprbp_PE=2_SV=4	1.00E-35	[illegible]	[illegible]
comp31562_c0_seq1.p2	sp|Q5BLD8|MT21A_DANRE_Methyltransferase-like_protein_21A_OS=Danio_rerio_GN=mettl21a_PE=2_SV=1	2.00E-14	[illegible]	[illegible]
comp31562_c0_seq4.p1				
comp31563_c1_seq1.p1	sp|Q07123|AMO2_ARTS1_Copper_methylamine_oxidase_OS=Arthrobacter_sp._(strain_P1)_GN=maoII_PE=1_SV=1	4.00E-128	[illegible]	[illegible]
comp31563_c1_seq2.p1	sp|Q07123|AMO2_ARTS1_Copper_methylamine_oxidase_OS=Arthrobacter_sp._(strain_P1)_GN=maoII_PE=1_SV=1	6.00E-65	[illegible]	[illegible]
comp31564_c0_seq1.p2				
comp31564_c0_seq2.p1				
comp31565_c0_seq5.p1	sp|O70196|PPCE_RAT_Prolyl_endopeptidase_OS=Rattus_norvegicus_GN=Prep_PE=1_SV=1	0	[illegible]	[illegible]
comp31565_c0_seq5.p2	sp|P0A8Y7|YIDA_SHIFL_Phosphatase_YidA_OS=Shigella_flexneri_GN=yidA_PE=3_SV=1	1.00E-20	[illegible]	[illegible]
comp31565_c0_seq6.p1	sp|P23687|PPCE_PIG_Prolyl_endopeptidase_OS=Sus_scrofa_GN=PREP_PE=1_SV=1	2.00E-83	[illegible]	[illegible]
comp31565_c0_seq6.p2	sp|O70196|PPCE_RAT_Prolyl_endopeptidase_OS=Rattus_norvegicus_GN=Prep_PE=1_SV=1	1.00E-92	[illegible]	[illegible]
comp31565_c0_seq6.p3	sp|P0A8Y7|YIDA_SHIFL_Phosphatase_YidA_OS=Shigella_flexneri_GN=yidA_PE=3_SV=1	1.00E-20	[illegible]	[illegible]
comp31566_c0_seq1.p1				
comp31566_c0_seq5.p1	sp|P97929|BRCA2_MOUSE_Breast_cancer_type_2_susceptibility_protein_homolog_OS=Mus_musculus_GN=Brca2_PE=1_SV=1	4.00E-33	[illegible]	[illegible]
comp31567_c0_seq2.p1	sp|Q9CPU4|MGST3_MOUSE_Microsomal_glutathione_S-transferase_3_OS=Mus_musculus_GN=Mgst3_PE=1_SV=1	3.00E-24	[illegible]	[illegible]
comp31568_c0_seq1.p1	sp|Q54NA6|MYBL_DICDI_Myb-like_protein_L_OS=Dictyostelium_discoideum_GN=mybL_PE=3_SV=1	1.00E-21	[illegible]	[illegible]
comp31569_c0_seq1.p1				
comp31569_c0_seq4.p1				
comp31569_c1_seq1.p1				
comp31569_c1_seq2.p3				
comp31570_c0_seq1.p1				
comp31570_c0_seq3.p1				
comp31571_c1_seq10.p1				
comp31571_c1_seq2.p2				
comp31571_c1_seq6.p1				
comp31571_c1_seq9.p1	sp|Q7T6Y2|YR831_MIMIV_Putative_serine/threonine-protein_kinase/receptor_R831_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R831_PE=4_SV=2	5.00E-13	[illegible]	[illegible]
comp31572_c0_seq1.p1				
comp31572_c0_seq4.p1				
comp31572_c0_seq5.p1				
comp31573_c0_seq1.p1				
comp31573_c0_seq3.p1	sp|Q5JM04|KAT3_ORYSJ_Potassium_channel_KAT3_OS=Oryza_sativa_subsp._japonica_GN=Os01g0756700_PE=2_SV=1	1.00E-27	[illegible]	[illegible]
comp31574_c0_seq1.p1	sp|Q84QU8|PPT2_ORYSJ_Phosphoenolpyruvate/phosphate_translocator_2,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=PPT2_PE=2_SV=1	3.00E-33	[illegible]	[illegible]
comp31574_c0_seq2.p2				
comp31574_c0_seq3.p1				
comp31576_c0_seq1.p1				
comp31576_c1_seq2.p1	sp|Q83CY8|BCP_COXBU_Putative_peroxiredoxin_bcp_OS=Coxiella_burnetii_(strain_RSA_493_/_Nine_Mile_phase_I)_GN=bcp_PE=1_SV=1	3.00E-28	[illegible]	[illegible]
comp31576_c1_seq8.p1				
comp31576_c1_seq9.p1	sp|P07374|UREA_CANEN_Urease_OS=Canavalia_ensiformis_PE=1_SV=3	0	[illegible]	[illegible]
comp31576_c1_seq9.p3	sp|Q47147|YAFJ_ECOLI_Putative_glutamine_amidotransferase_yafJ_OS=Escherichia_coli_(strain_K12)_GN=yafJ_PE=4_SV=1	2.00E-64	[illegible]	[illegible]
comp31578_c0_seq1.p1	sp|Q8L7W8|FUCO2_ARATH_Alpha-L-fucosidase_2_OS=Arabidopsis_thaliana_GN=At4g34260_PE=2_SV=1	4.00E-42	[illegible]	[illegible]
comp31579_c0_seq2.p1				
comp31579_c0_seq2.p2				
comp31580_c0_seq1.p1				
comp31580_c0_seq2.p1				
comp31580_c0_seq4.p1				
comp31580_c0_seq6.p1				
comp31580_c0_seq8.p1				
comp31581_c0_seq1.p1	sp|Q5RA75|F135A_PONAB_Protein_FAM135A_OS=Pongo_abelii_GN=FAM135A_PE=2_SV=1	8.00E-43		
comp31581_c0_seq5.p1	sp|Q5RA75|F135A_PONAB_Protein_FAM135A_OS=Pongo_abelii_GN=FAM135A_PE=2_SV=1	6.00E-26		
comp31581_c0_seq5.p4				
comp31581_c0_seq6.p1	sp|Q5RA75|F135A_PONAB_Protein_FAM135A_OS=Pongo_abelii_GN=FAM135A_PE=2_SV=1	8.00E-43		
comp31581_c0_seq7.p1	sp|Q5RA75|F135A_PONAB_Protein_FAM135A_OS=Pongo_abelii_GN=FAM135A_PE=2_SV=1	7.00E-26		
comp31582_c0_seq2.p1				
comp31583_c0_seq4.p1				
comp31583_c0_seq6.p1				
comp31584_c0_seq5.p1	sp|Q9CW03|SMC3_MOUSE_Structural_maintenance_of_chromosomes_protein_3_OS=Mus_musculus_GN=Smc3_PE=1_SV=2	0	[illegible]	[illegible]
comp31584_c0_seq5.p2	sp|P24821|TENA_HUMAN_Tenascin_OS=Homo_sapiens_GN=TNC_PE=1_SV=3	5.00E-18	[illegible]	[illegible]
comp31585_c0_seq1.p1				
comp31585_c0_seq1.p2	sp|Q08288|LYAR_MOUSE_Cell_growth-regulating_nucleolar_protein_OS=Mus_musculus_GN=Lyar_PE=1_SV=2	7.00E-25	[illegible]	[illegible]
comp31585_c0_seq1.p4				
comp31585_c0_seq2.p1				
comp31585_c0_seq2.p2				
comp31585_c1_seq1.p1	sp|Q504Q3|PAN2_HUMAN_PAB-dependent_poly(A)-specific_ribonuclease_subunit_2_OS=Homo_sapiens_GN=PAN2_PE=1_SV=3	2.00E-52	[illegible]	[illegible]
comp31586_c0_seq3.p1				
comp31587_c0_seq2.p1	sp|P40421|RDGC_DROME_Serine/threonine-protein_phosphatase_rdgC_OS=Drosophila_melanogaster_GN=rdgC_PE=2_SV=1	2.00E-71	[illegible]	[illegible]
comp31587_c0_seq3.p1				
comp31587_c0_seq5.p1				
comp31587_c1_seq2.p1	sp|Q923G5|ZDHC7_RAT_Palmitoyltransferase_ZDHHC7_OS=Rattus_norvegicus_GN=Zdhhc7_PE=1_SV=1	2.00E-42	[illegible]	[illegible]
comp31587_c1_seq4.p1	sp|Q923G5|ZDHC7_RAT_Palmitoyltransferase_ZDHHC7_OS=Rattus_norvegicus_GN=Zdhhc7_PE=1_SV=1	8.00E-43	[illegible]	[illegible]
comp31587_c3_seq11.p1	sp|P35249|RFC4_HUMAN_Replication_factor_C_subunit_4_OS=Homo_sapiens_GN=RFC4_PE=1_SV=2	6.00E-99	[illegible]	[illegible]
comp31587_c3_seq12.p1	sp|P35249|RFC4_HUMAN_Replication_factor_C_subunit_4_OS=Homo_sapiens_GN=RFC4_PE=1_SV=2	5.00E-111	[illegible]	[illegible]
comp31587_c3_seq12.p2	sp|P35249|RFC4_HUMAN_Replication_factor_C_subunit_4_OS=Homo_sapiens_GN=RFC4_PE=1_SV=2	2.00E-115	[illegible]	[illegible]
comp31587_c3_seq13.p1				
comp31587_c3_seq3.p1	sp|P59325|IF5_MOUSE_Eukaryotic_translation_initiation_factor_5_OS=Mus_musculus_GN=Eif5_PE=1_SV=1	5.00E-51	[illegible]	[illegible]
comp31587_c3_seq6.p1	sp|P35249|RFC4_HUMAN_Replication_factor_C_subunit_4_OS=Homo_sapiens_GN=RFC4_PE=1_SV=2	6.00E-99	[illegible]	[illegible]
comp31587_c3_seq9.p1	sp|P35249|RFC4_HUMAN_Replication_factor_C_subunit_4_OS=Homo_sapiens_GN=RFC4_PE=1_SV=2	2.00E-115	[illegible]	[illegible]
comp31587_c3_seq9.p2	sp|P35249|RFC4_HUMAN_Replication_factor_C_subunit_4_OS=Homo_sapiens_GN=RFC4_PE=1_SV=2	2.00E-115	[illegible]	[illegible]
comp31587_c4_seq1.p1	sp|P28583|CDPK_SOYBN_Calcium-dependent_protein_kinase_SK5_OS=Glycine_max_PE=1_SV=1	3.00E-74	[illegible]	[illegible]
comp31587_c4_seq2.p1	sp|Q8RWL2|CDPKT_ARATH_Calcium-dependent_protein_kinase_29_OS=Arabidopsis_thaliana_GN=CPK29_PE=2_SV=2	8.00E-67	[illegible]	[illegible]
comp31588_c0_seq10.p1				
comp31588_c0_seq11.p3				
comp31588_c0_seq14.p1				
comp31588_c0_seq2.p1				
comp31588_c0_seq8.p1				
comp31588_c0_seq9.p2				
comp31590_c0_seq3.p1				
comp31590_c0_seq5.p1				
comp31590_c0_seq6.p1				
comp31590_c0_seq8.p1				
comp31590_c0_seq9.p1	sp|Q5UQ40|UBC4_MIMIV_Probable_bifunctional_E2/E3_enzyme_R795_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R795_PE=3_SV=1	3.00E-34	[illegible]	[illegible]
comp31591_c0_seq13.p1				
comp31591_c0_seq4.p1	sp|Q9SK39|SBP3_ARATH_Probable_steroid-binding_protein_3_OS=Arabidopsis_thaliana_GN=MP3_PE=1_SV=1	7.00E-20	[illegible]	[illegible]
comp31591_c0_seq5.p1	sp|Q58DT5|ELMD3_BOVIN_ELMO_domain-containing_protein_3_OS=Bos_taurus_GN=ELMOD3_PE=2_SV=1	1.00E-26	[illegible]	[illegible]
comp31591_c0_seq9.p1	sp|Q58DT5|ELMD3_BOVIN_ELMO_domain-containing_protein_3_OS=Bos_taurus_GN=ELMOD3_PE=2_SV=1	2.00E-26	[illegible]	[illegible]
comp31591_c0_seq9.p3				
comp31592_c0_seq1.p1	sp|Q75DK1|SEC14_ASHGO_SEC14_cytosolic_factor_OS=Ashbya_gossypii_(strain_ATCC_10895_/_CBS_109.51_/_FGSC_9923_/_NRRL_Y-1056)_GN=SEC14_PE=3_SV=1	2.00E-18	[illegible]	[illegible]
comp31592_c0_seq2.p1				
comp31592_c0_seq3.p1	sp|A4K526|CQ061_BUFBG_UPF0451_protein_C17orf61_homolog_OS=Bufo_bufo_gargarizans_PE=3_SV=1	7.00E-15	[illegible]	[illegible]
comp31592_c0_seq4.p1				
comp31592_c0_seq4.p3				
comp31592_c0_seq6.p1	sp|Q75DK1|SEC14_ASHGO_SEC14_cytosolic_factor_OS=Ashbya_gossypii_(strain_ATCC_10895_/_CBS_109.51_/_FGSC_9923_/_NRRL_Y-1056)_GN=SEC14_PE=3_SV=1	7.00E-16	[illegible]	[illegible]
comp31592_c0_seq7.p1				
comp31592_c0_seq8.p1				
comp31592_c0_seq9.p1				
comp31592_c1_seq11.p1				
comp31592_c1_seq16.p1				
comp31592_c1_seq20.p1				
comp31592_c1_seq6.p1				
comp31592_c3_seq1.p1				
comp31593_c0_seq1.p1				
comp31594_c0_seq3.p2				
comp31595_c0_seq2.p1				
comp31595_c0_seq3.p1				
comp31595_c0_seq4.p1				
comp31596_c0_seq1.p1				
comp31596_c0_seq4.p1				
comp31596_c0_seq6.p1				
comp31596_c0_seq7.p1				
comp31598_c0_seq1.p1				
comp31598_c2_seq1.p1				
comp31599_c0_seq1.p1				
comp31599_c0_seq2.p1				
comp31599_c0_seq3.p1				
comp31599_c0_seq4.p1				
comp31599_c0_seq8.p1				
comp31601_c0_seq5.p1				
comp31601_c0_seq6.p1				
comp31601_c0_seq7.p1				
comp31602_c0_seq1.p2				
comp31602_c0_seq2.p1	sp|Q5UR85|YR636_MIMIV_Putative_FNIP_repeat-containing_protein_R636_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R636_PE=4_SV=1	2.00E-17		
comp31602_c0_seq4.p1				
comp31602_c0_seq5.p1	sp|Q5XIJ5|F108A_RAT_Abhydrolase_domain-containing_protein_FAM108A_OS=Rattus_norvegicus_GN=Fam108a_PE=2_SV=1	2.00E-16	[illegible]	[illegible]
comp31603_c0_seq2.p1	sp|Q9S775|PKL_ARATH_CHD3-type_chromatin-remodeling_factor_PICKLE_OS=Arabidopsis_thaliana_GN=PKL_PE=1_SV=1	2.00E-156	[illegible]	[illegible]
comp31604_c0_seq2.p2				
comp31606_c0_seq5.p2				
comp31607_c0_seq2.p1				
comp31608_c0_seq3.p1				
comp31609_c0_seq3.p1				
comp31609_c1_seq1.p1				
comp31609_c1_seq1.p4				
comp31609_c1_seq3.p1				
comp31609_c1_seq8.p1				
comp31610_c0_seq10.p1				
comp31610_c0_seq11.p1				
comp31610_c0_seq5.p1				
comp31611_c0_seq6.p1	sp|Q9R0Q9|MPU1_MOUSE_Mannose-P-dolichol_utilization_defect_1_protein_OS=Mus_musculus_GN=Mpdu1_PE=2_SV=1	2.00E-25	[illegible]	[illegible]
comp31611_c0_seq6.p2	sp|Q8C9A2|ENDOV_MOUSE_Endonuclease_V_OS=Mus_musculus_GN=Endov_PE=1_SV=2	8.00E-39	[illegible]	[illegible]
comp31611_c1_seq1.p1	sp|Q14746|COG2_HUMAN_Conserved_oligomeric_Golgi_complex_subunit_2_OS=Homo_sapiens_GN=COG2_PE=1_SV=1	8.00E-35	[illegible]	[illegible]
comp31611_c2_seq2.p1	sp|Q6ZRS2|SRCAP_HUMAN_Helicase_SRCAP_OS=Homo_sapiens_GN=SRCAP_PE=1_SV=3	5.00E-138	[illegible]	[illegible]
comp31611_c3_seq1.p1				
comp31611_c4_seq1.p1				
comp31611_c4_seq3.p1				
comp31611_c4_seq4.p1				
comp31611_c4_seq4.p3				
comp31612_c0_seq12.p1				
comp31612_c0_seq13.p1				
comp31612_c0_seq6.p1				
comp31612_c0_seq7.p1				
comp31613_c0_seq1.p1				
comp31613_c0_seq4.p1				
comp31615_c0_seq4.p1				
comp31617_c0_seq1.p1				
comp31618_c0_seq1.p1	sp|Q55909|Y305_SYNY3_TVP38/TMEM64_family_membrane_protein_slr0305_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0305_PE=3_SV=1	3.00E-26	[illegible]	[illegible]
comp31619_c0_seq10.p1				
comp31619_c0_seq16.p1				
comp31620_c0_seq1.p1				
comp31620_c0_seq2.p1				
comp31620_c0_seq3.p1				
comp31620_c0_seq4.p1				
comp31620_c0_seq9.p1				
comp31621_c0_seq2.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	3.00E-11	[illegible]	[illegible]
comp31621_c0_seq2.p2				
comp31621_c0_seq2.p7				
comp31621_c0_seq3.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	3.00E-11	[illegible]	[illegible]
comp31621_c0_seq3.p2				
comp31621_c0_seq3.p3				
comp31621_c0_seq3.p9				
comp31622_c0_seq1.p1	sp|Q659C4|LAR1B_HUMAN_La-related_protein_1B_OS=Homo_sapiens_GN=LARP1B_PE=1_SV=2	7.00E-12	[illegible]	[illegible]
comp31623_c0_seq1.p1	sp|B1WZK0|RIMM_CYAA5_Ribosome_maturation_factor_RimM_OS=Cyanothece_sp._(strain_ATCC_51142)_GN=rimM_PE=3_SV=1	1.00E-19	[illegible]	[illegible]
comp31624_c2_seq1.p1				
comp31624_c2_seq1.p2	sp|Q965Q4|SMS3_CAEEL_Putative_phosphatidylcholine:ceramide_cholinephosphotransferase_3_OS=Caenorhabditis_elegans_GN=sms-3_PE=2_SV=1	1.00E-14	[illegible]	[illegible]
comp31624_c2_seq2.p1				
comp31624_c2_seq4.p1				
comp31624_c2_seq5.p1				
comp31624_c2_seq5.p3				
comp31624_c2_seq6.p1				
comp31624_c2_seq7.p1	sp|Q6PB75|PAPD7_MOUSE_DNA_polymerase_sigma_OS=Mus_musculus_GN=Papd7_PE=2_SV=1	1.00E-13	[illegible]	[illegible]
comp31624_c2_seq7.p2	sp|Q965Q4|SMS3_CAEEL_Putative_phosphatidylcholine:ceramide_cholinephosphotransferase_3_OS=Caenorhabditis_elegans_GN=sms-3_PE=2_SV=1	1.00E-14	[illegible]	[illegible]
comp31625_c0_seq1.p1				
comp31625_c0_seq2.p1				
comp31626_c0_seq1.p1	sp|Q71ZJ8|DNAJ_LISMF_Chaperone_protein_DnaJ_OS=Listeria_monocytogenes_serotype_4b_(strain_F2365)_GN=dnaJ_PE=3_SV=1	2.00E-13	[illegible]	[illegible]
comp31626_c0_seq15.p1	sp|A0AIS3|DNAJ_LISW6_Chaperone_protein_DnaJ_OS=Listeria_welshimeri_serovar_6b_(strain_ATCC_35897_/_DSM_20650_/_SLCC5334)_GN=dnaJ_PE=3_SV=1	2.00E-17	[illegible]	[illegible]
comp31626_c0_seq7.p1	sp|A0AIS3|DNAJ_LISW6_Chaperone_protein_DnaJ_OS=Listeria_welshimeri_serovar_6b_(strain_ATCC_35897_/_DSM_20650_/_SLCC5334)_GN=dnaJ_PE=3_SV=1	6.00E-17	[illegible]	[illegible]
comp31626_c0_seq8.p1	sp|A0AIS3|DNAJ_LISW6_Chaperone_protein_DnaJ_OS=Listeria_welshimeri_serovar_6b_(strain_ATCC_35897_/_DSM_20650_/_SLCC5334)_GN=dnaJ_PE=3_SV=1	8.00E-17	[illegible]	[illegible]
comp31627_c0_seq1.p1	sp|Q6ZU11|YD002_HUMAN_Uncharacterized_protein_FLJ44066_OS=Homo_sapiens_PE=1_SV=1	6.00E-54		
comp31627_c0_seq1.p2	sp|P48293|RECA_SPIPL_Protein_RecA_OS=Spirulina_platensis_GN=recA_PE=3_SV=1	1.00E-142	[illegible]	[illegible]
comp31627_c0_seq2.p2				
comp31627_c0_seq5.p1	sp|Q6ZU11|YD002_HUMAN_Uncharacterized_protein_FLJ44066_OS=Homo_sapiens_PE=1_SV=1	1.00E-26		
comp31627_c1_seq3.p1	sp|Q9ZK14|CYSE_HELPJ_Serine_acetyltransferase_OS=Helicobacter_pylori_(strain_J99)_GN=cysE_PE=3_SV=1	3.00E-39	[illegible]	[illegible]
comp31627_c1_seq3.p2				
comp31627_c2_seq1.p1	sp|P79384|PCCB_PIG_Propionyl-CoA_carboxylase_beta_chain,_mitochondrial_OS=Sus_scrofa_GN=PCCB_PE=2_SV=1	0	[illegible]	[illegible]
comp31627_c2_seq3.p1	sp|Q9L4P4|CLPR_SYNE7_Putative_ATP-dependent_Clp_protease_proteolytic_subunit-like_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=clpR_PE=3_SV=1	7.00E-68	[illegible]	[illegible]
comp31628_c0_seq4.p1				
comp31628_c0_seq4.p2	sp|Q9H0R3|TM222_HUMAN_Transmembrane_protein_222_OS=Homo_sapiens_GN=TMEM222_PE=2_SV=2	1.00E-65	[illegible]	[illegible]
comp31628_c0_seq6.p1				
comp31628_c0_seq6.p2	sp|Q9H0R3|TM222_HUMAN_Transmembrane_protein_222_OS=Homo_sapiens_GN=TMEM222_PE=2_SV=2	1.00E-65	[illegible]	[illegible]
comp31629_c0_seq1.p1				
comp31629_c0_seq1.p2				
comp31629_c0_seq1.p3				
comp31629_c0_seq4.p1				
comp31629_c0_seq4.p2				
comp31629_c0_seq4.p3				
comp31629_c0_seq4.p4				
comp31630_c0_seq3.p1				
comp31630_c0_seq3.p2				
comp31631_c0_seq5.p1	sp|Q5Z859|MPK4_ORYSJ_Mitogen-activated_protein_kinase_4_OS=Oryza_sativa_subsp._japonica_GN=MPK4_PE=2_SV=1	3.00E-37	[illegible]	[illegible]
comp31631_c0_seq5.p2				
comp31632_c0_seq1.p1				
comp31632_c0_seq3.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	8.00E-13	[illegible]	[illegible]
comp31633_c0_seq2.p1				
comp31633_c0_seq2.p2	sp|Q6AYY8|ACATN_RAT_Acetyl-coenzyme_A_transporter_1_OS=Rattus_norvegicus_GN=Slc33a1_PE=2_SV=1	2.00E-150	[illegible]	[illegible]
comp31633_c0_seq5.p1	sp|Q6AYY8|ACATN_RAT_Acetyl-coenzyme_A_transporter_1_OS=Rattus_norvegicus_GN=Slc33a1_PE=2_SV=1	2.00E-150	[illegible]	[illegible]
comp31634_c0_seq1.p1				
comp31634_c1_seq1.p1				
comp31635_c0_seq1.p1	sp|Q9U1M8|MYOI_DICDI_Myosin-I_heavy_chain_OS=Dictyostelium_discoideum_GN=myoI_PE=1_SV=1	4.00E-89	[illegible]	[illegible]
comp31635_c0_seq4.p1	sp|Q9U1M8|MYOI_DICDI_Myosin-I_heavy_chain_OS=Dictyostelium_discoideum_GN=myoI_PE=1_SV=1	7.00E-85	[illegible]	[illegible]
comp31635_c0_seq6.p1				
comp31636_c0_seq2.p1				
comp31639_c0_seq10.p1	sp|Q31N27|ZDS_SYNE7_Probable_zeta-carotene_desaturase_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=zds_PE=3_SV=1	1.00E-15	[illegible]	[illegible]
comp31639_c0_seq12.p1	sp|Q31N27|ZDS_SYNE7_Probable_zeta-carotene_desaturase_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=zds_PE=3_SV=1	9.00E-19	[illegible]	[illegible]
comp31639_c0_seq5.p2				
comp31640_c0_seq1.p1	sp|Q09M02|CBPC5_MOUSE_Cytosolic_carboxypeptidase-like_protein_5_OS=Mus_musculus_GN=Agbl5_PE=1_SV=2	1.00E-23	[illegible]	[illegible]
comp31640_c0_seq3.p1	sp|Q8NDL9|CBPC5_HUMAN_Cytosolic_carboxypeptidase-like_protein_5_OS=Homo_sapiens_GN=AGBL5_PE=2_SV=1	2.00E-12	[illegible]	[illegible]
comp31641_c0_seq3.p1				
comp31641_c0_seq6.p1				
comp31642_c0_seq4.p1	sp|Q54KG3|FFR_DICDI_Protein_fat-free_homolog_OS=Dictyostelium_discoideum_GN=ffr_PE=3_SV=1	2.00E-36	[illegible]	[illegible]
comp31642_c0_seq6.p1	sp|Q3UMC0|SPAT5_MOUSE_Spermatogenesis-associated_protein_5_OS=Mus_musculus_GN=Spata5_PE=2_SV=2	3.00E-46	[illegible]	[illegible]
comp31642_c0_seq8.p1	sp|Q66GI4|PP179_ARATH_Pentatricopeptide_repeat-containing_protein_At2g32230,_mitochondrial_OS=Arabidopsis_thaliana_GN=At2g32230_PE=2_SV=1	2.00E-32	[illegible]	[illegible]
comp31642_c0_seq9.p1				
comp31642_c1_seq16.p1	sp|Q84UI5|MPK1_ORYSJ_Mitogen-activated_protein_kinase_1_OS=Oryza_sativa_subsp._japonica_GN=MPK1_PE=1_SV=1	2.00E-106	[illegible]	[illegible]
comp31642_c1_seq16.p2	sp|Q4UMH6|Y381_RICFE_Putative_ankyrin_repeat_protein_RF_0381_OS=Rickettsia_felis_(strain_ATCC_VR-1525_/_URRWXCal2)_GN=RF_0381_PE=4_SV=1	1.00E-16	GO:0015969	[illegible]
comp31642_c1_seq2.p1	sp|Q71S22|INVSA_XENLA_Inversin-A_OS=Xenopus_laevis_GN=invs-a_PE=1_SV=1	2.00E-13	[illegible]	[illegible]
comp31643_c0_seq3.p1	sp|Q6A009|LTN1_MOUSE_E3_ubiquitin-protein_ligase_listerin_OS=Mus_musculus_GN=Ltn1_PE=1_SV=3	8.00E-47	[illegible]	[illegible]
comp31643_c0_seq3.p3				
comp31643_c0_seq3.p6				
comp31644_c0_seq1.p1				
comp31644_c0_seq2.p1	sp|O97159|CHDM_DROME_Chromodomain-helicase-DNA-binding_protein_Mi-2_homolog_OS=Drosophila_melanogaster_GN=Mi-2_PE=1_SV=2	6.00E-11	[illegible]	[illegible]
comp31644_c0_seq2.p2				
comp31645_c0_seq13.p1				
comp31645_c0_seq18.p1				
comp31645_c0_seq18.p2				
comp31645_c0_seq19.p1				
comp31645_c0_seq19.p2				
comp31645_c0_seq22.p1				
comp31645_c0_seq5.p1				
comp31645_c0_seq7.p1				

comp31645_c0_seq7.p2				
comp31645_c0_seq7.p3				
comp31645_c0_seq8.p1				
comp31645_c0_seq8.p2				
comp31645_c0_seq8.p3				
comp31646_c0_seq1.p1	sp|O75691|UTP20_HUMAN_Small_subunit_processome_component_20_homolog_OS=Homo_sapiens_GN=UTP20_PE=1_SV=3	1.00E-22	GO:0000447,GO:0000462,GO:0000472,GO:0000480,GO:0005515,GO:0005515,GO:0005634,GO:0005654,GO:0005730,GO:0005730,GO:0005730,GO:0005737,GO:0006364,GO:0006364,GO:0008285,GO:0030686,GO:0030686,GO:0030688,GO:0032040,GO:0032040,GO:0044822,GO:0044822	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA),endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),protein binding,protein binding,nucleus,nucleoplasm,nucleolus,nucleolus,nucleolus,cytoplasm,rRNA processing,rRNA processing,negative regulation of cell proliferation,90S preribosome,90S preribosome,preribosome, small subunit precursor,small-subunit processome,small-subunit processome,poly(A) RNA binding,poly(A) RNA binding
comp31646_c0_seq1.p2	sp|Q5XG71|UTP20_MOUSE_Small_subunit_processome_component_20_homolog_OS=Mus_musculus_GN=Utp20_PE=2_SV=2	2.00E-19	GO:0000462,GO:0005634,GO:0005730,GO:0005730,GO:0005730,GO:0006364,GO:0006364,GO:0030686,GO:0032040	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),nucleus,nucleolus,nucleolus,nucleolus,rRNA processing,rRNA processing,90S preribosome,small-subunit processome
comp31647_c0_seq2.p1				
comp31647_c0_seq5.p1	sp|P46992|YJR1_YEAST_Cell_wall_protein_YJL171C_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YJL171C_PE=1_SV=2	5.00E-22	GO:0003674,GO:0005886,GO:0005886,GO:0008150,GO:0009277,GO:0016020,GO:0031225	molecular_function,plasma membrane,plasma membrane,biological_process,fungal-type cell wall,membrane,anchored component of membrane
comp31648_c0_seq1.p1				
comp31649_c0_seq1.p1				
comp31650_c0_seq10.p1				
comp31650_c0_seq17.p1	sp|B4NDG5|RTEL1_DROWI_Regulator_of_telomere_elongation_helicase_1_homolog_OS=Drosophila_willistoni_GN=GK24923_PE=3_SV=1	9.00E-12	GO:0000166,GO:0003676,GO:0003677,GO:0003677,GO:0004003,GO:0004003,GO:0004386,GO:0005524,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006139,GO:0006200,GO:0006281,GO:0006974,GO:0008026,GO:0010569,GO:0016787,GO:0016818,GO:0032508,GO:0032508,GO:0046872,GO:0051536,GO:0051539	nucleotide binding,nucleic acid binding,DNA binding,DNA binding,ATP-dependent DNA helicase activity,ATP-dependent DNA helicase activity,helicase activity,ATP binding,ATP binding,ATP binding,nucleus,nucleus,nucleus,nucleobase-containing compound metabolic process,ATP catabolic process,DNA repair,cellular response to DNA damage stimulus,ATP-dependent helicase activity,regulation of double-strand break repair via homologous recombination,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,DNA duplex unwinding,DNA duplex unwinding,metal ion binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp31650_c0_seq19.p1	sp|B4NDG5|RTEL1_DROWI_Regulator_of_telomere_elongation_helicase_1_homolog_OS=Drosophila_willistoni_GN=GK24923_PE=3_SV=1	7.00E-12	GO:0000166,GO:0003676,GO:0003677,GO:0003677,GO:0004003,GO:0004003,GO:0004386,GO:0005524,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006139,GO:0006200,GO:0006281,GO:0006974,GO:0008026,GO:0010569,GO:0016787,GO:0016818,GO:0032508,GO:0032508,GO:0046872,GO:0051536,GO:0051539	nucleotide binding,nucleic acid binding,DNA binding,DNA binding,ATP-dependent DNA helicase activity,ATP-dependent DNA helicase activity,helicase activity,ATP binding,ATP binding,ATP binding,nucleus,nucleus,nucleus,nucleobase-containing compound metabolic process,ATP catabolic process,DNA repair,cellular response to DNA damage stimulus,ATP-dependent helicase activity,regulation of double-strand break repair via homologous recombination,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,DNA duplex unwinding,DNA duplex unwinding,metal ion binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp31650_c0_seq19.p3				
comp31650_c0_seq20.p1				
comp31650_c0_seq20.p2				
comp31650_c0_seq4.p1				
comp31650_c0_seq5.p1				
comp31651_c0_seq3.p1	sp|Q28056|ASPH_BOVIN_Aspartyl/asparaginyl_beta-hydroxylase_OS=Bos_taurus_GN=ASPH_PE=1_SV=1	4.00E-11	GO:0004597,GO:0004597,GO:0005737,GO:0005783,GO:0005783,GO:0005789,GO:0005886,GO:0007389,GO:0008285,GO:0010524,GO:0016020,GO:0016020,GO:0016021,GO:0016491,GO:0018193,GO:0030176,GO:0031585,GO:0031647,GO:0032237,GO:0032541,GO:0033198,GO:0035108,GO:0042264,GO:0042264,GO:0045862,GO:0045893,GO:0046872,GO:0051213,GO:0055114,GO:0060021,GO:0060325,GO:0070588,GO:0071277,GO:0090316,GO:0097202,GO:1901879	peptide-aspartate beta-dioxygenase activity,peptide-aspartate beta-dioxygenase activity,cytoplasm,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,plasma membrane,pattern specification process,negative regulation of cell proliferation,positive regulation of calcium ion transport into cytosol,membrane,membrane,integral component of membrane,oxidoreductase activity,peptidyl-amino acid modification,integral component of endoplasmic reticulum membrane,regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity,regulation of protein stability,activation of store-operated calcium channel activity,cortical endoplasmic reticulum,response to ATP,limb morphogenesis,peptidyl-aspartic acid hydroxylation,peptidyl-aspartic acid hydroxylation,positive regulation of proteolysis,positive regulation of transcription, DNA-templated,metal ion binding,dioxygenase activity,oxidation-reduction process,palate development,face morphogenesis,calcium ion transmembrane transport,cellular response to calcium ion,positive regulation of intracellular protein transport,activation of cysteine-type endopeptidase activity,regulation of protein depolymerization
comp31651_c0_seq5.p1				
comp31651_c0_seq5.p3	sp|Q6RUV5|RAC1_RAT_Ras-related_C3_botulinum_toxin_substrate_1_OS=Rattus_norvegicus_GN=Rac1_PE=1_SV=1	4.00E-98	GO:0000139,GO:0000166,GO:0001891,GO:0001934,GO:0001934,GO:0002093,GO:0002551,GO:0003382,GO:0003924,GO:0003924,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005525,GO:0005525,GO:0005525,GO:0005525,GO:0005622,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005802,GO:0005829,GO:0005886,GO:0005886,GO:0006184,GO:0006184,GO:0006897,GO:0006911,GO:0006928,GO:0006935,GO:0006972,GO:0007010,GO:0007015,GO:0007155,GO:0007186,GO:0007264,GO:0007264,GO:0007411,GO:0008283,GO:0010592,GO:0016020,GO:0016020,GO:0016020,GO:0016023,GO:0016358,GO:0016477,GO:0016601,GO:0017137,GO:0019897,GO:0019899,GO:0019901,GO:0021799,GO:0021831,GO:0030027,GO:0030032,GO:0030036,GO:0030036,GO:0030041,GO:0030334,GO:0030334,GO:0030334,GO:0030742,GO:0030838,GO:0031410,GO:0031529,GO:0031996,GO:0032587,GO:0032707,GO:0034446,GO:0036464,GO:0042470,GO:0042826,GO:0042995,GO:0043552,GO:0043652,GO:0045216,GO:0045453,GO:0045740,GO:0048532,GO:0048813,GO:0048870,GO:0048870,GO:0051668,GO:0060071,GO:0060263,GO:0070062,GO:0071526,GO:0071542,GO:0072659,GO:0090103,GO:0097178	Golgi membrane,nucleotide binding,phagocytic cup,positive regulation of protein phosphorylation,positive regulation of protein phosphorylation,auditory receptor cell morphogenesis,mast cell chemotaxis,epithelial cell morphogenesis,GTPase activity,GTPase activity,protein binding,protein binding,protein binding,protein binding,GTP binding,GTP binding,GTP binding,GTP binding,intracellular,cytoplasm,cytoplasm,cytoplasm,cytoplasm,trans-Golgi network,cytosol,plasma membrane,plasma membrane,GTP catabolic process,GTP catabolic process,endocytosis,phagocytosis, engulfment,cellular component movement,chemotaxis,hyperosmotic response,cytoskeleton organization,actin filament organization,cell adhesion,G-protein coupled receptor signaling pathway,small GTPase mediated signal transduction,small GTPase mediated signal transduction,axon guidance,cell proliferation,positive regulation of lamellipodium assembly,membrane,membrane,membrane,cytoplasmic membrane-bounded vesicle,dendrite development,cell migration,Rac protein signal transduction,Rab GTPase binding,extrinsic component of plasma membrane,enzyme binding,protein kinase binding,cerebral cortex radially oriented cell migration,embryonic olfactory bulb interneuron precursor migration,lamellipodium,lamellipodium assembly,actin cytoskeleton organization,actin cytoskeleton organization,actin filament polymerization,regulation of cell migration,regulation of cell migration,regulation of cell migration,GTP-dependent protein binding,positive regulation of actin filament polymerization,cytoplasmic vesicle,ruffle organization,thioesterase binding,ruffle membrane,negative regulation of interleukin-23 production,substrate adhesion-dependent cell spreading,cytoplasmic ribonucleoprotein granule,melanosome,histone deacetylase binding,cell projection,positive regulation of phosphatidylinositol 3-kinase activity,engulfment of apoptotic cell,cell-cell junction organization,bone resorption,positive regulation of DNA replication,anatomical structure arrangement,dendrite morphogenesis,cell motility,cell motility,localization within membrane,Wnt signaling pathway, planar cell polarity pathway,regulation of respiratory burst,extracellular vesicular exosome,semaphorin-plexin signaling pathway,dopaminergic neuron differentiation,protein localization to plasma membrane,cochlea morphogenesis,ruffle assembly
comp31651_c0_seq5.p4				
comp31652_c0_seq1.p1				
comp31652_c0_seq1.p2	sp|O02467|ASPG_SPOFR_N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase_(Fragment)_OS=Spodoptera_frugiperda_PE=1_SV=1	3.00E-28	GO:0003948,GO:0005764,GO:0005764,GO:0006508,GO:0008233,GO:0016787,GO:0016787	N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity,lysosome,lysosome,proteolysis,peptidase activity,hydrolase activity,hydrolase activity
comp31652_c0_seq12.p1	sp|O02467|ASPG_SPOFR_N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase_(Fragment)_OS=Spodoptera_frugiperda_PE=1_SV=1	2.00E-57	GO:0003948,GO:0005764,GO:0005764,GO:0006508,GO:0008233,GO:0016787,GO:0016787	N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity,lysosome,lysosome,proteolysis,peptidase activity,hydrolase activity,hydrolase activity
comp31652_c0_seq12.p2				
comp31652_c0_seq12.p3				
comp31652_c0_seq12.p4				
comp31652_c0_seq13.p1				
comp31652_c0_seq13.p2	sp|O02467|ASPG_SPOFR_N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase_(Fragment)_OS=Spodoptera_frugiperda_PE=1_SV=1	2.00E-57	GO:0003948,GO:0005764,GO:0005764,GO:0006508,GO:0008233,GO:0016787,GO:0016787	N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity,lysosome,lysosome,proteolysis,peptidase activity,hydrolase activity,hydrolase activity
comp31652_c0_seq13.p3				
comp31652_c0_seq18.p1				
comp31652_c0_seq18.p2	sp|O02467|ASPG_SPOFR_N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase_(Fragment)_OS=Spodoptera_frugiperda_PE=1_SV=1	9.00E-51	GO:0003948,GO:0005764,GO:0005764,GO:0006508,GO:0008233,GO:0016787,GO:0016787	N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity,lysosome,lysosome,proteolysis,peptidase activity,hydrolase activity,hydrolase activity
comp31652_c0_seq18.p3				
comp31652_c0_seq3.p1	sp|O02467|ASPG_SPOFR_N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase_(Fragment)_OS=Spodoptera_frugiperda_PE=1_SV=1	9.00E-51	GO:0003948,GO:0005764,GO:0005764,GO:0006508,GO:0008233,GO:0016787,GO:0016787	N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity,lysosome,lysosome,proteolysis,peptidase activity,hydrolase activity,hydrolase activity
comp31652_c0_seq3.p2				
comp31652_c0_seq3.p3				
comp31652_c0_seq3.p4				
comp31652_c0_seq4.p1	sp|O02467|ASPG_SPOFR_N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase_(Fragment)_OS=Spodoptera_frugiperda_PE=1_SV=1	2.00E-57	GO:0003948,GO:0005764,GO:0005764,GO:0006508,GO:0008233,GO:0016787,GO:0016787	N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity,lysosome,lysosome,proteolysis,peptidase activity,hydrolase activity,hydrolase activity
comp31652_c0_seq4.p2				
comp31652_c0_seq4.p3				
comp31652_c0_seq4.p4				

comp31730_c0_seq4.p1	sp|P54873|HMCS_ARATH_Hydroxymethylglutaryl-CoA_synthase_OS=Arabidopsis_thaliana_GN=HMGS_PE=1_SV=2	1.00E-119
comp31730_c0_seq4.p3		
comp31730_c0_seq6.p1	sp|P54873|HMCS_ARATH_Hydroxymethylglutaryl-CoA_synthase_OS=Arabidopsis_thaliana_GN=HMGS_PE=1_SV=2	5.00E-118
comp31731_c0_seq3.p1		
comp31731_c2_seq2.p1	sp|Q042B4|TRML_LACGA_Putative_RNA_(cytidine(34)-2'-O)-methyltransferase_OS=Lactobacillus_gasseri_(strain_ATCC_33323_/_DSM_20243)_GN=LGAS_1346_PE=3_SV=2	6.00E-28
comp31731_c2_seq3.p1	sp|P41920|YRB1_YEAST_Ran-specific_GTPase-activating_protein_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YRB1_PE=1_SV=1	4.00E-31
comp31732_c0_seq7.p1		
comp31734_c0_seq1.p1		
comp31734_c0_seq2.p1	sp|Q9M364|ATX3_ARATH_Histone-lysine_N-methyltransferase_ATX3_OS=Arabidopsis_thaliana_GN=ATX3_PE=2_SV=2	4.00E-21
comp31735_c0_seq2.p1	sp|P36861|YPTV2_VOLCA_GTP-binding_protein_yptV2_OS=Volvox_carteri_GN=YPTV2_PE=3_SV=1	3.00E-37
comp31735_c0_seq2.p2		
comp31737_c0_seq3.p1	sp|O35604|NPC1_MOUSE_Niemann-Pick_C1_protein_OS=Mus_musculus_GN=Npc1_PE=1_SV=1	2.00E-15
comp31739_c0_seq4.p1	sp|Q76C99|RF1_ORYSI_Protein_Rf1,_mitochondrial_OS=Oryza_sativa_subsp._indica_GN=Rf1_PE=2_SV=1	2.00E-40
comp31739_c0_seq5.p1		
comp31739_c0_seq6.p1		
comp31741_c0_seq1.p1	sp|Q5E9T7|JADE1_BOVIN_Protein_Jade-1_OS=Bos_taurus_GN=PHF17_PE=2_SV=1	1.00E-25
comp31741_c0_seq3.p1	sp|Q8IYD8|FANCM_HUMAN_Fanconi_anemia_group_M_protein_OS=Homo_sapiens_GN=FANCM_PE=1_SV=2	7.00E-93
comp31741_c0_seq5.p1	sp|Q5E9T7|JADE1_BOVIN_Protein_Jade-1_OS=Bos_taurus_GN=PHF17_PE=2_SV=1	1.00E-25
comp31741_c0_seq5.p2		
comp31741_c0_seq8.p1	sp|Q8IYD8|FANCM_HUMAN_Fanconi_anemia_group_M_protein_OS=Homo_sapiens_GN=FANCM_PE=1_SV=2	2.00E-78
comp31742_c0_seq2.p1		
comp31742_c0_seq2.p2		
comp31742_c1_seq1.p1		
comp31743_c0_seq3.p1		
comp31743_c0_seq3.p2	sp|Q17QZ4|TFDP1_BOVIN_Transcription_factor_Dp-1_OS=Bos_taurus_GN=TFDP1_PE=2_SV=1	2.00E-55
comp31743_c0_seq4.p1		
comp31743_c0_seq4.p2	sp|Q17QZ4|TFDP1_BOVIN_Transcription_factor_Dp-1_OS=Bos_taurus_GN=TFDP1_PE=2_SV=1	2.00E-55
comp31744_c0_seq1.p1		
comp31744_c0_seq1.p5		
comp31745_c0_seq2.p1		
comp31745_c0_seq2.p2	sp|P25526|GABD_ECOLI_Succinate-semialdehyde_dehydrogenase_[NADP(+)]_GabD_OS=Escherichia_coli_(strain_K12)_GN=gabD_PE=1_SV=1	6.00E-111
comp31745_c0_seq5.p1		
comp31745_c0_seq5.p2	sp|Q8BWF0|SSDH_MOUSE_Succinate-semialdehyde_dehydrogenase,_mitochondrial_OS=Mus_musculus_GN=Aldh5a1_PE=1_SV=1	4.00E-150
comp31746_c0_seq2.p1		
comp31747_c0_seq2.p1		
comp31747_c0_seq4.p1		
comp31748_c0_seq2.p1		
comp31748_c0_seq3.p1		
comp31748_c0_seq6.p1		
comp31748_c0_seq7.p1		
comp31748_c0_seq9.p1		
comp31751_c0_seq1.p1	sp|Q8MKF1|THTPA_BOVIN_Thiamine-triphosphatase_OS=Bos_taurus_GN=THTPA_PE=1_SV=3	8.00E-19
comp31751_c0_seq12.p1		
comp31751_c0_seq14.p1	sp|Q8MKF1|THTPA_BOVIN_Thiamine-triphosphatase_OS=Bos_taurus_GN=THTPA_PE=1_SV=3	8.00E-19
comp31751_c0_seq14.p2		
comp31751_c0_seq15.p1	sp|Q8MKF1|THTPA_BOVIN_Thiamine-triphosphatase_OS=Bos_taurus_GN=THTPA_PE=1_SV=3	8.00E-19
comp31751_c0_seq16.p1	sp|Q9ZVT9|C2GR1_ARATH_C2_and_GRAM_domain-containing_protein_At1g03370_OS=Arabidopsis_thaliana_GN=At1g03370_PE=2_SV=4	5.00E-13
comp31751_c0_seq16.p2	sp|Q8MKF1|THTPA_BOVIN_Thiamine-triphosphatase_OS=Bos_taurus_GN=THTPA_PE=1_SV=3	8.00E-19
comp31751_c0_seq17.p1	sp|Q8MKF1|THTPA_BOVIN_Thiamine-triphosphatase_OS=Bos_taurus_GN=THTPA_PE=1_SV=3	8.00E-19
comp31751_c0_seq4.p1	sp|Q9ZVT9|C2GR1_ARATH_C2_and_GRAM_domain-containing_protein_At1g03370_OS=Arabidopsis_thaliana_GN=At1g03370_PE=2_SV=4	5.00E-13
comp31751_c0_seq4.p2	sp|Q8MKF1|THTPA_BOVIN_Thiamine-triphosphatase_OS=Bos_taurus_GN=THTPA_PE=1_SV=3	8.00E-19
comp31751_c0_seq7.p1	sp|Q8MKF1|THTPA_BOVIN_Thiamine-triphosphatase_OS=Bos_taurus_GN=THTPA_PE=1_SV=3	8.00E-19
comp31751_c0_seq7.p2		
comp31751_c0_seq9.p1	sp|Q8MKF1|THTPA_BOVIN_Thiamine-triphosphatase_OS=Bos_taurus_GN=THTPA_PE=1_SV=3	8.00E-19
comp31752_c1_seq15.p1	sp|P48467|KINH_NEUCR_Kinesin_heavy_chain_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=kin_PE=1_SV=2	2.00E-125
comp31752_c1_seq16.p1	sp|A6QLU8|NXN_BOVIN_Nucleoredoxin_OS=Bos_taurus_GN=NXN_PE=2_SV=1	5.00E-57
comp31752_c1_seq23.p1		
comp31752_c1_seq6.p1	sp|Q9ESJ1|CABL1_MOUSE_CDK5_and_ABL1_enzyme_substrate_1_OS=Mus_musculus_GN=Cables1_PE=1_SV=2	7.00E-20
comp31752_c1_seq8.p1	sp|P48467|KINH_NEUCR_Kinesin_heavy_chain_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=kin_PE=1_SV=2	2.00E-19
comp31752_c1_seq9.p1	sp|O43280|TREA_HUMAN_Trehalase_OS=Homo_sapiens_GN=TREH_PE=1_SV=2	1.00E-66
comp31752_c1_seq9.p2	sp|Q6N075|MFSD5_HUMAN_Major_facilitator_superfamily_domain-containing_protein_5_OS=Homo_sapiens_GN=MFSD5_PE=2_SV=2	3.00E-26
comp31753_c0_seq11.p1	sp|Q5PQM2|KLC4_RAT_Kinesin_light_chain_4_OS=Rattus_norvegicus_GN=Klc4_PE=2_SV=1	7.00E-19
comp31753_c0_seq12.p1	sp|Q2HJJ0|KLC4_BOVIN_Kinesin_light_chain_4_OS=Bos_taurus_GN=KLC4_PE=2_SV=2	7.00E-19
comp31753_c0_seq14.p1	sp|Q7Z494|NPHP3_HUMAN_Nephrocystin-3_OS=Homo_sapiens_GN=NPHP3_PE=1_SV=1	1.00E-43
comp31753_c0_seq9.p1	sp|Q5PQM2|KLC4_RAT_Kinesin_light_chain_4_OS=Rattus_norvegicus_GN=Klc4_PE=2_SV=1	1.00E-21
comp31754_c0_seq11.p1		
comp31754_c0_seq11.p3		
comp31755_c0_seq11.p1		
comp31755_c0_seq5.p1		
comp31755_c0_seq6.p1		
comp31755_c0_seq7.p1	sp|Q7TPS5|K0528_MOUSE_Uncharacterized_protein_KIAA0528_OS=Mus_musculus_GN=Kiaa0528_PE=1_SV=2	5.00E-13
comp31756_c1_seq2.p1		
comp31756_c1_seq3.p1		
comp31756_c1_seq3.p2		
comp31756_c2_seq3.p1		
comp31757_c0_seq2.p1		
comp31757_c0_seq2.p2	sp|Q86TL2|TM110_HUMAN_Transmembrane_protein_110_OS=Homo_sapiens_GN=TMEM110_PE=2_SV=1	3.00E-27
comp31757_c0_seq2.p6		
comp31757_c0_seq3.p1		
comp31757_c0_seq3.p2	sp|Q86TL2|TM110_HUMAN_Transmembrane_protein_110_OS=Homo_sapiens_GN=TMEM110_PE=2_SV=1	3.00E-27
comp31757_c0_seq3.p7		
comp31758_c0_seq5.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	2.00E-11
comp31760_c0_seq2.p1	sp|Q8VZR6|INT1_ARATH_Probable_inositol_transporter_1_OS=Arabidopsis_thaliana_GN=INT1_PE=2_SV=1	6.00E-103
comp31760_c0_seq3.p1		
comp31760_c0_seq3.p2		
comp31760_c0_seq4.p1		
comp31760_c0_seq6.p1	sp|Q96QE2|MYCT_HUMAN_Proton_myo-inositol_cotransporter_OS=Homo_sapiens_GN=SLC2A13_PE=1_SV=3	4.00E-49
comp31760_c0_seq8.p1		
comp31761_c0_seq1.p1	sp|C1FXW9|THOC2_DASNO_THO_complex_subunit_2_OS=Dasypus_novemcinctus_GN=THOC2_PE=3_SV=1	2.00E-14
comp31761_c0_seq5.p1	sp|B2KI97|THOC2_RHIFE_THO_complex_subunit_2_OS=Rhinolophus_ferrumequinum_GN=THOC2_PE=3_SV=1	2.00E-63
comp31762_c0_seq1.p1	sp|P78813|YCTB_SCHPO_ENTH_domain-containing_protein_C794.11c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC794.11c_PE=1_SV=2	3.00E-33
comp31762_c0_seq1.p4		
comp31762_c1_seq1.p1	sp|P0AFR6|YCIO_SHIFL_Uncharacterized_protein_yciO_OS=Shigella_flexneri_GN=yciO_PE=3_SV=1	1.00E-24
comp31762_c1_seq3.p1	sp|P0AFR6|YCIO_SHIFL_Uncharacterized_protein_yciO_OS=Shigella_flexneri_GN=yciO_PE=3_SV=1	1.00E-24
comp31764_c1_seq12.p1		
comp31764_c1_seq12.p2	sp|Q09809|YAB9_SCHPO_Uncharacterized_membrane_protein_C2G11.09_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC2G11.09_PE=2_SV=2	4.00E-20
comp31764_c1_seq12.p5		
comp31764_c1_seq3.p1		
comp31764_c1_seq3.p2		
comp31764_c1_seq7.p1	sp|Q09809|YAB9_SCHPO_Uncharacterized_membrane_protein_C2G11.09_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC2G11.09_PE=2_SV=2	4.00E-19
comp31764_c1_seq7.p5		
comp31764_c1_seq8.p1	sp|Q09809|YAB9_SCHPO_Uncharacterized_membrane_protein_C2G11.09_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC2G11.09_PE=2_SV=2	4.00E-20
comp31764_c1_seq8.p2	sp|Q06538|YL241_YEAST_Uncharacterized_membrane_protein_YLR241W_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YLR241W_PE=1_SV=1	6.00E-11
comp31764_c1_seq8.p4		
comp31765_c0_seq1.p1	sp|Q9SEI2|PS6AA_ARATH_26S_protease_regulatory_subunit_6A_homolog_A_OS=Arabidopsis_thaliana_GN=RPT5A_PE=2_SV=1	0
comp31765_c0_seq1.p2	sp|P53609|PGTB1_HUMAN_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Homo_sapiens_GN=PGGT1B_PE=1_SV=2	2.00E-47
comp31765_c0_seq1.p3	sp|Q8ZIK1|RLUA_YERPE_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Yersinia_pestis_GN=rluA_PE=3_SV=1	7.00E-41
comp31765_c0_seq12.p1	sp|Q9SEI2|PS6AA_ARATH_26S_protease_regulatory_subunit_6A_homolog_A_OS=Arabidopsis_thaliana_GN=RPT5A_PE=2_SV=1	0
comp31765_c0_seq12.p2	sp|Q8ZIK1|RLUA_YERPE_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Yersinia_pestis_GN=rluA_PE=3_SV=1	7.00E-41
comp31765_c0_seq12.p3	sp|P53609|PGTB1_HUMAN_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Homo_sapiens_GN=PGGT1B_PE=1_SV=2	1.00E-19
comp31765_c0_seq12.p4	sp|P53610|PGTB1_RAT_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Rattus_norvegicus_GN=Pggt1b_PE=1_SV=1	9.00E-21
comp31765_c0_seq14.p1	sp|Q9SEI2|PS6AA_ARATH_26S_protease_regulatory_subunit_6A_homolog_A_OS=Arabidopsis_thaliana_GN=RPT5A_PE=2_SV=1	0
comp31765_c0_seq14.p2	sp|Q8ZIK1|RLUA_YERPE_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Yersinia_pestis_GN=rluA_PE=3_SV=1	7.00E-41
comp31765_c0_seq14.p3	sp|P53609|PGTB1_HUMAN_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Homo_sapiens_GN=PGGT1B_PE=1_SV=2	6.00E-39
comp31765_c0_seq14.p4	sp|P53610|PGTB1_RAT_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Rattus_norvegicus_GN=Pggt1b_PE=1_SV=1	9.00E-21
comp31765_c0_seq19.p1	sp|Q9SEI2|PS6AA_ARATH_26S_protease_regulatory_subunit_6A_homolog_A_OS=Arabidopsis_thaliana_GN=RPT5A_PE=2_SV=1	0
comp31765_c0_seq19.p2	sp|Q8ZIK1|RLUA_YERPE_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Yersinia_pestis_GN=rluA_PE=3_SV=1	7.00E-41
comp31765_c0_seq19.p3	sp|P53609|PGTB1_HUMAN_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Homo_sapiens_GN=PGGT1B_PE=1_SV=2	2.00E-21
comp31765_c0_seq19.p4	sp|P53610|PGTB1_RAT_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Rattus_norvegicus_GN=Pggt1b_PE=1_SV=1	9.00E-21
comp31765_c0_seq20.p1	sp|Q9SEI2|PS6AA_ARATH_26S_protease_regulatory_subunit_6A_homolog_A_OS=Arabidopsis_thaliana_GN=RPT5A_PE=2_SV=1	0
comp31765_c0_seq20.p2	sp|Q8ZIK1|RLUA_YERPE_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Yersinia_pestis_GN=rluA_PE=3_SV=1	7.00E-41
comp31765_c0_seq20.p3	sp|P53609|PGTB1_HUMAN_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Homo_sapiens_GN=PGGT1B_PE=1_SV=2	7.00E-41
comp31765_c0_seq20.p5	sp|P53610|PGTB1_RAT_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Rattus_norvegicus_GN=Pggt1b_PE=1_SV=1	9.00E-21
comp31765_c0_seq6.p1	sp|Q9SEI2|PS6AA_ARATH_26S_protease_regulatory_subunit_6A_homolog_A_OS=Arabidopsis_thaliana_GN=RPT5A_PE=2_SV=1	0
comp31765_c0_seq6.p2	sp|P53609|PGTB1_HUMAN_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Homo_sapiens_GN=PGGT1B_PE=1_SV=2	1.00E-21
comp31765_c0_seq6.p3	sp|P53610|PGTB1_RAT_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Rattus_norvegicus_GN=Pggt1b_PE=1_SV=1	9.00E-21
comp31765_c0_seq9.p1	sp|Q9SEI2|PS6AA_ARATH_26S_protease_regulatory_subunit_6A_homolog_A_OS=Arabidopsis_thaliana_GN=RPT5A_PE=2_SV=1	0
comp31765_c0_seq9.p2	sp|P53609|PGTB1_HUMAN_Geranylgeranyl_transferase_type-1_subunit_beta_OS=Homo_sapiens_GN=PGGT1B_PE=1_SV=2	2.00E-49
comp31765_c0_seq9.p3	sp|Q8ZIK1|RLUA_YERPE_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Yersinia_pestis_GN=rluA_PE=3_SV=1	7.00E-41
comp31766_c0_seq2.p1		
comp31766_c1_seq1.p1		
comp31767_c0_seq12.p1	sp|Q61687|ATRX_MOUSE_Transcriptional_regulator_ATRX_OS=Mus_musculus_GN=Atrx_PE=1_SV=3	3.00E-45
comp31768_c0_seq1.p1		
comp31769_c0_seq1.p1		
comp31769_c0_seq1.p2	sp|Q110K2|RF3_TRIEI_Peptide_chain_release_factor_3_OS=Trichodesmium_erythraeum_(strain_IMS101)_GN=prfC_PE=3_SV=1	7.00E-23
comp31769_c0_seq3.p1	sp|B0JIY7|RF3_MICAN_Peptide_chain_release_factor_3_OS=Microcystis_aeruginosa_(strain_NIES-843)_GN=prfC_PE=3_SV=1	0
comp31769_c0_seq3.p2		
comp31769_c0_seq4.p1		
comp31769_c0_seq4.p3	sp|Q110K2|RF3_TRIEI_Peptide_chain_release_factor_3_OS=Trichodesmium_erythraeum_(strain_IMS101)_GN=prfC_PE=3_SV=1	7.00E-23
comp31769_c0_seq5.p1	sp|B0JIY7|RF3_MICAN_Peptide_chain_release_factor_3_OS=Microcystis_aeruginosa_(strain_NIES-843)_GN=prfC_PE=3_SV=1	0
comp31769_c0_seq5.p2		
comp31769_c0_seq6.p1		
comp31769_c0_seq6.p2	sp|Q31KM4|RF3_SYNE7_Peptide_chain_release_factor_3_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=prfC_PE=3_SV=1	7.00E-62
comp31769_c0_seq7.p1	sp|B0JIY7|RF3_MICAN_Peptide_chain_release_factor_3_OS=Microcystis_aeruginosa_(strain_NIES-843)_GN=prfC_PE=3_SV=1	0
comp31769_c0_seq7.p2		
comp31771_c0_seq1.p1		
comp31771_c0_seq10.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	9.00E-30
comp31771_c0_seq12.p2	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	2.00E-17
comp31771_c0_seq15.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	1.00E-28
comp31771_c0_seq17.p1		
comp31771_c0_seq18.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	4.00E-26
comp31771_c0_seq2.p1	sp|Q869L4|FNKA_DICDI_Probable_serine/threonine-protein_kinase_fnkA_OS=Dictyostelium_discoideum_GN=fnkA_PE=3_SV=1	8.00E-26
comp31771_c0_seq21.p1		
comp31771_c0_seq22.p1		
comp31771_c0_seq24.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	1.00E-16
comp31771_c0_seq26.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	1.00E-13
comp31771_c0_seq29.p1	sp|Q5UR85|YR636_MIMIV_Putative_FNIP_repeat-containing_protein_R636_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R636_PE=4_SV=1	9.00E-12
comp31771_c0_seq3.p1		
comp31771_c0_seq30.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	6.00E-32
comp31771_c0_seq32.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	4.00E-38
comp31771_c0_seq35.p2		
comp31771_c0_seq36.p1		
comp31771_c0_seq6.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	2.00E-21
comp31771_c0_seq7.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	1.00E-16
comp31772_c0_seq1.p1	sp|Q4WVM1|RAD5_ASPFU_DNA_repair_protein_rad5_OS=Neosartorya_fumigata_(strain_ATCC_MYA-4609_/_Af293_/_CBS_101355_/_FGSC_A1100)_GN=rad5_PE=3_SV=2	5.00E-16
comp31772_c0_seq13.p1	sp|Q9FIY7|SM3L3_ARATH_Putative_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A_member_3-like_3_OS=Arabidopsis_thaliana_GN=At5g43530_PE=3_SV=1	3.00E-31
comp31772_c0_seq2.p1	sp|Q9FIY7|SM3L3_ARATH_Putative_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A_member_3-like_3_OS=Arabidopsis_thaliana_GN=At5g43530_PE=3_SV=1	3.00E-31
comp31772_c0_seq3.p1		
comp31772_c0_seq5.p1	sp|Q9FNI6|SM3L2_ARATH_Putative_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A_member_3-like_2_OS=Arabidopsis_thaliana_GN=At5g22750_PE=2_SV=1	7.00E-27
comp31772_c0_seq9.p1	sp|Q9FNI6|SM3L2_ARATH_Putative_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A_member_3-like_2_OS=Arabidopsis_thaliana_GN=At5g22750_PE=2_SV=1	2.00E-63
comp31773_c0_seq2.p1		
comp31773_c0_seq3.p1	sp|Q4U2R1|HERC2_MOUSE_E3_ubiquitin-protein_ligase_HERC2_OS=Mus_musculus_GN=Herc2_PE=1_SV=3	5.00E-53
comp31773_c0_seq3.p2		
comp31773_c1_seq1.p1		
comp31774_c0_seq4.p1		
comp31775_c0_seq5.p1		
comp31775_c0_seq6.p1		
comp31776_c0_seq16.p1	sp|Q8K2I9|FBX18_MOUSE_F-box_only_protein_18_OS=Mus_musculus_GN=Fbxo18_PE=2_SV=1	1.00E-39
comp31776_c0_seq16.p3		
comp31776_c0_seq19.p1	sp|Q8K2I9|FBX18_MOUSE_F-box_only_protein_18_OS=Mus_musculus_GN=Fbxo18_PE=2_SV=1	2.00E-52
comp31776_c0_seq19.p2		
comp31776_c0_seq22.p1	sp|Q8K2I9|FBX18_MOUSE_F-box_only_protein_18_OS=Mus_musculus_GN=Fbxo18_PE=2_SV=1	1.00E-35
comp31776_c0_seq22.p2		
comp31776_c0_seq22.p4		
comp31776_c0_seq28.p1	sp|Q8K2I9|FBX18_MOUSE_F-box_only_protein_18_OS=Mus_musculus_GN=Fbxo18_PE=2_SV=1	3.00E-38
comp31776_c0_seq28.p2		
comp31776_c0_seq28.p3		
comp31776_c0_seq4.p1	sp|Q8K2I9|FBX18_MOUSE_F-box_only_protein_18_OS=Mus_musculus_GN=Fbxo18_PE=2_SV=1	2.00E-34
comp31776_c0_seq4.p2		
comp31776_c0_seq4.p3		
comp31776_c0_seq5.p1	sp|Q6NWJ4|DNJC2_DANRE_DnaJ_homolog_subfamily_C_member_2_OS=Danio_rerio_GN=dnajc2_PE=2_SV=1	3.00E-36
comp31776_c0_seq5.p3		
comp31776_c0_seq7.p1	sp|Q8K2I9|FBX18_MOUSE_F-box_only_protein_18_OS=Mus_musculus_GN=Fbxo18_PE=2_SV=1	4.00E-38
comp31776_c0_seq7.p2		
comp31776_c0_seq9.p1	sp|Q8K2I9|FBX18_MOUSE_F-box_only_protein_18_OS=Mus_musculus_GN=Fbxo18_PE=2_SV=1	2.00E-51
comp31776_c0_seq9.p4		
comp31777_c0_seq2.p1		
comp31777_c0_seq3.p1	sp|Q9D832|DNJB4_MOUSE_DnaJ_homolog_subfamily_B_member_4_OS=Mus_musculus_GN=Dnajb4_PE=2_SV=1	9.00E-13
comp31777_c0_seq4.p1		
comp31777_c0_seq6.p1		
comp31780_c0_seq1.p1		
comp31781_c0_seq1.p1		
comp31781_c0_seq1.p3		
comp31781_c0_seq4.p1		
comp31781_c0_seq5.p2		
comp31781_c0_seq7.p1		
comp31782_c0_seq12.p1	sp|O51039|Y006_BORBU_UPF0118_membrane_protein_BB_0006_OS=Borrelia_burgdorferi_(strain_ATCC_35210_/_B31_/_CIP_102532_/_DSM_4680)_GN=BB_0006_PE=3_SV=2	1.00E-11
comp31782_c0_seq17.p1	sp|P0AFS6|TQSA_SHIFL_AI-2_transport_protein_tqsA_OS=Shigella_flexneri_GN=tqsA_PE=3_SV=1	3.00E-20
comp31782_c0_seq21.p1	sp|O51039|Y006_BORBU_UPF0118_membrane_protein_BB_0006_OS=Borrelia_burgdorferi_(strain_ATCC_35210_/_B31_/_CIP_102532_/_DSM_4680)_GN=BB_0006_PE=3_SV=2	1.00E-19
comp31782_c0_seq21.p2		
comp31783_c0_seq6.p1	sp|P0CM60|VAC8_CRYNJ_Vacuolar_protein_8_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=VAC8_PE=3_SV=1	9.00E-38
comp31783_c0_seq6.p2	sp|O28972|Y1297_ARCFU_Cell_division_cycle_protein_48_homolog_AF_1297_OS=Archaeoglobus_fulgidus_(strain_ATCC_49558_/_VC-16_/_DSM_4304_/_JCM_9628_/_NBRC_100126)_GN=AF_1297_PE=3_SV=1	1.00E-178
comp31783_c0_seq7.p1	sp|P0CM60|VAC8_CRYNJ_Vacuolar_protein_8_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=VAC8_PE=3_SV=1	8.00E-38
comp31783_c0_seq7.p2	sp|O28972|Y1297_ARCFU_Cell_division_cycle_protein_48_homolog_AF_1297_OS=Archaeoglobus_fulgidus_(strain_ATCC_49558_/_VC-16_/_DSM_4304_/_JCM_9628_/_NBRC_100126)_GN=AF_1297_PE=3_SV=1	1.00E-178
comp31783_c0_seq7.p7		
comp31783_c0_seq9.p1	sp|Q8NB90|SPAT5_HUMAN_Spermatogenesis-associated_protein_5_OS=Homo_sapiens_GN=SPATA5_PE=1_SV=3	3.00E-33
comp31784_c0_seq2.p1		
comp31785_c0_seq3.p2		
comp31785_c0_seq4.p1	sp|Q969S3|ZN622_HUMAN_Zinc_finger_protein_622_OS=Homo_sapiens_GN=ZNF622_PE=1_SV=1	6.00E-37
comp31785_c0_seq4.p2		
comp31786_c0_seq7.p1	sp|A7SKJ3|DPH2_NEMVE_Diphthamide_biosynthesis_protein_2_OS=Nematostella_vectensis_GN=dph2_PE=3_SV=1	1.00E-49
comp31786_c0_seq7.p2	sp|Q5R7X9|RAD1_PONAB_Cell_cycle_checkpoint_protein_RAD1_OS=Pongo_abelii_GN=RAD1_PE=2_SV=1	1.00E-31
comp31786_c0_seq7.p3	sp|Q60441|MPU1_CRIGR_Mannose-P-dolichol_utilization_defect_1_protein_OS=Cricetulus_griseus_GN=MPDU1_PE=2_SV=2	1.00E-16
comp31788_c0_seq1.p1		
comp31788_c0_seq2.p1		
comp31788_c1_seq2.p1		
comp31788_c1_seq4.p1	sp|P97366|EVI5_MOUSE_Ecotropic_viral_integration_site_5_protein_OS=Mus_musculus_GN=Evi5_PE=1_SV=2	7.00E-16
comp31789_c0_seq2.p2		
comp31789_c0_seq3.p1		
comp31789_c0_seq4.p1		
comp31789_c0_seq7.p1		
comp31789_c0_seq9.p1		
comp31790_c0_seq4.p1	sp|P05659|MYSN_ACACA_Myosin-2_heavy_chain,_non_muscle_OS=Acanthamoeba_castellanii_PE=3_SV=1	9.00E-11
comp31790_c1_seq3.p1		
comp31791_c0_seq10.p1		
comp31791_c0_seq11.p1		
comp31791_c0_seq9.p1		
comp31793_c0_seq1.p1	sp|Q5SSW2|PSME4_MOUSE_Proteasome_activator_complex_subunit_4_OS=Mus_musculus_GN=Psme4_PE=1_SV=1	6.00E-16
comp31795_c0_seq2.p1		
comp31796_c0_seq1.p1		
comp31797_c0_seq3.p1	sp|Q92616|GCN1L_HUMAN_Translational_activator_GCN1_OS=Homo_sapiens_GN=GCN1L1_PE=1_SV=6	0
comp31797_c0_seq3.p2		
comp31798_c0_seq6.p1	sp|Q8GYL3|ULP1A_ARATH_Ubiquitin-like-specific_protease_1A_OS=Arabidopsis_thaliana_GN=ULP1A_PE=2_SV=2	3.00E-34
comp31798_c0_seq8.p1		
comp31799_c0_seq1.p1		
comp31800_c0_seq1.p1		
comp31800_c0_seq11.p1	sp|P20054|PYR1_DICDI_Protein_PYR1-3_OS=Dictyostelium_discoideum_GN=pyr1-3_PE=1_SV=3	0
comp31800_c0_seq17.p1		
comp31800_c2_seq1.p1	sp|P20054|PYR1_DICDI_Protein_PYR1-3_OS=Dictyostelium_discoideum_GN=pyr1-3_PE=1_SV=3	0
comp31801_c0_seq10.p1		
comp31801_c0_seq18.p1		
comp31801_c0_seq19.p1		
comp31801_c0_seq24.p1		
comp31801_c0_seq27.p1		
comp31802_c0_seq1.p1	sp|P54002|YTH3_CAEEL_Putative_glycosyltransferase_C14A4.3_OS=Caenorhabditis_elegans_GN=C14A4.3_PE=1_SV=2	1.00E-76
comp31802_c1_seq4.p1		
comp31803_c0_seq3.p1	sp|Q8T9W1|TAGD_DICDI_Serine_protease/ABC_transporter_B_family_protein_tagD_OS=Dictyostelium_discoideum_GN=tagD_PE=3_SV=1	2.00E-13
comp31803_c0_seq3.p2	sp|Q9LJU2|PDI53_ARATH_Protein_disulfide-isomerase_5-3_OS=Arabidopsis_thaliana_GN=PDIL5-3_PE=2_SV=1	3.00E-61
comp31803_c0_seq4.p1		
comp31803_c0_seq5.p1	sp|Q9LJU2|PDI53_ARATH_Protein_disulfide-isomerase_5-3_OS=Arabidopsis_thaliana_GN=PDIL5-3_PE=2_SV=1	3.00E-23
comp31804_c0_seq3.p1		
comp31805_c0_seq4.p1		
comp31805_c0_seq4.p16		
comp31805_c0_seq4.p2	sp|A2BF66|HORM1_DANRE_HORMA_domain-containing_protein_1_OS=Danio_rerio_GN=hormad1_PE=2_SV=1	6.00E-14
comp31805_c0_seq4.p3		
comp31805_c0_seq4.p6		
comp31805_c0_seq8.p1	sp|Q11L51|RLME_MESSB_Ribosomal_RNA_large_subunit_methyltransferase_E_OS=Mesorhizobium_sp._(strain_BNC1)_GN=rlmE_PE=3_SV=1	3.00E-17
comp31805_c0_seq8.p4		
comp31805_c0_seq8.p8		
comp31805_c0_seq9.p1		
comp31806_c0_seq5.p1		
comp31807_c0_seq1.p1	sp|Q6DRB1|GLE1_DANRE_Nucleoporin_GLE1_OS=Danio_rerio_GN=gle1_PE=2_SV=2	2.00E-16
comp31807_c0_seq2.p1	sp|Q6DRB1|GLE1_DANRE_Nucleoporin_GLE1_OS=Danio_rerio_GN=gle1_PE=2_SV=2	2.00E-16
comp31808_c0_seq2.p1	sp|Q923G2|RPAB3_MOUSE_DNA-directed_RNA_polymerases_I,_II,_and_III_subunit_RPABC3_OS=Mus_musculus_GN=Polr2h_PE=2_SV=3	2.00E-42
comp31808_c0_seq8.p1	sp|Q9MAT5|ANM42_ARATH_Probable_protein_arginine_N-methyltransferase_4.2_OS=Arabidopsis_thaliana_GN=PRMT4.2_PE=1_SV=1	2.00E-103
comp31808_c0_seq8.p6		
comp31808_c0_seq9.p1	sp|P38074|HMT1_YEAST_HNRNP_arginine_N-methyltransferase_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=HMT1_PE=1_SV=1	3.00E-64
comp31808_c0_seq9.p2	sp|O04714|GCR1_ARATH_G-protein_coupled_receptor_1_OS=Arabidopsis_thaliana_GN=GCR1_PE=1_SV=1	3.00E-18
comp31809_c0_seq2.p1	sp|Q8VCH0|THIKB_MOUSE_3-ketoacyl-CoA_thiolase_B,_peroxisomal_OS=Mus_musculus_GN=Acaa1b_PE=2_SV=1	9.00E-58
comp31809_c0_seq3.p1	sp|Q06850|CDPK1_ARATH_Calcium-dependent_protein_kinase_1_OS=Arabidopsis_thaliana_GN=CPK1_PE=1_SV=1	3.00E-98
comp31809_c0_seq4.p1	sp|Q06850|CDPK1_ARATH_Calcium-dependent_protein_kinase_1_OS=Arabidopsis_thaliana_GN=CPK1_PE=1_SV=1	3.00E-98
comp31809_c0_seq5.p1	sp|Q8VCH0|THIKB_MOUSE_3-ketoacyl-CoA_thiolase_B,_peroxisomal_OS=Mus_musculus_GN=Acaa1b_PE=2_SV=1	5.00E-145
comp31810_c0_seq1.p1		
comp31810_c0_seq3.p1		
comp31811_c0_seq2.p1		
comp31811_c0_seq4.p1		
comp31811_c0_seq8.p1		
comp31812_c0_seq5.p1	sp|Q7YRZ2|APTX_BOVIN_Aprataxin_OS=Bos_taurus_GN=APTX_PE=2_SV=1	3.00E-36
comp31813_c0_seq3.p1		
comp31814_c0_seq4.p1	sp|Q8G6Z9|PEPD_BIFLO_Dipeptidase_OS=Bifidobacterium_longum_(strain_NCC_2705)_GN=pepD_PE=1_SV=1	1.00E-19
comp31814_c0_seq4.p2	sp|P42856|ZB14_MAIZE_14_kDa_zinc-binding_protein_OS=Zea_mays_GN=ZBP14_PE=1_SV=1	5.00E-37
comp31815_c0_seq3.p1	sp|Q3YL57|NHX8_ARATH_Sodium/hydrogen_exchanger_8_OS=Arabidopsis_thaliana_GN=NHX8_PE=2_SV=1	1.00E-17
comp31815_c0_seq4.p1		
comp31815_c0_seq5.p1	sp|Q3YL57|NHX8_ARATH_Sodium/hydrogen_exchanger_8_OS=Arabidopsis_thaliana_GN=NHX8_PE=2_SV=1	2.00E-76

comp31816_c1_seq12.p1	sp|P61315|G3ST3_MOUSE_Galactose-3-O-sulfotransferase_3_OS=Mus_musculus_GN=Gal3st3_PE=2_SV=1	5.00E-14	GO:0001733,GO:0005575,GO:0005794,GO:0005794,GO:0009058,GO:0016020,GO:0016021,GO:0016021,GO:0016740,GO:0032580,GO:0050694
comp31816_c1_seq8.p1			
comp31816_c1_seq8.p2			
comp31817_c0_seq2.p1			
comp31817_c0_seq3.p1			
comp31817_c1_seq1.p2			
comp31817_c2_seq1.p1			
comp31818_c0_seq2.p1	sp|Q39161|NIR_ARATH_Ferredoxin--nitrite_reductase,_chloroplastic_OS=Arabidopsis_thaliana_GN=NIR1_PE=1_SV=1	8.00E-139	GO:0005739,GO:0009507,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009570,GO:0009570,GO:0009570,GO:0010167,GO:0010167,GO:0015706,GO:0016020,GO:0016491,GO:0016491,GO:0019344,GO:0020037,GO:0042128,GO:0042128,GO:0046872,GO:0048046,GO:0048307,GO:0050421,GO:0051536,GO:0051536,GO:0051539,GO:0055114,GO:0055114,GO:0055114,GO:0005829
comp31818_c0_seq4.p1			
comp31818_c0_seq5.p1	sp|Q51879|NIR_PHOLA_Ferredoxin--nitrite_reductase_OS=Phormidium_laminosum_GN=nirA_PE=3_SV=1	5.00E-16	GO:0016491,GO:0016491,GO:0020037,GO:0042128,GO:0046872,GO:0048307,GO:0051536,GO:0051536,GO:0051539,GO:0055114,GO:0055114,GO:0055114
comp31819_c1_seq2.p1			
comp31820_c0_seq1.p1			
comp31820_c0_seq2.p1	sp|Q91447|MP2K1_SERCA_Dual_specificity_mitogen-activated_protein_kinase_kinase_1_(Fragment)_OS=Serinus_canaria_GN=MAP2K1_PE=2_SV=1	4.00E-28	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004713,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005815,GO:0005856,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0018108
comp31820_c0_seq3.p1			
comp31821_c0_seq3.p1	sp|Q875Q8|MYO2_LACKL_Myosin-2_OS=Lachancea_kluyveri_GN=MYO2_PE=3_SV=1	4.00E-164	GO:0000166,GO:0003774,GO:0003779,GO:0005524,GO:0005524,GO:0006810,GO:0007049,GO:0008152,GO:0015031,GO:0016459,GO:0016459,GO:0051015
comp31821_c0_seq5.p1	sp|P47808|MYSH_ACACA_High_molecular_weight_form_of_myosin-1_OS=Acanthamoeba_castellanii_PE=4_SV=1	1.00E-85	GO:0000166,GO:0003774,GO:0003779,GO:0005524,GO:0005524,GO:0005856,GO:0008152,GO:0016459,GO:0016459
comp31821_c0_seq5.p2	sp|P47808|MYSH_ACACA_High_molecular_weight_form_of_myosin-1_OS=Acanthamoeba_castellanii_PE=4_SV=1	3.00E-71	GO:0000166,GO:0003774,GO:0003779,GO:0005524,GO:0005524,GO:0005856,GO:0008152,GO:0016459,GO:0016459
comp31822_c0_seq2.p1			
comp31823_c0_seq1.p1	sp|Q5XTS1|PLPL8_RABIT_Calcium-independent_phospholipase_A2-gamma_OS=Oryctolagus_cuniculus_GN=PNPLA8_PE=1_SV=1	2.00E-55	GO:0000139,GO:0004622,GO:0005737,GO:0005783,GO:0005789,GO:0005794,GO:0006629,GO:0006629,GO:0008152,GO:0016020,GO:0016021,GO:0016042,GO:0016787,GO:0048471
comp31824_c0_seq6.p1			
comp31825_c0_seq1.p1			
comp31825_c0_seq2.p1			
comp31825_c0_seq2.p3			
comp31825_c0_seq2.p8			
comp31826_c0_seq1.p1	sp|Q8CGF6|WDR47_MOUSE_WD_repeat-containing_protein_47_OS=Mus_musculus_GN=Wdr47_PE=1_SV=2	5.00E-31	GO:0003674,GO:0005575,GO:0005737,GO:0005856,GO:0005856,GO:0005874,GO:0007275,GO:0008150
comp31827_c0_seq1.p1			
comp31827_c0_seq6.p1			
comp31828_c0_seq1.p1			
comp31828_c0_seq1.p2			
comp31828_c0_seq1.p8			
comp31829_c0_seq1.p1	sp|Q9Y4P9|SPEF1_HUMAN_Sperm_flagellar_protein_1_OS=Homo_sapiens_GN=SPEF1_PE=1_SV=3	2.00E-36	GO:0003674,GO:0005575,GO:0005737,GO:0005737,GO:0005737,GO:0005856,GO:0005929,GO:0005930,GO:0008150,GO:0031514,GO:0031514,GO:0042995
comp31829_c0_seq2.p1	sp|Q9Y4P9|SPEF1_HUMAN_Sperm_flagellar_protein_1_OS=Homo_sapiens_GN=SPEF1_PE=1_SV=3	2.00E-36	GO:0003674,GO:0005575,GO:0005737,GO:0005737,GO:0005737,GO:0005856,GO:0005929,GO:0005930,GO:0008150,GO:0031514,GO:0031514,GO:0042995
comp31829_c0_seq3.p1	sp|Q9Y4P9|SPEF1_HUMAN_Sperm_flagellar_protein_1_OS=Homo_sapiens_GN=SPEF1_PE=1_SV=3	2.00E-35	GO:0003674,GO:0005575,GO:0005737,GO:0005737,GO:0005737,GO:0005856,GO:0005929,GO:0005930,GO:0008150,GO:0031514,GO:0031514,GO:0042995
comp31829_c0_seq4.p1	sp|Q58DA1|SPEF1_BOVIN_Sperm_flagellar_protein_1_OS=Bos_taurus_GN=SPEF1_PE=2_SV=1	6.00E-44	GO:0005737,GO:0005737,GO:0005737,GO:0005856,GO:0005929,GO:0005930,GO:0031514,GO:0031514,GO:0042995
comp31829_c0_seq6.p1			
comp31830_c0_seq2.p1			
comp31830_c0_seq3.p1			
comp31830_c0_seq4.p1	sp|Q9Y7R4|SET1_SCHPO_Histone-lysine_N-methyltransferase,_H3_lysine-4_specific_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=set1_PE=1_SV=1	5.00E-51	GO:0000166,GO:0000723,GO:0000790,GO:0003676,GO:0003723,GO:0005515,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0005737,GO:0006338,GO:0008168,GO:0016568,GO:0016740,GO:0018024,GO:0018024,GO:0018024,GO:0032259,GO:0034968,GO:0042800,GO:0048188,GO:0048188,GO:0051568,GO:0006342
comp31831_c0_seq1.p1	sp|A5USV3|TGT_ROSS1_Queuine_tRNA-ribosyltransferase_OS=Roseiflexus_sp._(strain_RS-1)_GN=tgt_PE=3_SV=1	4.00E-100	GO:0006400,GO:0008033,GO:0008033,GO:0008033,GO:0008479,GO:0008479,GO:0008479,GO:0008616,GO:0008616,GO:0008616,GO:0008616,GO:0016740,GO:0016757,GO:0046872
comp31832_c0_seq10.p1			
comp31832_c0_seq15.p1			
comp31832_c0_seq18.p1	sp|P0DD25|PEPDA_STRPQ_Probable_dipeptidase_A_OS=Streptococcus_pyogenes_serotype_M3_(strain_SSI-1)_GN=pepDA_PE=3_SV=1	8.00E-22	GO:0006508,GO:0006508,GO:0008233,GO:0016787,GO:0016805,GO:0016805
comp31832_c0_seq18.p2			
comp31834_c0_seq1.p1			
comp31834_c0_seq5.p1			
comp31834_c0_seq9.p1	sp|O89114|DNJB5_MOUSE_DnaJ_homolog_subfamily_B_member_5_OS=Mus_musculus_GN=Dnajb5_PE=2_SV=1	1.00E-13	GO:0000122,GO:0005515,GO:0005634,GO:0005829,GO:0005829,GO:0006457,GO:0006986,GO:0051082,GO:0051082,GO:0051087
comp31836_c0_seq2.p1	sp|Q54K57|TPSA_DICDI_Alpha,alpha-trehalose-phosphate_synthase_[UDP-forming]_A_OS=Dictyostelium_discoideum_GN=tpsA_PE=2_SV=1	9.00E-113	GO:0003824,GO:0003825,GO:0003825,GO:0005575,GO:0005975,GO:0005992,GO:0016740,GO:0016757
comp31836_c0_seq2.p2	sp|Q8HY87|RNZ2_MACFA_Zinc_phosphodiesterase_ELAC_protein_2_OS=Macaca_fascicularis_GN=ELAC2_PE=2_SV=1	9.00E-37	GO:0004518,GO:0004519,GO:0005634,GO:0005634,GO:0005634,GO:0005739,GO:0005739,GO:0005739,GO:0008033,GO:0008033,GO:0016787,GO:0046872,GO:0072684
comp31836_c0_seq2.p3			
comp31836_c0_seq2.p6	sp|Q54K57|TPSA_DICDI_Alpha,alpha-trehalose-phosphate_synthase_[UDP-forming]_A_OS=Dictyostelium_discoideum_GN=tpsA_PE=2_SV=1	3.00E-17	GO:0003824,GO:0003825,GO:0003825,GO:0005575,GO:0005975,GO:0005992,GO:0016740,GO:0016757
comp31836_c0_seq4.p1	sp|Q54K57|TPSA_DICDI_Alpha,alpha-trehalose-phosphate_synthase_[UDP-forming]_A_OS=Dictyostelium_discoideum_GN=tpsA_PE=2_SV=1	5.00E-138	GO:0003824,GO:0003825,GO:0003825,GO:0005575,GO:0005975,GO:0005992,GO:0016740,GO:0016757
comp31836_c0_seq4.p2	sp|Q8HY87|RNZ2_MACFA_Zinc_phosphodiesterase_ELAC_protein_2_OS=Macaca_fascicularis_GN=ELAC2_PE=2_SV=1	9.00E-37	GO:0004518,GO:0004519,GO:0005634,GO:0005634,GO:0005634,GO:0005739,GO:0005739,GO:0005739,GO:0008033,GO:0008033,GO:0016787,GO:0046872,GO:0072684
comp31836_c0_seq4.p3			
comp31836_c2_seq2.p1			
comp31836_c2_seq4.p2			
comp31836_c2_seq7.p1			
comp31836_c2_seq8.p1			
comp31836_c2_seq8.p2	sp|Q53RE8|ANR39_HUMAN_Ankyrin_repeat_domain-containing_protein_39_OS=Homo_sapiens_GN=ANKRD39_PE=1_SV=1	3.00E-21	GO:0003674,GO:0005575,GO:0008150
comp31837_c0_seq2.p1			
comp31838_c0_seq10.p1			
comp31838_c0_seq12.p1	sp|Q755I4|GYP5_ASHGO_GTPase-activating_protein_GYP5_OS=Ashbya_gossypii_(strain_ATCC_10895_/_CBS_109.51_/_FGSC_9923_/_NRRL_Y-1056)_GN=GYP5_PE=3_SV=1	6.00E-15	GO:0005096,GO:0005097,GO:0005737,GO:0005737,GO:0006810,GO:0006887,GO:0015031,GO:0016192,GO:0032313,GO:0032851,GO:0043547
comp31838_c0_seq3.p1			
comp31838_c0_seq4.p1	sp|Q755I4|GYP5_ASHGO_GTPase-activating_protein_GYP5_OS=Ashbya_gossypii_(strain_ATCC_10895_/_CBS_109.51_/_FGSC_9923_/_NRRL_Y-1056)_GN=GYP5_PE=3_SV=1	6.00E-15	GO:0005096,GO:0005097,GO:0005737,GO:0005737,GO:0006810,GO:0006887,GO:0015031,GO:0016192,GO:0032313,GO:0032851,GO:0043547
comp31839_c0_seq1.p1			
comp31839_c0_seq2.p1			
comp31839_c0_seq3.p1	sp|Q5RKI3|DPOLL_RAT_DNA_polymerase_lambda_OS=Rattus_norvegicus_GN=Poll_PE=2_SV=1	1.00E-63	GO:0003674,GO:0003677,GO:0003677,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0005575,GO:0005634,GO:0005634,GO:0005634,GO:0006260,GO:0006281,GO:0006281,GO:0006289,GO:0006974,GO:0008150,GO:0016740,GO:0016779,GO:0016779,GO:0016829,GO:0034061,GO:0046872,GO:0071897
comp31839_c0_seq4.p1			
comp31839_c0_seq7.p1	sp|Q5RKI3|DPOLL_RAT_DNA_polymerase_lambda_OS=Rattus_norvegicus_GN=Poll_PE=2_SV=1	5.00E-45	GO:0003674,GO:0003677,GO:0003677,GO:0003887,GO:0003887,GO:0003887,GO:0003887,GO:0005575,GO:0005634,GO:0005634,GO:0005634,GO:0006260,GO:0006281,GO:0006281,GO:0006289,GO:0006974,GO:0008150,GO:0016740,GO:0016779,GO:0016779,GO:0016829,GO:0034061,GO:0046872,GO:0071897
comp31839_c0_seq8.p1			
comp31840_c0_seq1.p1	sp|Q6TBX7|LUT1_ARATH_Carotene_epsilon-monooxygenase,_chloroplastic_OS=Arabidopsis_thaliana_GN=CYP97C1_PE=1_SV=1	2.00E-23	GO:0004497,GO:0005506,GO:0006636,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009941,GO:0009941,GO:0009965,GO:0009974,GO:0010103,GO:0015995,GO:0016020,GO:0016117,GO:0016117,GO:0016117,GO:0016491,GO:0016556,GO:0016705,GO:0019288,GO:0020037,GO:0030154,GO:0031969,GO:0046872,GO:0055114,GO:0055114
comp31840_c0_seq10.p1			
comp31840_c0_seq12.p1			
comp31840_c0_seq12.p2			
comp31840_c0_seq14.p1	sp|O64636|C76C1_ARATH_Cytochrome_P450_76C1_OS=Arabidopsis_thaliana_GN=CYP76C1_PE=2_SV=1	4.00E-18	GO:0004497,GO:0005506,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016102,GO:0016491,GO:0016705,GO:0016709,GO:0020037,GO:0044550,GO:0046872,GO:0055114,GO:0055114
comp31840_c0_seq16.p1	sp|O64636|C76C1_ARATH_Cytochrome_P450_76C1_OS=Arabidopsis_thaliana_GN=CYP76C1_PE=2_SV=1	7.00E-16	GO:0004497,GO:0005506,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016102,GO:0016491,GO:0016705,GO:0016709,GO:0020037,GO:0044550,GO:0046872,GO:0055114,GO:0055114
comp31841_c0_seq11.p1	sp|Q7ZYA0|LMBD2_XENLA_LMBR1_domain-containing_protein_2_OS=Xenopus_laevis_GN=lmbrd2_PE=2_SV=1	5.00E-37	GO:0016020,GO:0016020,GO:0016021
comp31841_c0_seq3.p1	sp|O94599|YC8B_SCHPO_LIMR_family_protein_C622.11_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC622.11_PE=2_SV=1	4.00E-12	GO:0000139,GO:0003674,GO:0005737,GO:0005794,GO:0005794,GO:0008150,GO:0016020,GO:0016021
comp31841_c0_seq6.p1	sp|O94599|YC8B_SCHPO_LIMR_family_protein_C622.11_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC622.11_PE=2_SV=1	4.00E-12	GO:0000139,GO:0003674,GO:0005737,GO:0005794,GO:0005794,GO:0008150,GO:0016020,GO:0016021
comp31841_c1_seq1.p1			
comp31841_c1_seq1.p4			
comp31841_c1_seq1.p5			
comp31842_c0_seq1.p1	sp|O34340|FABF_BACSU_3-oxoacyl-[acyl-carrier-protein]_synthase_2_OS=Bacillus_subtilis_GN=fabF_PE=3_SV=1	2.00E-124	GO:0003824,GO:0006629,GO:0006631,GO:0006633,GO:0006633,GO:0006633,GO:0008152,GO:0016740,GO:0016746,GO:0016747,GO:0033817
comp31842_c0_seq1.p2	sp|B0JXE2|FABH_MICAN_3-oxoacyl-[acyl-carrier-protein]_synthase_3_OS=Microcystis_aeruginosa_(strain_NIES-843)_GN=fabH_PE=3_SV=1	2.00E-125	GO:0003824,GO:0003824,GO:0004315,GO:0005737,GO:0005737,GO:0005737,GO:0006629,GO:0006631,GO:0006633,GO:0006633,GO:0006633,GO:0006633,GO:0008152,GO:0008152,GO:0008610,GO:0016740,GO:0016746,GO:0016747,GO:0033818,GO:0033818
comp31842_c1_seq1.p1	sp|Q9MAK9|PS10B_ARATH_26S_protease_regulatory_subunit_S10B_homolog_B_OS=Arabidopsis_thaliana_GN=RPT4B_PE=2_SV=1	2.00E-140	GO:0000166,GO:0000502,GO:0000502,GO:0005524,GO:0005524,GO:0005618,GO:0005634,GO:0005634,GO:0005730,GO:0005737,GO:0005737,GO:0005737,GO:0005886,GO:0009506,GO:0016020,GO:0016787,GO:0030163,GO:0030244,GO:0048193,GO:0005829
comp31842_c2_seq10.p2			
comp31842_c2_seq10.p4			
comp31842_c2_seq6.p1			
comp31842_c2_seq7.p1			
comp31842_c2_seq7.p2			
comp31842_c2_seq7.p5			
comp31842_c2_seq9.p1			
comp31842_c2_seq9.p3	sp|Q54PJ1|PRS10_DICDI_26S_protease_regulatory_subunit_10B_OS=Dictyostelium_discoideum_GN=psmC6_PE=1_SV=1	8.00E-57	GO:0000166,GO:0000502,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0016787,GO:0030163,GO:0044351
comp31842_c3_seq1.p2			
comp31843_c0_seq2.p2			
comp31843_c0_seq2.p4			
comp31843_c0_seq3.p1	sp|Q10137|SEC14_SCHPO_Sec14_cytosolic_factor_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=sec14_PE=2_SV=1	1.00E-17	GO:0000281,GO:0005215,GO:0005622,GO:0005628,GO:0005628,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0006810,GO:0006810,GO:0006893,GO:0008525,GO:0008526,GO:0008526,GO:0010570,GO:0015031,GO:0015914,GO:0016020,GO:0030437,GO:0030437,GO:0030437,GO:0032153,GO:0035838,GO:0048193,GO:0051286,GO:0051286,GO:0060187
comp31843_c0_seq4.p1			
comp31844_c0_seq1.p1			
comp31844_c0_seq10.p1			
comp31844_c0_seq10.p2	sp|Q8L850|PI5K9_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_9_OS=Arabidopsis_thaliana_GN=PIP5K9_PE=1_SV=2	8.00E-30	GO:0000166,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005829,GO:0005975,GO:0006520,GO:0016020,GO:0016020,GO:0016020,GO:0016301,GO:0016307,GO:0016308,GO:0016308,GO:0016310,GO:0016740,GO:0046488,GO:0046854,GO:0046854,GO:0046854
comp31844_c0_seq11.p1			
comp31844_c0_seq14.p1			
comp31844_c0_seq15.p1			
comp31844_c0_seq19.p1			
comp31844_c0_seq2.p1	sp|Q71A37|PHLP3_DICDI_Phosducin-like_protein_3_OS=Dictyostelium_discoideum_GN=phlp3_PE=2_SV=1	1.00E-31	GO:0003674,GO:0005575,GO:0008150,GO:0045454
comp31844_c0_seq21.p1	sp|Q1JPG1|RS10B_BOVIN_Radial_spoke_head_10_homolog_B_OS=Bos_taurus_GN=RSPH10B_PE=2_SV=2	7.00E-37	
comp31844_c0_seq22.p1			
comp31844_c0_seq5.p1			
comp31844_c0_seq6.p2			
comp31844_c0_seq7.p1			
comp31844_c0_seq8.p1			
comp31844_c2_seq2.p1			
comp31844_c2_seq2.p2			
comp31845_c0_seq2.p1	sp|P26182|ACT_ACHBI_Actin_OS=Achlya_bisexualis_PE=3_SV=1	0	GO:0000166,GO:0005524,GO:0005737,GO:0005856,GO:0005856
comp31846_c0_seq2.p1			
comp31847_c0_seq2.p1	sp|Q9S7C0|HSP7O_ARATH_Heat_shock_70_kDa_protein_14_OS=Arabidopsis_thaliana_GN=HSP70-14_PE=1_SV=1	4.00E-152	GO:0000166,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0005886,GO:0009408,GO:0046686
comp31847_c0_seq2.p4			
comp31847_c1_seq1.p1			
comp31848_c0_seq9.p1			
comp31850_c0_seq10.p1	sp|O75808|CAN15_HUMAN_Calpain-15_OS=Homo_sapiens_GN=SOLH_PE=1_SV=1	1.00E-17	GO:0003700,GO:0004198,GO:0004198,GO:0004198,GO:0005622,GO:0005737,GO:0006355,GO:0006508,GO:0006508,GO:0006508,GO:0008233,GO:0008233,GO:0008234,GO:0008234,GO:0008270,GO:0016787,GO:0046872
comp31850_c0_seq11.p1	sp|O75808|CAN15_HUMAN_Calpain-15_OS=Homo_sapiens_GN=SOLH_PE=1_SV=1	1.00E-17	GO:0003700,GO:0004198,GO:0004198,GO:0004198,GO:0005622,GO:0005737,GO:0006355,GO:0006508,GO:0006508,GO:0006508,GO:0008233,GO:0008233,GO:0008234,GO:0008234,GO:0008270,GO:0016787,GO:0046872
comp31850_c0_seq2.p1			
comp31850_c0_seq3.p1	sp|Q9JLG8|CAN15_MOUSE_Calpain-15_OS=Mus_musculus_GN=Solh_PE=1_SV=1	7.00E-31	GO:0004198,GO:0004198,GO:0005622,GO:0005737,GO:0006508,GO:0006508,GO:0006508,GO:0008233,GO:0008234,GO:0008270,GO:0016787,GO:0046872
comp31850_c0_seq4.p1	sp|Q8T9W2|ABCB5_DICDI_ABC_transporter_B_family_member_5_OS=Dictyostelium_discoideum_GN=abcB5_PE=3_SV=1	2.00E-169	GO:0000166,GO:0005215,GO:0005524,GO:0005524,GO:0005739,GO:0005743,GO:0006200,GO:0006810,GO:0006810,GO:0006810,GO:0006879,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016887,GO:0031154,GO:0042626,GO:0042626,GO:0042626,GO:0043190,GO:0055085,GO:0055085
comp31850_c0_seq4.p2	sp|D0NP70|LIPA_PHYIT_Lipoyl_synthase,_mitochondrial_OS=Phytophthora_infestans_(strain_T30-4)_GN=PITG_14852_PE=3_SV=1	7.00E-148	GO:0003824,GO:0005739,GO:0005739,GO:0005739,GO:0009107,GO:0009107,GO:0009249,GO:0016740,GO:0016783,GO:0016992,GO:0016992,GO:0016992,GO:0046872,GO:0051536,GO:0051536,GO:0051539,GO:0051539,GO:0051539
comp31850_c0_seq5.p1			
comp31850_c0_seq7.p1	sp|Q9LVM1|AB25B_ARATH_ABC_transporter_B_family_member_25,_mitochondrial_OS=Arabidopsis_thaliana_GN=ABCB25_PE=1_SV=1	0	GO:0000166,GO:0005215,GO:0005524,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0006200,GO:0006777,GO:0006810,GO:0006810,GO:0006811,GO:0006879,GO:0006879,GO:0009507,GO:0009555,GO:0009630,GO:0009658,GO:0009941,GO:0009941,GO:0010288,GO:0010380,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016887,GO:0042626,GO:0042626,GO:0046686,GO:0048364,GO:0050790,GO:0051276,GO:0055072,GO:0055085,GO:0055085
comp31850_c0_seq7.p2	sp|D0NP70|LIPA_PHYIT_Lipoyl_synthase,_mitochondrial_OS=Phytophthora_infestans_(strain_T30-4)_GN=PITG_14852_PE=3_SV=1	7.00E-148	GO:0003824,GO:0005739,GO:0005739,GO:0005739,GO:0009107,GO:0009107,GO:0009249,GO:0016740,GO:0016783,GO:0016992,GO:0016992,GO:0016992,GO:0046872,GO:0051536,GO:0051536,GO:0051539,GO:0051539,GO:0051539
comp31850_c0_seq9.p1	sp|Q9JLG8|CAN15_MOUSE_Calpain-15_OS=Mus_musculus_GN=Solh_PE=1_SV=1	5.00E-31	GO:0004198,GO:0004198,GO:0005622,GO:0005737,GO:0006508,GO:0006508,GO:0006508,GO:0008233,GO:0008234,GO:0008270,GO:0016787,GO:0046872
comp31851_c0_seq1.p1			
comp31851_c0_seq3.p1	sp|Q54RZ2|YIPF6_DICDI_Protein_YIPF6_homolog_OS=Dictyostelium_discoideum_GN=yipf6_PE=3_SV=2	5.00E-58	GO:0003674,GO:0008150,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0044351
comp31851_c0_seq3.p2			
comp31851_c0_seq4.p1			
comp31851_c1_seq1.p1			
comp31851_c1_seq2.p1			
comp31851_c1_seq4.p1			
comp31851_c1_seq5.p1	sp|A0JND4|SBNO2_BOVIN_Protein_strawberry_notch_homolog_2_OS=Bos_taurus_GN=SBNO2_PE=2_SV=1	3.00E-61	GO:0002281,GO:0002281,GO:0003674,GO:0005575,GO:0006351,GO:0006355,GO:0006355,GO:0008150,GO:0030282,GO:0030316,GO:0045892,GO:0045892,GO:0045944,GO:0050727,GO:0050727,GO:0061430,GO:0072674,GO:0072675
comp31851_c1_seq5.p12			
comp31851_c1_seq5.p2	sp|A6QR09|SAMC_BOVIN_S-adenosylmethionine_mitochondrial_carrier_protein_OS=Bos_taurus_GN=SLC25A26_PE=2_SV=1	4.00E-13	GO:0000095,GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0006810,GO:0015805,GO:0016020,GO:0016021,GO:0055085,GO:1901962
comp31851_c1_seq9.p1	sp|Q9SNQ2|ANM42_ORYSJ_Probable_protein_arginine_N-methyltransferase_4.2_OS=Oryza_sativa_subsp._japonica_GN=PRMT4.2_PE=2_SV=1	3.00E-101	GO:0005829,GO:0006479,GO:0006479,GO:0008168,GO:0008168,GO:0008168,GO:0008469,GO:0008469,GO:0009909,GO:0010228,GO:0016277,GO:0016740,GO:0016740,GO:0019919,GO:0032259,GO:0032259,GO:0034968,GO:0034969,GO:0035241,GO:0035242
comp31851_c1_seq9.p2	sp|Q08448|YO059_YEAST_Putative_lipase_YOR059C_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YOR059C_PE=1_SV=1	3.00E-11	GO:0004622,GO:0004622,GO:0005811,GO:0005811,GO:0005811,GO:0005811,GO:0006629,GO:0016020,GO:0016020,GO:0016021,GO:0016042,GO:0016787,GO:0055088
comp31851_c2_seq1.p1			
comp31851_c2_seq2.p1			
comp31854_c0_seq10.p1			
comp31854_c0_seq10.p3			
comp31854_c0_seq10.p6			
comp31854_c0_seq2.p2			
comp31854_c0_seq2.p3			
comp31854_c0_seq3.p1			
comp31855_c0_seq13.p1			
comp31855_c0_seq5.p1			
comp31855_c1_seq1.p1	sp|Q5PP37|ATXR2_ARATH_Histone-lysine_N-methyltransferase_ATXR2_OS=Arabidopsis_thaliana_GN=ATXR2_PE=2_SV=1	5.00E-14	GO:0005634,GO:0005634,GO:0008168,GO:0016568,GO:0016740,GO:0018024,GO:0032259,GO:0034968,GO:0046872
comp31855_c1_seq4.p1			
comp31856_c1_seq1.p1			
comp31856_c1_seq12.p1			
comp31856_c1_seq13.p1			
comp31856_c1_seq15.p1	sp|Q9BX10|GTPB2_HUMAN_GTP-binding_protein_2_OS=Homo_sapiens_GN=GTPBP2_PE=2_SV=1	3.00E-35	GO:0000166,GO:0003924,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005525,GO:0005525,GO:0006184,GO:0008150,GO:0043231
comp31856_c1_seq15.p2			
comp31856_c1_seq18.p1	sp|Q9BX10|GTPB2_HUMAN_GTP-binding_protein_2_OS=Homo_sapiens_GN=GTPBP2_PE=2_SV=1	3.00E-35	GO:0000166,GO:0003924,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005525,GO:0005525,GO:0006184,GO:0008150,GO:0043231
comp31856_c1_seq18.p5			
comp31856_c1_seq19.p1	sp|Q9BX10|GTPB2_HUMAN_GTP-binding_protein_2_OS=Homo_sapiens_GN=GTPBP2_PE=2_SV=1	3.00E-35	GO:0000166,GO:0003924,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005525,GO:0005525,GO:0006184,GO:0008150,GO:0043231
comp31856_c1_seq19.p2			
comp31856_c1_seq2.p1	sp|Q9BX10|GTPB2_HUMAN_GTP-binding_protein_2_OS=Homo_sapiens_GN=GTPBP2_PE=2_SV=1	3.00E-35	GO:0000166,GO:0003924,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005525,GO:0005525,GO:0006184,GO:0008150,GO:0043231
comp31856_c1_seq2.p11			
comp31856_c1_seq3.p6			
comp31856_c1_seq5.p1	sp|Q9BX10|GTPB2_HUMAN_GTP-binding_protein_2_OS=Homo_sapiens_GN=GTPBP2_PE=2_SV=1	3.00E-35	GO:0000166,GO:0003924,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005525,GO:0005525,GO:0006184,GO:0008150,GO:0043231
comp31856_c1_seq6.p3			
comp31856_c1_seq9.p1			
comp31857_c0_seq1.p2	sp|P19275|VTP3_TTV1V_Viral_protein_TPX_OS=Thermoproteus_tenax_virus_1_(strain_VT3)_PE=4_SV=1	2.00E-17	
comp31857_c3_seq11.p2			
comp31857_c3_seq17.p2			
comp31857_c3_seq19.p1			
comp31858_c0_seq1.p1			
comp31859_c1_seq1.p1			
comp31859_c1_seq1.p4			
comp31859_c1_seq12.p3			
comp31859_c1_seq2.p1			
comp31859_c1_seq4.p1	sp|Q9ERI6|RDH14_MOUSE_Retinol_dehydrogenase_14_OS=Mus_musculus_GN=Rdh14_PE=1_SV=1	2.00E-34	GO:0001649,GO:0003674,GO:0005634,GO:0005739,GO:0005765,GO:0005783,GO:0008152,GO:0016020,GO:0016491,GO:0016491,GO:0055114
comp31859_c1_seq7.p1			
comp31859_c1_seq7.p2			
comp31859_c1_seq8.p1			
comp31859_c1_seq8.p2			
comp31859_c1_seq8.p7			
comp31859_c1_seq9.p1			
comp31861_c0_seq2.p1	sp|Q8N9H8|MUT7_HUMAN_Probable_exonuclease_mut-7_homolog_OS=Homo_sapiens_GN=EXD3_PE=1_SV=3	6.00E-15	GO:0003676,GO:0004518,GO:0004527,GO:0005634,GO:0005737,GO:0006139,GO:0008408,GO:0008408,GO:0016787,GO:0046872,GO:0090305,GO:0090305,GO:0090305,GO:0090305
comp31861_c0_seq3.p2			
comp31861_c0_seq4.p1	sp|P43603|LSB3_YEAST_LAS_seventeen-binding_protein_3_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=LSB3_PE=1_SV=3	2.00E-54	GO:0003674,GO:0005515,GO:0005737,GO:0005737,GO:0051666,GO:0051666
comp31862_c0_seq1.p1	sp|A5ILG0|MUTS_THEP1_DNA_mismatch_repair_protein_MutS_OS=Thermotoga_petrophila_(strain_RKU-1_/_ATCC_BAA-488_/_DSM_13995)_GN=mutS_PE=3_SV=1	9.00E-25	GO:0000166,GO:0003677,GO:0003684,GO:0005524,GO:0005524,GO:0005524,GO:0006281,GO:0006298,GO:0006298,GO:0006974,GO:0030983
comp31862_c0_seq1.p4	sp|Q9V4N3|CYB5_DROME_Cytochrome_b5_OS=Drosophila_melanogaster_GN=Cyt-b5_PE=2_SV=1	4.00E-21	GO:0005783,GO:0005789,GO:0005811,GO:0012505,GO:0016020,GO:0016021,GO:0020037,GO:0031090,GO:0035206,GO:0043231,GO:0045610,GO:0046872,GO:0055114
comp31863_c0_seq10.p1	sp|B8J2B6|GPDA_DESDA_Glycerol-3-phosphate_dehydrogenase_[NAD(P)+]_OS=Desulfovibrio_desulfuricans_(strain_ATCC_27774_/_DSM_6949)_GN=gpsA_PE=3_SV=1	1.00E-74	GO:0004367,GO:0004367,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005975,GO:0006072,GO:0006629,GO:0006650,GO:0008654,GO:0008654,GO:0009331,GO:0016491,GO:0016491,GO:0016616,GO:0036439,GO:0046167,GO:0046168,GO:0047952,GO:0047952,GO:0050662,GO:0051287,GO:0055114,GO:0055114
comp31863_c0_seq10.p2			
comp31863_c0_seq12.p1			
comp31863_c0_seq12.p2			
comp31863_c0_seq12.p4	sp|Q3A8M2|GPDA_PELCD_Glycerol-3-phosphate_dehydrogenase_[NAD(P)+]_OS=Pelobacter_carbinolicus_(strain_DSM_2380_/_Gra_Bd_1)_GN=gpsA_PE=3_SV=1	7.00E-60	GO:0004367,GO:0004367,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005975,GO:0006072,GO:0006629,GO:0006650,GO:0008654,GO:0008654,GO:0009331,GO:0016491,GO:0016491,GO:0016616,GO:0036439,GO:0046167,GO:0046168,GO:0047952,GO:0047952,GO:0050662,GO:0051287,GO:0055114,GO:0055114
comp31863_c0_seq3.p2			
comp31863_c0_seq4.p1			
comp31863_c0_seq5.p1	sp|Q6KCD5|NIPBL_MOUSE_Nipped-B-like_protein_OS=Mus_musculus_GN=Nipbl_PE=1_SV=1	1.00E-32	GO:0000122,GO:0000785,GO:0003007,GO:0003151,GO:0003682,GO:0005634,GO:0005634,GO:0005634,GO:0006974,GO:0007049,GO:0007064,GO:0007420,GO:0007507,GO:0007605,GO:0008022,GO:0019827,GO:0031065,GO:0032116,GO:0032116,GO:0034088,GO:0034088,GO:0034613,GO:0035115,GO:0035136,GO:0035261,GO:0036033,GO:0040018,GO:0042471,GO:0042634,GO:0042826,GO:0045444,GO:0045778,GO:0045892,GO:0045944,GO:0045995,GO:0047485,GO:0048557,GO:0048589,GO:0048592,GO:0048638,GO:0048701,GO:0048703,GO:0050890,GO:0060325,GO:0061010,GO:0061038,GO:0070062,GO:0070087,GO:0071481
comp31863_c0_seq7.p1			
comp31863_c0_seq8.p1			
comp31863_c0_seq8.p2			
comp31863_c0_seq8.p4	sp|Q3A8M2|GPDA_PELCD_Glycerol-3-phosphate_dehydrogenase_[NAD(P)+]_OS=Pelobacter_carbinolicus_(strain_DSM_2380_/_Gra_Bd_1)_GN=gpsA_PE=3_SV=1	7.00E-60	GO:0004367,GO:0004367,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005975,GO:0006072,GO:0006629,GO:0006650,GO:0008654,GO:0008654,GO:0009331,GO:0016491,GO:0016491,GO:0016616,GO:0036439,GO:0046167,GO:0046168,GO:0047952,GO:0047952,GO:0050662,GO:0051287,GO:0055114,GO:0055114
comp31863_c1_seq1.p1	sp|P50430|ARSB_RAT_Arylsulfatase_B_OS=Rattus_norvegicus_GN=Arsb_PE=2_SV=2	7.00E-92	GO:0003824,GO:0003943,GO:0003943,GO:0004065,GO:0004065,GO:0005739,GO:0005764,GO:0005764,GO:0005764,GO:0005791,GO:0005794,GO:0006914,GO:0007417,GO:0007584,GO:0008152,GO:0008484,GO:0008484,GO:0009268,GO:0009986,GO:0010632,GO:0010976,GO:0016787,GO:0043627,GO:0046872,GO:0051597,GO:0061580,GO:0070062
comp31863_c1_seq1.p6			
comp31863_c1_seq3.p1	sp|Q9SX85|SEC3A_ARATH_Exocyst_complex_component_SEC3A_OS=Arabidopsis_thaliana_GN=SEC3A_PE=1_SV=1	1.00E-16	GO:0005737,GO:0005829,GO:0005856,GO:0005886,GO:0005886,GO:0006810,GO:0006887,GO:0009524,GO:0016020
comp31863_c1_seq3.p2			
comp31863_c1_seq3.p4			
comp31864_c0_seq5.p1			
comp31865_c0_seq3.p1	sp|Q86AS0|Y4399_DICDI_Probable_helicase_DDB_G0274399_OS=Dictyostelium_discoideum_GN=DDB_G0274399_PE=3_SV=1	7.00E-65	GO:0000166,GO:0003674,GO:0004386,GO:0005524,GO:0005575,GO:0005634,GO:0005634,GO:0008150,GO:0008152,GO:0008152,GO:0016787
comp31866_c0_seq1.p1	sp|Q80X72|LRC15_MOUSE_Leucine-rich_repeat-containing_protein_15_OS=Mus_musculus_GN=Lrrc15_PE=2_SV=1	2.00E-13	GO:0001968,GO:0005518,GO:0016020,GO:0016020,GO:0016021,GO:0030335,GO:0043236,GO:0046813,GO:0070062,GO:0090005
comp31866_c0_seq11.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	6.00E-11	GO:0003674,GO:0005576,GO:0005576,GO:0008150,GO:0070062,GO:0072562
comp31866_c0_seq17.p1			
comp31866_c0_seq19.p2			
comp31866_c0_seq2.p1	sp|Q80X72|LRC15_MOUSE_Leucine-rich_repeat-containing_protein_15_OS=Mus_musculus_GN=Lrrc15_PE=2_SV=1	4.00E-13	GO:0001968,GO:0005518,GO:0016020,GO:0016020,GO:0016021,GO:0030335,GO:0043236,GO:0046813,GO:0070062,GO:0090005
comp31866_c0_seq20.p1			
comp31866_c0_seq20.p3			
comp31867_c1_seq2.p1			
comp31867_c1_seq2.p2			
comp31867_c1_seq3.p2			
comp31867_c1_seq5.p1			
comp31867_c1_seq5.p2			
comp31868_c0_seq1.p1	sp|P23585|HXT2_YEAST_High-affinity_glucose_transporter_HXT2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=HXT2_PE=1_SV=1	7.00E-63	GO:0005215,GO:0005353,GO:0005355,GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006810,GO:0008643,GO:0015146,GO:0015578,GO:0015750,GO:0015755,GO:0015758,GO:0015761,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0022857,GO:0022891,GO:0055085
comp31870_c0_seq1.p1	sp|P64956|Y2253_MYCBO_Uncharacterized_protein_Mb2253c_OS=Mycobacterium_bovis_GN=Mb2253c_PE=4_SV=1	9.00E-16	GO:0003676,GO:0004523,GO:0090502
comp31870_c1_seq2.p1			
comp31870_c1_seq3.p1	sp|Q54U63|LVSC_DICDI_BEACH_domain-containing_protein_lvsC_OS=Dictyostelium_discoideum_GN=lvsC_PE=4_SV=2	3.00E-135	GO:0005543,GO:0012505,GO:0016197,GO:0019898
comp31870_c1_seq3.p2			
comp31871_c1_seq1.p2			
comp31871_c1_seq2.p1	sp|Q2PFW9|NOVA1_MACFA_RNA-binding_protein_Nova-1_OS=Macaca_fascicularis_GN=NOVA1_PE=2_SV=1	1.00E-25	GO:0003723,GO:0003723,GO:0005634,GO:0005634
comp31871_c1_seq3.p1	sp|Q5ZK62|ACAP2_CHICK_Arf-GAP_with_coiled-coil,_ANK_repeat_and_PH_domain-containing_protein_2_OS=Gallus_gallus_GN=ACAP2_PE=2_SV=1	5.00E-16	GO:0005096,GO:0005768,GO:0008060,GO:0008270,GO:0010008,GO:0010008,GO:0016020,GO:0032312,GO:0036010,GO:0043547,GO:0043547,GO:0046872,GO:1990090
comp31871_c1_seq4.p1	sp|Q2PFW9|NOVA1_MACFA_RNA-binding_protein_Nova-1_OS=Macaca_fascicularis_GN=NOVA1_PE=2_SV=1	2.00E-25	GO:0003723,GO:0003723,GO:0005634,GO:0005634
comp31871_c1_seq4.p2			
comp31872_c0_seq17.p2	sp|P45545|YHFS_ECOLI_Uncharacterized_protein_yhfS_OS=Escherichia_coli_(strain_K12)_GN=yhfS_PE=4_SV=1	5.00E-54	GO:0003824,GO:0009058,GO:0030170
comp31873_c0_seq3.p1			
comp31875_c0_seq1.p1	sp|Q8R127|SCPDL_MOUSE_Saccharopine_dehydrogenase-like_oxidoreductase_OS=Mus_musculus_GN=Sccpdh_PE=2_SV=1	5.00E-83	GO:0003674,GO:0005634,GO:0005739,GO:0005739,GO:0005811,GO:0008150,GO:0016020,GO:0016491,GO:0016491,GO:0030496,GO:0055114,GO:0055114
comp31876_c0_seq11.p1			
comp31876_c0_seq13.p1			
comp31876_c0_seq16.p1			
comp31876_c0_seq2.p1			
comp31876_c0_seq4.p1			
comp31878_c0_seq2.p1			
comp31879_c0_seq1.p1			
comp31879_c0_seq2.p1			
comp31879_c0_seq3.p1	sp|Q57629|Y165_METJA_Uncharacterized_protein_MJ0165_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ0165_PE=4_SV=1	3.00E-32	GO:0005886,GO:0005886,GO:0006189,GO:0016020,GO:0016021
comp31879_c0_seq3.p2	sp|Q1L987|ATPF1_DANRE_ATP_synthase_mitochondrial_F1_complex_assembly_factor_1_OS=Danio_rerio_GN=atpaf1_PE=2_SV=1	2.00E-11	GO:0005739,GO:0005739,GO:0005739,GO:0006461
comp31879_c0_seq4.p1			
comp31879_c0_seq6.p1			
comp31879_c0_seq9.p2			
comp31880_c0_seq1.p2	sp|Q9ST27|PHOT2_ORYSJ_Phototropin-2_OS=Oryza_sativa_subsp._japonica_GN=PHOT2_PE=1_SV=1	2.00E-15	GO:0000023,GO:0000155,GO:0000155,GO:0000160,GO:0000160,GO:0000166,GO:0000166,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004871,GO:0004871,GO:0005524,GO:0005524,GO:0005524,GO:0005794,GO:0005886,GO:0006364,GO:0006468,GO:0006468,GO:0007165,GO:0007165,GO:0009637,GO:0009638,GO:0009644,GO:0009744,GO:0009785,GO:0009881,GO:0009881,GO:0009882,GO:0009882,GO:0009902,GO:0010027,GO:0010103,GO:0010114,GO:0010118,GO:0010155,GO:0010181,GO:0010207,GO:0010218,GO:0010362,GO:0016020,GO:0016301,GO:0016301,GO:0016310,GO:0016310,GO:0016556,GO:0016740,GO:0016740,GO:0016772,GO:0016772,GO:0018298,GO:0018298,GO:0019252,GO:0019761,GO:0023014,GO:0034660,GO:0035304,GO:0042793,GO:0042802,GO:0043085,GO:0045893,GO:0046777,GO:0050896,GO:0050896
comp31880_c0_seq7.p1	sp|Q9ST27|PHOT2_ORYSJ_Phototropin-2_OS=Oryza_sativa_subsp._japonica_GN=PHOT2_PE=1_SV=1	5.00E-28	GO:0000023,GO:0000155,GO:0000155,GO:0000160,GO:0000160,GO:0000166,GO:0000166,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004871,GO:0004871,GO:0005524,GO:0005524,GO:0005524,GO:0005794,GO:0005886,GO:0006364,GO:0006468,GO:0006468,GO:0007165,GO:0007165,GO:0009637,GO:0009638,GO:0009644,GO:0009744,GO:0009785,GO:0009881,GO:0009881,GO:0009882,GO:0009882,GO:0009902,GO:0010027,GO:0010103,GO:0010114,GO:0010118,GO:0010155,GO:0010181,GO:0010207,GO:0010218,GO:0010362,GO:0016020,GO:0016301,GO:0016301,GO:0016310,GO:0016310,GO:0016556,GO:0016740,GO:0016740,GO:0016772,GO:0016772,GO:0018298,GO:0018298,GO:0019252,GO:0019761,GO:0023014,GO:0034660,GO:0035304,GO:0042793,GO:0042802,GO:0043085,GO:0045893,GO:0046777,GO:0050896,GO:0050896
comp31881_c1_seq1.p1			
comp31881_c1_seq1.p2			
comp31881_c1_seq2.p1			
comp31881_c1_seq3.p1			
comp31882_c0_seq1.p1			
comp31882_c1_seq1.p1			
comp31882_c1_seq11.p1			
comp31882_c1_seq13.p1			
comp31882_c1_seq15.p1			
comp31882_c1_seq2.p1			
comp31882_c1_seq5.p1			
comp31882_c1_seq6.p1			
comp31882_c1_seq7.p1			
comp31882_c1_seq9.p1			
comp31884_c0_seq1.p3			
comp31884_c0_seq11.p1	sp|O89114|DNJB5_MOUSE_DnaJ_homolog_subfamily_B_member_5_OS=Mus_musculus_GN=Dnajb5_PE=2_SV=1	4.00E-15	GO:0000122,GO:0005515,GO:0005634,GO:0005829,GO:0005829,GO:0006457,GO:0006986,GO:0051082,GO:0051082,GO:0051087
comp31884_c0_seq11.p2			
comp31884_c0_seq13.p1			
comp31884_c0_seq13.p3			
comp31884_c0_seq13.p4			
comp31884_c0_seq14.p1			
comp31884_c0_seq14.p2			
comp31884_c0_seq14.p4			
comp31884_c0_seq15.p1	sp|O89114|DNJB5_MOUSE_DnaJ_homolog_subfamily_B_member_5_OS=Mus_musculus_GN=Dnajb5_PE=2_SV=1	4.00E-15	GO:0000122,GO:0005515,GO:0005634,GO:0005829,GO:0005829,GO:0006457,GO:0006986,GO:0051082,GO:0051082,GO:0051087
comp31884_c0_seq15.p2			
comp31884_c0_seq16.p1			
comp31884_c0_seq16.p2			
comp31884_c0_seq16.p4			
comp31884_c0_seq17.p1			
comp31884_c0_seq17.p2			
comp31884_c0_seq17.p4			
comp31884_c0_seq3.p1	sp|O89114|DNJB5_MOUSE_DnaJ_homolog_subfamily_B_member_5_OS=Mus_musculus_GN=Dnajb5_PE=2_SV=1	4.00E-15	GO:0000122,GO:0005515,GO:0005634,GO:0005829,GO:0005829,GO:0006457,GO:0006986,GO:0051082,GO:0051082,GO:0051087
comp31884_c0_seq3.p2			
comp31884_c0_seq5.p1			
comp31884_c0_seq5.p3			
comp31884_c0_seq5.p4			
comp31884_c0_seq8.p1			
comp31884_c0_seq8.p3			
comp31884_c0_seq8.p4			
comp31885_c0_seq1.p1			
comp31885_c0_seq6.p1			
comp31886_c0_seq3.p2	sp|Q9SD61|C3H42_ARATH_Zinc_finger_CCCH_domain-containing_protein_42_OS=Arabidopsis_thaliana_GN=At3g47120_PE=2_SV=1	7.00E-11	GO:0000166,GO:0003676,GO:0003677,GO:0003723,GO:0008150,GO:0046872,GO:0046872
comp31886_c0_seq7.p1			
comp31887_c0_seq12.p3			
comp31887_c0_seq15.p1			
comp31887_c0_seq4.p1			
comp31887_c0_seq7.p1			
comp31887_c0_seq7.p2			
comp31887_c0_seq7.p5			
comp31887_c0_seq7.p6			
comp31887_c0_seq8.p2			
comp31888_c0_seq1.p1			
comp31889_c0_seq1.p2			
comp31889_c0_seq2.p1			
comp31890_c0_seq3.p1			
comp31892_c0_seq2.p1	sp|Q5RF73|TMM19_PONAB_Transmembrane_protein_19_OS=Pongo_abelii_GN=TMEM19_PE=2_SV=1	1.00E-41	GO:0016020,GO:0016020,GO:0016021,GO:0016021
comp31892_c0_seq3.p1	sp|Q5RF73|TMM19_PONAB_Transmembrane_protein_19_OS=Pongo_abelii_GN=TMEM19_PE=2_SV=1	4.00E-26	GO:0016020,GO:0016020,GO:0016021,GO:0016021
comp31892_c1_seq1.p1			
comp31892_c1_seq10.p1			
comp31892_c1_seq10.p2			
comp31892_c1_seq13.p1			
comp31892_c1_seq14.p1			
comp31892_c1_seq21.p1	sp|Q9LT17|BBR_ARATH_E3_ubiquitin_ligase_BIG_BROTHER-related_OS=Arabidopsis_thaliana_GN=BBR_PE=2_SV=1	5.00E-17	GO:0004842,GO:0008270,GO:0016567,GO:0016567,GO:0016874,GO:0046872,GO:0051865
comp31892_c1_seq22.p1			
comp31892_c1_seq6.p2			
comp31892_c1_seq8.p1			
comp31893_c0_seq1.p1			
comp31893_c1_seq2.p1			
comp31893_c1_seq4.p1			
comp31893_c1_seq6.p1			
comp31893_c1_seq6.p3			
comp31895_c0_seq1.p1			
comp31895_c1_seq1.p1			
comp31895_c2_seq13.p1	sp|P0CB49|YLPM1_RAT_YLP_motif-containing_protein_1_OS=Rattus_norvegicus_GN=Ylpm1_PE=1_SV=1	3.00E-45	GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0016607
comp31895_c2_seq14.p1			
comp31895_c2_seq14.p4			
comp31895_c2_seq15.p1			
comp31895_c2_seq2.p1			
comp31895_c2_seq2.p2			
comp31895_c2_seq3.p1			
comp31895_c2_seq4.p1			
comp31895_c2_seq5.p1			
comp31895_c2_seq6.p1			
comp31895_c2_seq7.p1			
comp31895_c2_seq8.p1			
comp31895_c3_seq1.p1			
comp31895_c3_seq2.p1			
comp31895_c3_seq3.p1			
comp31896_c0_seq1.p1			
comp31896_c0_seq2.p1			
comp31896_c0_seq3.p1			
comp31896_c1_seq1.p1	sp|Q8HXQ5|MRP1_BOVIN_Multidrug_resistance-associated_protein_1_OS=Bos_taurus_GN=ABCC1_PE=2_SV=1	0	GO:0000166,GO:0005215,GO:0005524,GO:0005524,GO:0005886,GO:0005886,GO:0006200,GO:0006810,GO:0006810,GO:0008152,GO:0016020,GO:0016021,GO:0016021,GO:0016787,GO:0016887,GO:0042626,GO:0055085
comp31896_c2_seq11.p1			
comp31896_c2_seq2.p1			
comp31896_c2_seq23.p1			
comp31896_c2_seq24.p1			
comp31896_c2_seq27.p1			
comp31896_c2_seq28.p1			
comp31896_c2_seq30.p1			
comp31896_c2_seq30.p3			
comp31896_c2_seq30.p4			
comp31896_c2_seq31.p1			
comp31896_c2_seq33.p2			
comp31896_c2_seq33.p3			
comp31896_c2_seq34.p1			
comp31896_c2_seq35.p2			
comp31896_c2_seq5.p1			
comp31896_c2_seq5.p2			
comp31896_c2_seq8.p1	sp|Q54X16|U559_DICDI_UPF0559_protein_OS=Dictyostelium_discoideum_GN=DDB_G0279265_PE=3_SV=2	6.00E-57	GO:0003674,GO:0005575,GO:0005634,GO:0005634,GO:0008150
comp31897_c0_seq1.p1			
comp31897_c0_seq4.p1			
comp31897_c0_seq6.p1			
comp31898_c0_seq1.p2			
comp31898_c0_seq13.p1	sp|Q9SH30|HMA5_ARATH_Putative_copper-transporting_ATPase_HMA5_OS=Arabidopsis_thaliana_GN=HMA5_PE=2_SV=2	2.00E-129	GO:0000166,GO:0000166,GO:0005507,GO:0005524,GO:0006810,GO:0006811,GO:0006812,GO:0006825,GO:0008152,GO:0010043,GO:0010273,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016787,GO:0019829,GO:0030001,GO:0046688,GO:0046872,GO:0046872,GO:0098655
comp31898_c0_seq13.p2	sp|Q08647|PUS7_YEAST_Multisubstrate_pseudouridine_synthase_7_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PUS7_PE=1_SV=1	3.00E-37	GO:0000455,GO:0001522,GO:0003723,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0006364,GO:0006397,GO:0008033,GO:0008380,GO:0009451,GO:0009982,GO:0009982,GO:0009982,GO:0009982,GO:0016853,GO:0031119,GO:0031120,GO:0031120,GO:0031120,GO:0042254,GO:1990481,GO:1990481
comp31898_c0_seq14.p1			
comp31898_c0_seq17.p2			
comp31898_c0_seq3.p1			
comp31898_c0_seq5.p1			
comp31899_c0_seq1.p1			
comp31899_c0_seq7.p1			
comp31899_c0_seq8.p1			
comp31899_c0_seq9.p1			
comp31900_c0_seq1.p1			
comp31900_c0_seq5.p1			
comp31900_c0_seq5.p2			
comp31901_c0_seq1.p1			
comp31901_c0_seq14.p1			
comp31901_c0_seq15.p1			

comp31901_c0_seq16.p1	sp|Q9SHJ3|CALS7_ARATH_Callose_synthase_7_OS=Arabidopsis_thaliana_GN=CALS7_PE=2_SV=3	1.00E-108	[illegible]	[illegible]
comp31901_c0_seq17.p1				
comp31901_c0_seq18.p1				
comp31901_c0_seq20.p1	sp|Q3B724|CALS5_ARATH_Callose_synthase_5_OS=Arabidopsis_thaliana_GN=CALS5_PE=1_SV=1	3.00E-31	[illegible]	[illegible]
comp31901_c0_seq21.p1	sp|Q9ZT82|CALSC_ARATH_Callose_synthase_12_OS=Arabidopsis_thaliana_GN=CALS12_PE=1_SV=1	0	[illegible]	[illegible]
comp31901_c0_seq22.p1				
comp31901_c0_seq24.p1				
comp31901_c0_seq4.p1				
comp31901_c0_seq5.p1				
comp31901_c0_seq8.p1				
comp31903_c0_seq1.p1				
comp31903_c0_seq1.p3				
comp31903_c0_seq3.p1	sp|Q86HG9|Y9871_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0271682_OS=Dictyostelium_discoideum_GN=DDB_G0271682_PE=3_SV=2	5.00E-26	[illegible]	[illegible]
comp31903_c0_seq3.p2				
comp31903_c0_seq4.p1				
comp31903_c0_seq7.p1				
comp31905_c0_seq4.p1				
comp31905_c0_seq5.p1				
comp31905_c0_seq5.p2				
comp31906_c0_seq1.p1	sp|Q500Y9|NADHK_ARATH_NADH_kinase_OS=Arabidopsis_thaliana_GN=NADK3_PE=1_SV=1	6.00E-43	[illegible]	[illegible]
comp31906_c1_seq1.p1	sp|Q8VCN9|TBCC_MOUSE_Tubulin-specific_chaperone_C_OS=Mus_musculus_GN=Tbcc_PE=2_SV=1	8.00E-36	[illegible]	[illegible]
comp31906_c1_seq18.p1	sp|P84239|H3_URECA_Histone_H3_OS=Urechis_caupo_PE=1_SV=2	2.00E-74	[illegible]	[illegible]
comp31906_c1_seq2.p1	sp|Q8VCN9|TBCC_MOUSE_Tubulin-specific_chaperone_C_OS=Mus_musculus_GN=Tbcc_PE=2_SV=1	2.00E-45	[illegible]	[illegible]
comp31906_c1_seq3.p1				
comp31906_c1_seq4.p1	sp|Q8VCN9|TBCC_MOUSE_Tubulin-specific_chaperone_C_OS=Mus_musculus_GN=Tbcc_PE=2_SV=1	8.00E-36	[illegible]	[illegible]
comp31906_c1_seq7.p1	sp|Q8VCN9|TBCC_MOUSE_Tubulin-specific_chaperone_C_OS=Mus_musculus_GN=Tbcc_PE=2_SV=1	2.00E-45	[illegible]	[illegible]
comp31906_c1_seq8.p1	sp|Q8VCN9|TBCC_MOUSE_Tubulin-specific_chaperone_C_OS=Mus_musculus_GN=Tbcc_PE=2_SV=1	8.00E-36	[illegible]	[illegible]
comp31907_c0_seq2.p1				
comp31907_c0_seq4.p1				
comp31908_c0_seq1.p1				
comp31908_c1_seq1.p1	sp|Q6AYB5|SRP54_RAT_Signal_recognition_particle_54_kDa_protein_OS=Rattus_norvegicus_GN=Srp54_PE=2_SV=1	3.00E-20	[illegible]	[illegible]
comp31908_c1_seq2.p1	sp|P14576|SRP54_MOUSE_Signal_recognition_particle_54_kDa_protein_OS=Mus_musculus_GN=Srp54_PE=1_SV=2	3.00E-96	[illegible]	[illegible]
comp31908_c1_seq3.p1	sp|P14576|SRP54_MOUSE_Signal_recognition_particle_54_kDa_protein_OS=Mus_musculus_GN=Srp54_PE=1_SV=2	8.00E-88	[illegible]	[illegible]
comp31908_c1_seq4.p1	sp|P14576|SRP54_MOUSE_Signal_recognition_particle_54_kDa_protein_OS=Mus_musculus_GN=Srp54_PE=1_SV=2	8.00E-88	[illegible]	[illegible]
comp31908_c1_seq4.p2	sp|Q6AYB5|SRP54_RAT_Signal_recognition_particle_54_kDa_protein_OS=Rattus_norvegicus_GN=Srp54_PE=2_SV=1	8.00E-20	[illegible]	[illegible]
comp31908_c1_seq6.p1				
comp31908_c1_seq7.p1	sp|P14576|SRP54_MOUSE_Signal_recognition_particle_54_kDa_protein_OS=Mus_musculus_GN=Srp54_PE=1_SV=2	2.00E-151	[illegible]	[illegible]
comp31909_c0_seq11.p1	sp|Q5MB13|ABCG2_MACMU_ATP-binding_cassette_sub-family_G_member_2_OS=Macaca_mulatta_GN=ABCG2_PE=2_SV=1	1.00E-48	[illegible]	[illegible]
comp31909_c0_seq13.p1	sp|Q9MAG3|AB24G_ARATH_ABC_transporter_G_family_member_24_OS=Arabidopsis_thaliana_GN=ABCG24_PE=1_SV=2	4.00E-12	[illegible]	[illegible]
comp31909_c0_seq13.p2				
comp31909_c0_seq2.p1	sp|Q9MAH4|AB10G_ARATH_ABC_transporter_G_family_member_10_OS=Arabidopsis_thaliana_GN=ABCG10_PE=3_SV=1	1.00E-26	[illegible]	[illegible]
comp31909_c0_seq2.p2				
comp31909_c0_seq21.p1				
comp31909_c0_seq21.p2				
comp31909_c0_seq24.p1	sp|Q9M2V6|AB17G_ARATH_ABC_transporter_G_family_member_17_OS=Arabidopsis_thaliana_GN=ABCG17_PE=2_SV=1	1.00E-54	[illegible]	[illegible]
comp31909_c0_seq24.p2	sp|Q56ZZ7|PLST4_ARATH_Plastidic_glucose_transporter_4_OS=Arabidopsis_thaliana_GN=At5g16150_PE=1_SV=2	2.00E-62	[illegible]	[illegible]
comp31909_c0_seq33.p1	sp|Q9MAG3|AB24G_ARATH_ABC_transporter_G_family_member_24_OS=Arabidopsis_thaliana_GN=ABCG24_PE=1_SV=2	4.00E-11	[illegible]	[illegible]
comp31909_c0_seq38.p1	sp|Q9M2V6|AB17G_ARATH_ABC_transporter_G_family_member_17_OS=Arabidopsis_thaliana_GN=ABCG17_PE=2_SV=1	2.00E-56	[illegible]	[illegible]
comp31909_c0_seq38.p2	sp|Q5MB13|ABCG2_MACMU_ATP-binding_cassette_sub-family_G_member_2_OS=Macaca_mulatta_GN=ABCG2_PE=2_SV=1	1.00E-49	[illegible]	[illegible]
comp31909_c0_seq38.p3	sp|Q56ZZ7|PLST4_ARATH_Plastidic_glucose_transporter_4_OS=Arabidopsis_thaliana_GN=At5g16150_PE=1_SV=2	2.00E-62	[illegible]	[illegible]
comp31909_c0_seq42.p1	sp|Q5MB13|ABCG2_MACMU_ATP-binding_cassette_sub-family_G_member_2_OS=Macaca_mulatta_GN=ABCG2_PE=2_SV=1	1.00E-49	[illegible]	[illegible]
comp31909_c0_seq42.p2	sp|Q56ZZ7|PLST4_ARATH_Plastidic_glucose_transporter_4_OS=Arabidopsis_thaliana_GN=At5g16150_PE=1_SV=2	2.00E-62	[illegible]	[illegible]
comp31909_c0_seq42.p3	sp|Q3E9B8|AB23G_ARATH_ABC_transporter_G_family_member_23_OS=Arabidopsis_thaliana_GN=ABCG23_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp31909_c0_seq42.p4	sp|Q9MAG3|AB24G_ARATH_ABC_transporter_G_family_member_24_OS=Arabidopsis_thaliana_GN=ABCG24_PE=1_SV=2	4.00E-12	[illegible]	[illegible]
comp31911_c0_seq1.p1	sp|Q8N122|RPTOR_HUMAN_Regulatory-associated_protein_of_mTOR_OS=Homo_sapiens_GN=RPTOR_PE=1_SV=1	8.00E-89	[illegible]	[illegible]
comp31912_c0_seq2.p1				
comp31912_c0_seq2.p2	sp|Q54XZ0|MFEB_DICDI_Probable_enoyl-CoA_hydratase_2_OS=Dictyostelium_discoideum_GN=mfeB_PE=2_SV=1	3.00E-39	[illegible]	[illegible]
comp31912_c0_seq3.p1				
comp31912_c0_seq4.p2				
comp31912_c0_seq5.p1				
comp31914_c0_seq1.p1	sp|Q5UP39|YR873_MIMIV_Putative_ankyrin_repeat_protein_R873_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R873_PE=4_SV=1	2.00E-17		
comp31914_c0_seq2.p1				
comp31914_c1_seq3.p1				
comp31916_c0_seq4.p1	sp|P72772|CHLD_SYNY3_Magnesium-chelatase_subunit_ChlD_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=chlD_PE=3_SV=1	1.00E-104	[illegible]	[illegible]
comp31916_c0_seq4.p2	sp|P46250|SEC14_CANAL_SEC14_cytosolic_factor_OS=Candida_albicans_(strain_SC5314_/_ATCC_MYA-2876)_GN=SEC14_PE=2_SV=1	7.00E-15	[illegible]	[illegible]
comp31916_c0_seq4.p4				
comp31917_c0_seq1.p1	sp|Q9XIE6|ALA3_ARATH_Phospholipid-transporting_ATPase_3_OS=Arabidopsis_thaliana_GN=ALA3_PE=1_SV=2	3.00E-112	[illegible]	[illegible]
comp31917_c0_seq1.p2				
comp31919_c0_seq2.p1				
comp31919_c0_seq2.p3	sp|A0JMD2|LST2_DANRE_Lateral_signaling_target_protein_2_homolog_OS=Danio_rerio_GN=zfyve28_PE=2_SV=1	3.00E-12	[illegible]	[illegible]
comp31919_c0_seq4.p1				
comp31920_c0_seq4.p1	sp|P35525|CLCN2_RAT_Chloride_channel_protein_2_OS=Rattus_norvegicus_GN=Clcn2_PE=2_SV=1	6.00E-42	[illegible]	[illegible]
comp31922_c0_seq1.p1				
comp31922_c0_seq1.p2				
comp31922_c0_seq6.p1				
comp31922_c0_seq6.p2				
comp31923_c0_seq15.p1	sp|P51567|AFC2_ARATH_Serine/threonine-protein_kinase_AFC2_OS=Arabidopsis_thaliana_GN=AFC2_PE=1_SV=1	1.00E-77	[illegible]	[illegible]
comp31923_c0_seq3.p1	sp|P06245|KAPB_YEAST_cAMP-dependent_protein_kinase_type_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TPK2_PE=1_SV=2	1.00E-20	[illegible]	[illegible]
comp31923_c0_seq3.p3				
comp31923_c0_seq4.p1	sp|P51567|AFC2_ARATH_Serine/threonine-protein_kinase_AFC2_OS=Arabidopsis_thaliana_GN=AFC2_PE=1_SV=1	1.00E-26	[illegible]	[illegible]
comp31923_c0_seq5.p2				
comp31923_c0_seq8.p1	sp|P51567|AFC2_ARATH_Serine/threonine-protein_kinase_AFC2_OS=Arabidopsis_thaliana_GN=AFC2_PE=1_SV=1	5.00E-83	[illegible]	[illegible]
comp31923_c0_seq9.p1				
comp31923_c2_seq1.p1				
comp31924_c0_seq1.p1	sp|Q9H5Z1|DHX35_HUMAN_Probable_ATP-dependent_RNA_helicase_DHX35_OS=Homo_sapiens_GN=DHX35_PE=1_SV=2	0	[illegible]	[illegible]
comp31924_c0_seq2.p1	sp|O22899|DHX15_ARATH_Probable_pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_OS=Arabidopsis_thaliana_GN=At2g47250_PE=2_SV=1	1.00E-59	[illegible]	[illegible]
comp31924_c0_seq3.p1	sp|O22899|DHX15_ARATH_Probable_pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_OS=Arabidopsis_thaliana_GN=At2g47250_PE=2_SV=1	3.00E-35	[illegible]	[illegible]
comp31924_c0_seq5.p1	sp|O22899|DHX15_ARATH_Probable_pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_OS=Arabidopsis_thaliana_GN=At2g47250_PE=2_SV=1	0	[illegible]	[illegible]
comp31924_c0_seq6.p1	sp|O22899|DHX15_ARATH_Probable_pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_OS=Arabidopsis_thaliana_GN=At2g47250_PE=2_SV=1	1.00E-131	[illegible]	[illegible]
comp31924_c0_seq6.p2	sp|P53131|PRP43_YEAST_Pre-mRNA-splicing_factor_ATP-dependent_RNA_helicase_PRP43_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PRP43_PE=1_SV=1	3.00E-37	[illegible]	[illegible]
comp31925_c0_seq1.p1				
comp31926_c0_seq3.p1				
comp31927_c0_seq3.p1				
comp31929_c0_seq1.p1				
comp31929_c0_seq3.p1				
comp31929_c0_seq8.p1				
comp31930_c0_seq1.p3				
comp31931_c0_seq1.p1				
comp31931_c0_seq1.p2	sp|Q9Z1Z1|E2AK3_RAT_Eukaryotic_translation_initiation_factor_2-alpha_kinase_3_OS=Rattus_norvegicus_GN=Eif2ak3_PE=1_SV=1	5.00E-24	[illegible]	[illegible]
comp31932_c0_seq5.p1				
comp31933_c0_seq11.p1	sp|O94296|YOOC_SCHPO_Probable_phospholipid-transporting_ATPase_C887.12_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC887.12_PE=2_SV=1	4.00E-108	[illegible]	[illegible]
comp31933_c0_seq11.p7	sp|Q9P241|AT10D_HUMAN_Probable_phospholipid-transporting_ATPase_VD_OS=Homo_sapiens_GN=ATP10D_PE=2_SV=3	1.00E-14	[illegible]	[illegible]
comp31933_c0_seq3.p1	sp|O94296|YOOC_SCHPO_Probable_phospholipid-transporting_ATPase_C887.12_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC887.12_PE=2_SV=1	6.00E-108	[illegible]	[illegible]
comp31933_c0_seq3.p7	sp|Q9P241|AT10D_HUMAN_Probable_phospholipid-transporting_ATPase_VD_OS=Homo_sapiens_GN=ATP10D_PE=2_SV=3	1.00E-14	[illegible]	[illegible]
comp31933_c0_seq4.p1	sp|Q29449|AT8A1_BOVIN_Probable_phospholipid-transporting_ATPase_IA_OS=Bos_taurus_GN=ATP8A1_PE=1_SV=2	6.00E-39	[illegible]	[illegible]
comp31933_c0_seq6.p1	sp|Q9XIE6|ALA3_ARATH_Phospholipid-transporting_ATPase_3_OS=Arabidopsis_thaliana_GN=ALA3_PE=1_SV=2	5.00E-40	[illegible]	[illegible]
comp31933_c0_seq6.p4	sp|Q9P241|AT10D_HUMAN_Probable_phospholipid-transporting_ATPase_VD_OS=Homo_sapiens_GN=ATP10D_PE=2_SV=3	1.00E-14	[illegible]	[illegible]
comp31933_c0_seq7.p2				
comp31934_c0_seq1.p1	sp|P74334|ACOX_SYNY3_Apocarotenoid-15,15'-oxygenase_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll1541_PE=1_SV=1	5.00E-41	[illegible]	[illegible]
comp31935_c0_seq2.p1	sp|Q8BGW1|FTO_MOUSE_Alpha-ketoglutarate-dependent_dioxygenase_FTO_OS=Mus_musculus_GN=Fto_PE=1_SV=1	3.00E-43	[illegible]	[illegible]
comp31935_c0_seq3.p1	sp|Q6ZIK0|GTOMC_ORYSJ_Probable_tocopherol_O-methyltransferase,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=VTE4_PE=2_SV=1	2.00E-53	[illegible]	[illegible]
comp31935_c0_seq7.p1	sp|Q6ZIK0|GTOMC_ORYSJ_Probable_tocopherol_O-methyltransferase,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=VTE4_PE=2_SV=1	2.00E-49	[illegible]	[illegible]
comp31937_c0_seq2.p1				
comp31937_c1_seq7.p1				
comp31938_c0_seq4.p1	sp|P11029|ACAC_CHICK_Acetyl-CoA_carboxylase_OS=Gallus_gallus_GN=ACAC_PE=1_SV=1	5.00E-128	[illegible]	[illegible]
comp31938_c0_seq5.p1	sp|Q13085|ACACA_HUMAN_Acetyl-CoA_carboxylase_1_OS=Homo_sapiens_GN=ACACA_PE=1_SV=2	0	[illegible]	[illegible]
comp31939_c0_seq2.p1				
comp31939_c0_seq3.p1				
comp31939_c0_seq3.p2				
comp31939_c0_seq5.p1				
comp31939_c0_seq5.p2				
comp31939_c0_seq7.p1				
comp31940_c0_seq10.p1				
comp31940_c0_seq12.p1				
comp31940_c0_seq18.p1				
comp31940_c0_seq20.p1				
comp31940_c0_seq23.p1				
comp31940_c0_seq24.p1				
comp31941_c0_seq1.p1				
comp31941_c0_seq2.p1	sp|Q8CBH5|MFSD6_MOUSE_Major_facilitator_superfamily_domain-containing_protein_6_OS=Mus_musculus_GN=Mfsd6_PE=1_SV=1	1.00E-13	[illegible]	[illegible]
comp31941_c0_seq3.p1	sp|B0UYT5|MFD6B_DANRE_Major_facilitator_superfamily_domain-containing_protein_6-B_OS=Danio_rerio_GN=mfsd6b_PE=3_SV=1	8.00E-22	[illegible]	[illegible]
comp31941_c0_seq6.p1	sp|Q8CBH5|MFSD6_MOUSE_Major_facilitator_superfamily_domain-containing_protein_6_OS=Mus_musculus_GN=Mfsd6_PE=1_SV=1	7.00E-15	[illegible]	[illegible]
comp31943_c0_seq14.p1	sp|Q9H9H8|APAF_DANRE_Apoptotic_protease-activating_factor_1_OS=Danio_rerio_GN=apaf1_PE=2_SV=1	5.00E-12	[illegible]	[illegible]
comp31943_c0_seq15.p1				
comp31943_c0_seq22.p1				
comp31943_c0_seq26.p1				
comp31943_c0_seq26.p2				
comp31943_c0_seq28.p1				
comp31943_c0_seq28.p2				
comp31943_c0_seq3.p1	sp|Q9H9H8|APAF_DANRE_Apoptotic_protease-activating_factor_1_OS=Danio_rerio_GN=apaf1_PE=2_SV=1	6.00E-15	[illegible]	[illegible]
comp31943_c0_seq5.p1	sp|Q9H9H8|APAF_DANRE_Apoptotic_protease-activating_factor_1_OS=Danio_rerio_GN=apaf1_PE=2_SV=1	2.00E-11	[illegible]	[illegible]
comp31946_c0_seq2.p1	sp|Q91628|ORC2_XENLA_Origin_recognition_complex_subunit_2_OS=Xenopus_laevis_GN=orc2_PE=2_SV=1	3.00E-15	[illegible]	[illegible]
comp31947_c0_seq1.p1				
comp31947_c0_seq1.p6				
comp31948_c0_seq10.p1				
comp31948_c0_seq11.p1	sp|P11730|KCC2G_RAT_Calcium/calmodulin-dependent_protein_kinase_type_II_subunit_gamma_OS=Rattus_norvegicus_GN=Camk2g_PE=2_SV=1	2.00E-54	[illegible]	[illegible]
comp31948_c0_seq5.p1	sp|Q8BW96|KCC1D_MOUSE_Calcium/calmodulin-dependent_protein_kinase_type_1D_OS=Mus_musculus_GN=Camk1d_PE=1_SV=2	8.00E-39	[illegible]	[illegible]
comp31948_c0_seq5.p2	sp|P08414|KCC4_MOUSE_Calcium/calmodulin-dependent_protein_kinase_type_IV_OS=Mus_musculus_GN=Camk4_PE=1_SV=2	7.00E-49	[illegible]	[illegible]
comp31948_c0_seq9.p2				
comp31950_c0_seq17.p1				
comp31950_c0_seq19.p1	sp|Q9CPV0|TM107_MOUSE_Transmembrane_protein_107_OS=Mus_musculus_GN=Tmem107_PE=2_SV=1	2.00E-16	[illegible]	[illegible]
comp31950_c0_seq3.p2				
comp31950_c0_seq9.p1				
comp31951_c0_seq1.p1	sp|Q6GFF5|PUTP_STAAR_Sodium/proline_symporter_OS=Staphylococcus_aureus_(strain_MRSA252)_GN=putP_PE=3_SV=1	1.00E-23	[illegible]	[illegible]
comp31953_c0_seq2.p1	sp|Q9ESJ0|XPO4_MOUSE_Exportin-4_OS=Mus_musculus_GN=Xpo4_PE=1_SV=2	4.00E-36	[illegible]	[illegible]
comp31953_c0_seq2.p2	sp|Q9C0E2|XPO4_HUMAN_Exportin-4_OS=Homo_sapiens_GN=XPO4_PE=1_SV=2	3.00E-17	[illegible]	[illegible]
comp31953_c0_seq3.p1	sp|Q5ZMR9|XPO4_CHICK_Exportin-4_OS=Gallus_gallus_GN=XPO4_PE=2_SV=1	8.00E-54	[illegible]	[illegible]
comp31953_c0_seq6.p1	sp|Q9C0E2|XPO4_HUMAN_Exportin-4_OS=Homo_sapiens_GN=XPO4_PE=1_SV=2	3.00E-17	[illegible]	[illegible]
comp31953_c0_seq6.p2	sp|Q9ESJ0|XPO4_MOUSE_Exportin-4_OS=Mus_musculus_GN=Xpo4_PE=1_SV=2	1.00E-33	[illegible]	[illegible]
comp31953_c0_seq7.p1	sp|Q5ZMR9|XPO4_CHICK_Exportin-4_OS=Gallus_gallus_GN=XPO4_PE=2_SV=1	4.00E-51	[illegible]	[illegible]
comp31954_c0_seq2.p1				
comp31954_c0_seq3.p1				
comp31954_c1_seq10.p2				
comp31954_c1_seq15.p1				
comp31954_c1_seq2.p1				
comp31955_c0_seq6.p2				
comp31955_c0_seq6.p4				
comp31956_c0_seq3.p1				
comp31957_c0_seq3.p1	sp|P68182|KAPCB_RAT_cAMP-dependent_protein_kinase_catalytic_subunit_beta_OS=Rattus_norvegicus_GN=Prkacb_PE=1_SV=2	3.00E-40	[illegible]	[illegible]
comp31958_c0_seq4.p1				
comp31958_c0_seq7.p1				
comp31958_c1_seq2.p1				
comp31958_c1_seq3.p1				
comp31958_c2_seq1.p1				
comp31958_c2_seq2.p1				
comp31958_c2_seq3.p1				
comp31958_c2_seq3.p2				
comp31958_c3_seq1.p2				
comp31958_c3_seq1.p3				
comp31959_c0_seq10.p1				
comp31959_c0_seq11.p1	sp|Q54TA1|DRKC_DICDI_Probable_serine/threonine-protein_kinase_drkC_OS=Dictyostelium_discoideum_GN=drkC_PE=3_SV=1	2.00E-33	[illegible]	[illegible]
comp31959_c0_seq11.p3				
comp31959_c0_seq12.p1	sp|Q2XWK0|SVOP_XENLA_Synaptic_vesicle_2-related_protein_OS=Xenopus_laevis_GN=svop_PE=2_SV=1	1.00E-48	[illegible]	[illegible]
comp31959_c0_seq7.p1	sp|Q6MEC9|SYN_PARUW_Asparagine--tRNA_ligase_OS=Protochlamydia_amoebophila_(strain_UWE25)_GN=asnS_PE=3_SV=1	9.00E-169	[illegible]	[illegible]
comp31959_c0_seq8.p2				
comp31959_c0_seq9.p2				
comp31960_c0_seq5.p1	sp|O95394|AGM1_HUMAN_Phosphoacetylglucosamine_mutase_OS=Homo_sapiens_GN=PGM3_PE=1_SV=1	5.00E-135	[illegible]	[illegible]
comp31962_c0_seq2.p1	sp|P44263|Y1586_HAEIN_Uncharacterized_protein_HI_1586_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=HI_1586_PE=4_SV=1	3.00E-26	[illegible]	[illegible]
comp31962_c0_seq5.p1				
comp31963_c1_seq1.p1				
comp31963_c1_seq3.p1				
comp31963_c1_seq4.p1				
comp31964_c0_seq1.p2				
comp31965_c0_seq1.p3				
comp31965_c0_seq3.p1				
comp31966_c0_seq1.p1				
comp31966_c0_seq2.p1				
comp31966_c0_seq2.p2				
comp31966_c1_seq11.p1	sp|Q9FT74|RQL1_ARATH_ATP-dependent_DNA_helicase_Q-like_1_OS=Arabidopsis_thaliana_GN=RECQL1_PE=2_SV=1	2.00E-114	[illegible]	[illegible]
comp31966_c1_seq3.p2				
comp31966_c1_seq8.p1	sp|B2ZFP3|SMAL1_DANRE_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A-like_protein_1_OS=Danio_rerio_GN=smarcal1_PE=2_SV=1	2.00E-51	[illegible]	[illegible]
comp31966_c1_seq9.p1	sp|B4F769|SMAL1_RAT_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A-like_protein_1_OS=Rattus_norvegicus_GN=Smarcal1_PE=2_SV=1	3.00E-34	[illegible]	[illegible]
comp31966_c2_seq2.p1				
comp31966_c2_seq2.p3				
comp31966_c2_seq6.p1	sp|Q40412|ABA2_NICPL_Zeaxanthin_epoxidase,_chloroplastic_OS=Nicotiana_plumbaginifolia_GN=ABA2_PE=1_SV=1	2.00E-19	[illegible]	[illegible]
comp31966_c2_seq8.p1	sp|Q32KJ8|ARSI_RAT_Arylsulfatase_I_OS=Rattus_norvegicus_GN=Arsi_PE=2_SV=1	6.00E-78	[illegible]	[illegible]
comp31966_c2_seq9.p1	sp|Q5FYB1|ARSI_HUMAN_Arylsulfatase_I_OS=Homo_sapiens_GN=ARSI_PE=1_SV=1	4.00E-76	[illegible]	[illegible]
comp31966_c2_seq9.p2	sp|Q28CH3|UAP1L_XENTR_UDP-N-acetylhexosamine_pyrophosphorylase-like_protein_1_OS=Xenopus_tropicalis_GN=uap1l1_PE=2_SV=1	2.00E-114	[illegible]	[illegible]
comp31967_c0_seq3.p1				
comp31967_c0_seq6.p1				
comp31967_c0_seq7.p1				
comp31967_c0_seq7.p2				
comp31968_c0_seq1.p1	sp|Q9EPU0|RENT1_MOUSE_Regulator_of_nonsense_transcripts_1_OS=Mus_musculus_GN=Upf1_PE=1_SV=2	3.00E-52	[illegible]	[illegible]
comp31968_c0_seq2.p1				
comp31968_c0_seq3.p1				
comp31968_c0_seq4.p1	sp|Q9FJR0|RENT1_ARATH_Regulator_of_nonsense_transcripts_1_homolog_OS=Arabidopsis_thaliana_GN=UPF1_PE=1_SV=2	0	[illegible]	[illegible]
comp31970_c0_seq1.p1				
comp31970_c0_seq10.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	2.00E-14	[illegible]	[illegible]
comp31970_c0_seq11.p1				
comp31970_c0_seq4.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	3.00E-18	[illegible]	[illegible]
comp31970_c0_seq5.p1				
comp31970_c0_seq7.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	2.00E-18	[illegible]	[illegible]
comp31973_c0_seq5.p1				
comp31973_c0_seq6.p1				
comp31973_c0_seq7.p1				
comp31974_c0_seq1.p1	sp|Q8BL06|UBP54_MOUSE_Inactive_ubiquitin_carboxyl-terminal_hydrolase_54_OS=Mus_musculus_GN=Usp54_PE=1_SV=2	5.00E-13	[illegible]	[illegible]
comp31975_c0_seq1.p1				
comp31975_c1_seq1.p1				
comp31975_c1_seq2.p1				
comp31975_c1_seq5.p1				
comp31975_c2_seq1.p1	sp|P58338|OCD1_RHIME_Ornithine_cyclodeaminase_1_OS=Rhizobium_meliloti_(strain_1021)_GN=ocd1_PE=3_SV=1	3.00E-47	GO:0008473,GO:0016829,GO:0055129	[illegible]
comp31975_c2_seq1.p2				
comp31975_c2_seq1.p3				
comp31977_c0_seq1.p1				
comp31977_c0_seq1.p2				
comp31977_c0_seq7.p1	sp|B2FQP3|ASPN_STRMK_Peptidyl-Asp_metalloendopeptidase_OS=Stenotrophomonas_maltophilia_(strain_K279a)_GN=Smlt0970_PE=3_SV=1	9.00E-14	[illegible]	[illegible]
comp31977_c0_seq8.p1	sp|B2FQP3|ASPN_STRMK_Peptidyl-Asp_metalloendopeptidase_OS=Stenotrophomonas_maltophilia_(strain_K279a)_GN=Smlt0970_PE=3_SV=1	9.00E-14	[illegible]	[illegible]
comp31977_c0_seq9.p1				
comp31978_c0_seq2.p2				
comp31978_c0_seq2.p4				
comp31978_c0_seq4.p1	sp|Q2KIJ5|KDSR_BOVIN_3-ketodihydrosphingosine_reductase_OS=Bos_taurus_GN=KDSR_PE=2_SV=1	3.00E-71	[illegible]	[illegible]
comp31979_c0_seq1.p2				
comp31980_c0_seq1.p1				
comp31980_c0_seq2.p1				
comp31980_c0_seq4.p1				
comp31980_c0_seq5.p1				
comp31981_c0_seq3.p1	sp|O75191|XYLB_HUMAN_Xylulose_kinase_OS=Homo_sapiens_GN=XYLB_PE=1_SV=3	2.00E-111	[illegible]	[illegible]
comp31983_c0_seq5.p1	sp|Q3B7D0|HEM6_RAT_Coproporphyrinogen-III_oxidase,_mitochondrial_OS=Rattus_norvegicus_GN=Cpox_PE=2_SV=1	2.00E-75	[illegible]	[illegible]
comp31983_c0_seq5.p2				
comp31984_c0_seq1.p1	sp|P31692|ADT_PARKE_ADP,ATP_carrier_protein_OS=Parachlorella_kessleri_PE=3_SV=1	9.00E-114	[illegible]	[illegible]
comp31984_c1_seq5.p1	sp|Q07282|TCR5_ECOLX_Tetracycline_resistance_protein,_class_E_OS=Escherichia_coli_GN=tetA_PE=3_SV=1	3.00E-19	[illegible]	[illegible]
comp31984_c1_seq8.p1	sp|Q07282|TCR5_ECOLX_Tetracycline_resistance_protein,_class_E_OS=Escherichia_coli_GN=tetA_PE=3_SV=1	5.00E-19	[illegible]	[illegible]
comp31984_c2_seq3.p1				
comp31984_c3_seq1.p1	sp|Q1LZA1|CAH1_BOVIN_Carbonic_anhydrase_1_OS=Bos_taurus_GN=CA1_PE=2_SV=3	1.00E-25	[illegible]	[illegible]
comp31984_c3_seq4.p1	sp|Q9ERQ8|CAH7_MOUSE_Carbonic_anhydrase_7_OS=Mus_musculus_GN=Ca7_PE=1_SV=2	1.00E-20	[illegible]	[illegible]
comp31985_c0_seq1.p1	sp|Q9C0V4|YOM2_SCHPO_Uncharacterized_protein_PB7E8.02_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBPB7E8.02_PE=2_SV=1	9.00E-23	[illegible]	[illegible]
comp31985_c0_seq3.p1				
comp31986_c0_seq1.p1				
comp31986_c0_seq1.p2	sp|A2QVV2|CREC_ASPNC_Probable_catabolite_repression_protein_creC_OS=Aspergillus_niger_(strain_CBS_513.88_/_FGSC_A1513)_GN=creC_PE=3_SV=1	1.00E-29	[illegible]	[illegible]
comp31986_c0_seq2.p1	sp|A2QVV2|CREC_ASPNC_Probable_catabolite_repression_protein_creC_OS=Aspergillus_niger_(strain_CBS_513.88_/_FGSC_A1513)_GN=creC_PE=3_SV=1	1.00E-29	[illegible]	[illegible]
comp31986_c0_seq3.p1				
comp31986_c0_seq3.p2	sp|A2QVV2|CREC_ASPNC_Probable_catabolite_repression_protein_creC_OS=Aspergillus_niger_(strain_CBS_513.88_/_FGSC_A1513)_GN=creC_PE=3_SV=1	1.00E-29	[illegible]	[illegible]
comp31986_c0_seq5.p1	sp|A2QVV2|CREC_ASPNC_Probable_catabolite_repression_protein_creC_OS=Aspergillus_niger_(strain_CBS_513.88_/_FGSC_A1513)_GN=creC_PE=3_SV=1	1.00E-29	[illegible]	[illegible]
comp31987_c0_seq1.p1				
comp31987_c0_seq2.p1				
comp31988_c0_seq2.p1				
comp31989_c0_seq3.p1				
comp31989_c0_seq3.p2	sp|P33144|BIMB_EMENI_Separin_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=bimB_PE=3_SV=2	3.00E-40	[illegible]	[illegible]
comp31989_c0_seq3.p3				
comp31991_c0_seq1.p1				
comp31991_c0_seq2.p1				
comp31991_c0_seq3.p1				
comp31991_c0_seq4.p1				
comp31991_c0_seq6.p1				
comp31993_c0_seq3.p1				
comp31993_c0_seq4.p1				
comp31994_c0_seq1.p1	sp|Q5RKH7|CB018_RAT_Transmembrane_protein_C2orf18_homolog_OS=Rattus_norvegicus_PE=2_SV=1	2.00E-36	[illegible]	[illegible]
comp31996_c0_seq1.p1	sp|O89042|DPOLA_RAT_DNA_polymerase_alpha_catalytic_subunit_(Fragment)_OS=Rattus_norvegicus_GN=Pola1_PE=2_SV=1	8.00E-132	[illegible]	[illegible]
comp31996_c0_seq3.p1				
comp31997_c0_seq2.p1				
comp31997_c0_seq3.p1				
comp31997_c0_seq3.p8				
comp31997_c0_seq5.p1				
comp31999_c1_seq1.p1	sp|Q8SPQ7|FMO3_MACMU_Dimethylaniline_monooxygenase_[N-oxide-forming]_3_OS=Macaca_mulatta_GN=FMO3_PE=2_SV=3	6.00E-14	[illegible]	[illegible]
comp31999_c1_seq12.p1	sp|Q9FWW9|GSXL2_ARATH_Flavin-containing_monooxygenase_FMO_GS-OX-like_2_OS=Arabidopsis_thaliana_GN=At1g12200_PE=2_SV=1	3.00E-45	[illegible]	[illegible]
comp31999_c1_seq14.p1	sp|Q9FWW9|GSXL2_ARATH_Flavin-containing_monooxygenase_FMO_GS-OX-like_2_OS=Arabidopsis_thaliana_GN=At1g12200_PE=2_SV=1	2.00E-45	[illegible]	[illegible]
comp31999_c1_seq2.p1				
comp31999_c1_seq6.p1				
comp31999_c2_seq10.p1				
comp31999_c2_seq4.p1	sp|P0C605|KGP1_MOUSE_cGMP-dependent_protein_kinase_1_OS=Mus_musculus_GN=Prkg1_PE=1_SV=1	5.00E-105	[illegible]	[illegible]
comp31999_c2_seq4.p3	sp|Q9V3B6|CWC15_DROME_Protein_CWC15_homolog_OS=Drosophila_melanogaster_GN=c12.1_PE=2_SV=1	2.00E-12	[illegible]	[illegible]
comp31999_c2_seq6.p1	sp|P31319|KAPR_APLCA_cAMP-dependent_protein_kinase_regulatory_subunit_OS=Aplysia_californica_PE=2_SV=2	2.00E-51	[illegible]	[illegible]
comp32000_c1_seq15.p1				
comp32000_c1_seq19.p1				
comp32000_c1_seq3.p1				
comp32001_c0_seq1.p1	sp|Q944Q0|WNK8_ARATH_Serine/threonine-protein_kinase_WNK8_OS=Arabidopsis_thaliana_GN=WNK8_PE=1_SV=1	9.00E-85	[illegible]	[illegible]
comp32001_c0_seq11.p1	sp|Q944Q0|WNK8_ARATH_Serine/threonine-protein_kinase_WNK8_OS=Arabidopsis_thaliana_GN=WNK8_PE=1_SV=1	7.00E-85	[illegible]	[illegible]
comp32001_c0_seq19.p1	sp|Q944Q0|WNK8_ARATH_Serine/threonine-protein_kinase_WNK8_OS=Arabidopsis_thaliana_GN=WNK8_PE=1_SV=1	4.00E-85	[illegible]	[illegible]
comp32001_c0_seq24.p1	sp|Q944Q0|WNK8_ARATH_Serine/threonine-protein_kinase_WNK8_OS=Arabidopsis_thaliana_GN=WNK8_PE=1_SV=1	7.00E-85	[illegible]	[illegible]
comp32001_c0_seq28.p1	sp|Q944Q0|WNK8_ARATH_Serine/threonine-protein_kinase_WNK8_OS=Arabidopsis_thaliana_GN=WNK8_PE=1_SV=1	5.00E-85	[illegible]	[illegible]
comp32001_c0_seq36.p1	sp|Q944Q0|WNK8_ARATH_Serine/threonine-protein_kinase_WNK8_OS=Arabidopsis_thaliana_GN=WNK8_PE=1_SV=1	7.00E-85	[illegible]	[illegible]
comp32001_c0_seq37.p1	sp|Q944Q0|WNK8_ARATH_Serine/threonine-protein_kinase_WNK8_OS=Arabidopsis_thaliana_GN=WNK8_PE=1_SV=1	7.00E-85	[illegible]	[illegible]

comp32001_c0_seq46.p1	sp|Q944Q0|WNK8_ARATH_Serine/threonine-protein_kinase_WNK8_OS=Arabidopsis_thaliana_GN=WNK8_PE=1_SV=1	5.00E-85	GO:0000166,GO:0004672,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006468,GO:0006468,GO:0006468,GO:0006865,GO:0006888,GO:0009909,GO:0009911,GO:0010228,GO:0010228,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016926,GO:0042802,GO:0043090,GO:0046777,GO:0048573,GO:0050665	nucleotide binding,protein kinase activity,protein kinase activity,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,nucleus,nucleus,protein phosphorylation,protein phosphorylation,protein phosphorylation,amino acid transport,ER to Golgi vesicle-mediated transport,regulation of flower development,positive regulation of flower development,vegetative to reproductive phase transition of meristem,vegetative to reproductive phase transition of meristem,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,protein desumoylation,identical protein binding,amino acid import,protein autophosphorylation,photoperiodism, flowering,hydrogen peroxide biosynthetic process
comp32001_c0_seq50.p1	sp|Q944Q0|WNK8_ARATH_Serine/threonine-protein_kinase_WNK8_OS=Arabidopsis_thaliana_GN=WNK8_PE=1_SV=1	4.00E-85	GO:0000166,GO:0004672,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006468,GO:0006468,GO:0006468,GO:0006865,GO:0006888,GO:0009909,GO:0009911,GO:0010228,GO:0010228,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016926,GO:0042802,GO:0043090,GO:0046777,GO:0048573,GO:0050665	nucleotide binding,protein kinase activity,protein kinase activity,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,nucleus,nucleus,protein phosphorylation,protein phosphorylation,protein phosphorylation,amino acid transport,ER to Golgi vesicle-mediated transport,regulation of flower development,positive regulation of flower development,vegetative to reproductive phase transition of meristem,vegetative to reproductive phase transition of meristem,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,protein desumoylation,identical protein binding,amino acid import,protein autophosphorylation,photoperiodism, flowering,hydrogen peroxide biosynthetic process
comp32001_c0_seq54.p1	sp|Q944Q0|WNK8_ARATH_Serine/threonine-protein_kinase_WNK8_OS=Arabidopsis_thaliana_GN=WNK8_PE=1_SV=1	1.00E-84	GO:0000166,GO:0004672,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006468,GO:0006468,GO:0006468,GO:0006865,GO:0006888,GO:0009909,GO:0009911,GO:0010228,GO:0010228,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016926,GO:0042802,GO:0043090,GO:0046777,GO:0048573,GO:0050665	nucleotide binding,protein kinase activity,protein kinase activity,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,nucleus,nucleus,protein phosphorylation,protein phosphorylation,protein phosphorylation,amino acid transport,ER to Golgi vesicle-mediated transport,regulation of flower development,positive regulation of flower development,vegetative to reproductive phase transition of meristem,vegetative to reproductive phase transition of meristem,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,protein desumoylation,identical protein binding,amino acid import,protein autophosphorylation,photoperiodism, flowering,hydrogen peroxide biosynthetic process
comp32001_c0_seq55.p1	sp|Q944Q0|WNK8_ARATH_Serine/threonine-protein_kinase_WNK8_OS=Arabidopsis_thaliana_GN=WNK8_PE=1_SV=1	4.00E-85	GO:0000166,GO:0004672,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006468,GO:0006468,GO:0006468,GO:0006865,GO:0006888,GO:0009909,GO:0009911,GO:0010228,GO:0010228,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016926,GO:0042802,GO:0043090,GO:0046777,GO:0048573,GO:0050665	nucleotide binding,protein kinase activity,protein kinase activity,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,nucleus,nucleus,protein phosphorylation,protein phosphorylation,protein phosphorylation,amino acid transport,ER to Golgi vesicle-mediated transport,regulation of flower development,positive regulation of flower development,vegetative to reproductive phase transition of meristem,vegetative to reproductive phase transition of meristem,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,protein desumoylation,identical protein binding,amino acid import,protein autophosphorylation,photoperiodism, flowering,hydrogen peroxide biosynthetic process
comp32001_c1_seq1.p1	sp|Q875X3|MYO2A_NAUCC_Myosin-2A_OS=Naumovozyma_castellii_(strain_ATCC_76901_/_CBS_4309_/_NBRC_1992_/_NRRL_Y-12630)_GN=MYO2A_PE=3_SV=2	5.00E-82	GO:0000166,GO:0003774,GO:0003779,GO:0005524,GO:0005524,GO:0006810,GO:0007049,GO:0008152,GO:0015031,GO:0016459,GO:0016459,GO:0051015	nucleotide binding,motor activity,actin binding,ATP binding,ATP binding,transport,cell cycle,metabolic process,protein transport,myosin complex,myosin complex,actin filament binding
comp32001_c1_seq4.p1	sp|Q875X3|MYO2A_NAUCC_Myosin-2A_OS=Naumovozyma_castellii_(strain_ATCC_76901_/_CBS_4309_/_NBRC_1992_/_NRRL_Y-12630)_GN=MYO2A_PE=3_SV=2	5.00E-82	GO:0000166,GO:0003774,GO:0003779,GO:0005524,GO:0005524,GO:0006810,GO:0007049,GO:0008152,GO:0015031,GO:0016459,GO:0016459,GO:0051015	nucleotide binding,motor activity,actin binding,ATP binding,ATP binding,transport,cell cycle,metabolic process,protein transport,myosin complex,myosin complex,actin filament binding
comp32001_c1_seq4.p2	sp|Q9C5V6|TOP6B_ARATH_DNA_topoisomerase_6_subunit_B_OS=Arabidopsis_thaliana_GN=TOP6B_PE=1_SV=1	0	GO:0000166,GO:0000278,GO:0000902,GO:0003002,GO:0003677,GO:0003677,GO:0003677,GO:0003916,GO:0003918,GO:0003918,GO:0003918,GO:0003918,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006200,GO:0006200,GO:0006200,GO:0006200,GO:0006265,GO:0006265,GO:0006355,GO:0006396,GO:0007155,GO:0007389,GO:0009330,GO:0009330,GO:0009741,GO:0010026,GO:0010090,GO:0016853,GO:0033043,GO:0042023,GO:0042802,GO:0043687,GO:0045010,GO:0045893,GO:0048449	nucleotide binding,mitotic cell cycle,cell morphogenesis,regionalization,DNA binding,DNA binding,DNA binding,DNA topoisomerase activity,DNA topoisomerase type II (ATP-hydrolyzing) activity,DNA topoisomerase type II (ATP-hydrolyzing) activity,DNA topoisomerase type II (ATP-hydrolyzing) activity,DNA topoisomerase type II (ATP-hydrolyzing) activity,protein binding,protein binding,protein binding,ATP binding,ATP binding,ATP binding,nucleus,nucleus,nucleus,ATP catabolic process,ATP catabolic process,ATP catabolic process,ATP catabolic process,DNA topological change,DNA topological change,regulation of transcription, DNA-templated,RNA processing,cell adhesion,pattern specification process,DNA topoisomerase complex (ATP-hydrolyzing),DNA topoisomerase complex (ATP-hydrolyzing),response to brassinosteroid,trichome differentiation,trichome morphogenesis,isomerase activity,regulation of organelle organization,DNA endoreduplication,identical protein binding,post-translational protein modification,actin nucleation,positive regulation of transcription, DNA-templated,floral organ formation
comp32002_c0_seq1.p2	sp|P11759|ALGD_PSEAE_GDP-mannose_6-dehydrogenase_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=algD_PE=1_SV=2	7.00E-16	GO:0016491,GO:0016616,GO:0042121,GO:0042121,GO:0042121,GO:0042121,GO:0047919,GO:0047919,GO:0047919,GO:0051287,GO:0051287,GO:0055114,GO:0055114	oxidoreductase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,alginic acid biosynthetic process,alginic acid biosynthetic process,alginic acid biosynthetic process,alginic acid biosynthetic process,GDP-mannose 6-dehydrogenase activity,GDP-mannose 6-dehydrogenase activity,GDP-mannose 6-dehydrogenase activity,NAD binding,NAD binding,oxidation-reduction process,oxidation-reduction process
comp32002_c0_seq2.p2	sp|P11759|ALGD_PSEAE_GDP-mannose_6-dehydrogenase_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=algD_PE=1_SV=2	7.00E-16	GO:0016491,GO:0016616,GO:0042121,GO:0042121,GO:0042121,GO:0042121,GO:0047919,GO:0047919,GO:0047919,GO:0051287,GO:0051287,GO:0055114,GO:0055114	oxidoreductase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,alginic acid biosynthetic process,alginic acid biosynthetic process,alginic acid biosynthetic process,alginic acid biosynthetic process,GDP-mannose 6-dehydrogenase activity,GDP-mannose 6-dehydrogenase activity,GDP-mannose 6-dehydrogenase activity,NAD binding,NAD binding,oxidation-reduction process,oxidation-reduction process
comp32002_c0_seq6.p1	sp|O05973|UDG_RICPR_UDP-glucose_6-dehydrogenase_OS=Rickettsia_prowazekii_(strain_Madrid_E)_GN=udg_PE=3_SV=1	4.00E-17	GO:0000271,GO:0003979,GO:0003979,GO:0006065,GO:0016491,GO:0016616,GO:0051287,GO:0055114,GO:0055114	polysaccharide biosynthetic process,UDP-glucose 6-dehydrogenase activity,UDP-glucose 6-dehydrogenase activity,UDP-glucuronate biosynthetic process,oxidoreductase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp32003_c0_seq16.p1				
comp32004_c0_seq1.p1	sp|P22699|GUN6_DICDI_Endoglucanase_OS=Dictyostelium_discoideum_GN=celA_PE=2_SV=1	6.00E-12	GO:0000272,GO:0003824,GO:0004553,GO:0005975,GO:0005975,GO:0008152,GO:0008810,GO:0016787,GO:0016798,GO:0030245,GO:0030435	polysaccharide catabolic process,catalytic activity,hydrolase activity, hydrolyzing O-glycosyl compounds,carbohydrate metabolic process,carbohydrate metabolic process,metabolic process,cellulase activity,hydrolase activity,hydrolase activity, acting on glycosyl bonds,cellulose catabolic process,sporulation resulting in formation of a cellular spore
comp32004_c0_seq2.p1				
comp32005_c0_seq2.p1				
comp32005_c0_seq3.p1	sp|Q9ZS88|DER22_ARATH_Derlin-2.2_OS=Arabidopsis_thaliana_GN=DER2.2_PE=2_SV=1	4.00E-64	GO:0005783,GO:0005789,GO:0016020,GO:0016021	endoplasmic reticulum,endoplasmic reticulum membrane,membrane,integral component of membrane
comp32006_c1_seq1.p1				
comp32006_c1_seq13.p1				
comp32006_c1_seq14.p2	sp|Q94C12|NDBAB_ARATH_NADH_dehydrogenase_[ubiquinone]_1_beta_subcomplex_subunit_10-B_OS=Arabidopsis_thaliana_GN=At3g18410_PE=2_SV=1	1.00E-11	GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005747,GO:0005747,GO:0009853,GO:0016020,GO:0031966,GO:0045271,GO:0055114,GO:0070469	mitochondrion,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial respiratory chain complex I,mitochondrial respiratory chain complex I,photorespiration,membrane,mitochondrial membrane,respiratory chain complex I,oxidation-reduction process,respiratory chain
comp32006_c1_seq9.p1				
comp32008_c0_seq2.p1	sp|Q5RG45|CP135_DANRE_Centrosomal_protein_of_135_kDa_OS=Danio_rerio_GN=cep135_PE=2_SV=2	5.00E-19	GO:0005737,GO:0005814,GO:0005856,GO:0007099,GO:0010457	cytoplasm,centriole,cytoskeleton,centriole replication,centriole-centriole cohesion
comp32009_c0_seq2.p1				
comp32009_c0_seq4.p1				
comp32010_c0_seq11.p1				
comp32010_c0_seq12.p1				
comp32010_c0_seq12.p3				
comp32010_c0_seq13.p1				
comp32010_c0_seq14.p1				
comp32010_c0_seq14.p2				
comp32010_c0_seq14.p4				
comp32010_c0_seq3.p1				
comp32010_c0_seq6.p1				
comp32010_c0_seq7.p1				
comp32010_c0_seq7.p2				
comp32012_c0_seq2.p1				
comp32012_c0_seq3.p1				
comp32013_c0_seq1.p1				
comp32014_c0_seq10.p1				
comp32014_c0_seq10.p2				
comp32014_c0_seq14.p1				
comp32014_c0_seq2.p1				
comp32014_c0_seq3.p1				
comp32014_c0_seq4.p1				
comp32014_c0_seq7.p1				
comp32014_c0_seq9.p1				

comp32082_c1_seq8.p1				
comp32082_c1_seq9.p1				
comp32082_c4_seq3.p1				
comp32083_c0_seq10.p1	sp|O66534|RIBD_AQUAE_Riboflavin_biosynthesis_protein_RibD_OS=Aquifex_aeolicus_(strain_VF5)_GN=ribD_PE=3_SV=1	9.00E-14	GO:0003824,GO:0003824,GO:0008152,GO:0008270,GO:0008703,GO:0008703,GO:0008835,GO:0008835,GO:0009231,GO:0009231,GO:0009231,GO:0016491,GO:0016787,GO:0016787,GO:0046872,GO:0050661,GO:0055114,GO:0055114	[illegible]
comp32083_c0_seq4.p1	sp|O66534|RIBD_AQUAE_Riboflavin_biosynthesis_protein_RibD_OS=Aquifex_aeolicus_(strain_VF5)_GN=ribD_PE=3_SV=1	7.00E-20	GO:0003824,GO:0003824,GO:0008152,GO:0008270,GO:0008703,GO:0008703,GO:0008835,GO:0008835,GO:0009231,GO:0009231,GO:0009231,GO:0016491,GO:0016787,GO:0016787,GO:0046872,GO:0050661,GO:0055114,GO:0055114	[illegible]
comp32083_c0_seq6.p1	sp|Q9QZA2|PDC6I_RAT_Programmed_cell_death_6-interacting_protein_OS=Rattus_norvegicus_GN=Pdcd6ip_PE=1_SV=2	1.00E-50	GO:0001772,GO:0005737,GO:0005737,GO:0005737,GO:0005815,GO:0005829,GO:0005829,GO:0005856,GO:0006810,GO:0006915,GO:0007049,GO:0015031,GO:0016020,GO:0017124,GO:0042470,GO:0042803,GO:0046983,GO:0048306,GO:0051301,GO:0070062	[illegible]
comp32083_c0_seq6.p2	sp|O66534|RIBD_AQUAE_Riboflavin_biosynthesis_protein_RibD_OS=Aquifex_aeolicus_(strain_VF5)_GN=ribD_PE=3_SV=1	1.00E-19	GO:0003824,GO:0003824,GO:0008152,GO:0008270,GO:0008703,GO:0008703,GO:0008835,GO:0008835,GO:0009231,GO:0009231,GO:0009231,GO:0016491,GO:0016787,GO:0016787,GO:0046872,GO:0050661,GO:0055114,GO:0055114	[illegible]
comp32085_c0_seq2.p1	sp|P37039|NCPR_CAVPO_NADPH--cytochrome_P450_reductase_OS=Cavia_porcellus_GN=POR_PE=2_SV=2	3.00E-136	GO:0003958,GO:0003958,GO:0005506,GO:0005783,GO:0005789,GO:0010181,GO:0016020,GO:0016491,GO:0016491,GO:0055114,GO:0055114	[illegible]
comp32085_c0_seq3.p1	sp|Q9SB48|ATR1_ARATH_NADPH--cytochrome_P450_reductase_1_OS=Arabidopsis_thaliana_GN=ATR1_PE=1_SV=1	3.00E-116	GO:0003958,GO:0003958,GO:0003958,GO:0005506,GO:0005783,GO:0005783,GO:0005789,GO:0005829,GO:0006888,GO:0006979,GO:0009698,GO:0009698,GO:0009737,GO:0010181,GO:0016020,GO:0016491,GO:0016491,GO:0055114,GO:0055114	[illegible]
comp32086_c0_seq1.p1				
comp32086_c0_seq11.p2				
comp32086_c0_seq15.p2				
comp32086_c0_seq17.p2				
comp32086_c0_seq5.p1				
comp32086_c0_seq6.p2				
comp32086_c0_seq7.p1				
comp32087_c0_seq6.p1				
comp32088_c1_seq11.p1				
comp32088_c1_seq17.p1				
comp32088_c1_seq21.p1				
comp32088_c1_seq21.p2				
comp32088_c1_seq22.p1				
comp32088_c1_seq4.p1				
comp32088_c1_seq6.p1				
comp32089_c0_seq10.p1	sp|Q9NW15|ANO10_HUMAN_Anoctamin-10_OS=Homo_sapiens_GN=ANO10_PE=1_SV=2	6.00E-43	GO:0005227,GO:0005229,GO:0005622,GO:0005622,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006812,GO:0006821,GO:0016020,GO:0016020,GO:0016021,GO:0034220,GO:0055085,GO:0098655,GO:1902476,GO:0005229	[illegible]
comp32089_c0_seq12.p1	sp|Q9NW15|ANO10_HUMAN_Anoctamin-10_OS=Homo_sapiens_GN=ANO10_PE=1_SV=2	6.00E-43	GO:0005227,GO:0005229,GO:0005622,GO:0005622,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006812,GO:0006821,GO:0016020,GO:0016020,GO:0016021,GO:0034220,GO:0055085,GO:0098655,GO:1902476,GO:0005229	[illegible]
comp32089_c0_seq2.p1				
comp32089_c0_seq2.p2				
comp32089_c0_seq3.p1				
comp32090_c1_seq1.p1				
comp32090_c1_seq1.p3				
comp32090_c1_seq11.p1	sp|Q8DJ32|LEU1_THEEB_2-isopropylmalate_synthase_OS=Thermosynechococcus_elongatus_(strain_BP-1)_GN=leuA_PE=3_SV=1	0	GO:0003824,GO:0003852,GO:0003852,GO:0003852,GO:0008652,GO:0009082,GO:0009098,GO:0009098,GO:0009098,GO:0009098,GO:0016740,GO:0019752,GO:0046912	[illegible]
comp32090_c1_seq14.p1				
comp32090_c1_seq16.p2	sp|Q9C550|LEU12_ARATH_2-isopropylmalate_synthase_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=IPMS2_PE=1_SV=1	5.00E-29	GO:0003824,GO:0003852,GO:0003852,GO:0003852,GO:0003852,GO:0003852,GO:0008652,GO:0009082,GO:0009098,GO:0009098,GO:0009098,GO:0009098,GO:0009098,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009941,GO:0016740,GO:0016829,GO:0019752,GO:0046912	[illegible]
comp32090_c1_seq20.p1				
comp32090_c1_seq23.p1				
comp32090_c1_seq27.p2	sp|Q9C550|LEU12_ARATH_2-isopropylmalate_synthase_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=IPMS2_PE=1_SV=1	2.00E-20	GO:0003824,GO:0003852,GO:0003852,GO:0003852,GO:0003852,GO:0003852,GO:0008652,GO:0009082,GO:0009098,GO:0009098,GO:0009098,GO:0009098,GO:0009098,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009941,GO:0016740,GO:0016829,GO:0019752,GO:0046912	[illegible]
comp32090_c1_seq28.p1				
comp32090_c1_seq29.p1				
comp32090_c1_seq31.p1				
comp32090_c1_seq38.p1				
comp32090_c1_seq5.p1				
comp32091_c0_seq10.p1	sp|Q7PZD5|K0664_ANOGA_Protein_KIAA0664_homolog_OS=Anopheles_gambiae_GN=AGAP011851_PE=3_SV=4	4.00E-20	GO:0005737,GO:0005737,GO:0005737,GO:0007005,GO:0048312	[illegible]
comp32091_c0_seq8.p1	sp|O15818|K0664_DICDI_Protein_KIAA0664_homolog_OS=Dictyostelium_discoideum_GN=cluA_PE=1_SV=2	1.00E-13	GO:0000266,GO:0000281,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0007005,GO:0008053,GO:0048312,GO:0048312	[illegible]
comp32092_c0_seq1.p1				
comp32092_c0_seq3.p1				
comp32092_c0_seq3.p2				
comp32092_c0_seq4.p1				
comp32092_c0_seq4.p2				
comp32092_c0_seq5.p1				
comp32093_c0_seq3.p1				
comp32093_c0_seq3.p2				
comp32094_c0_seq2.p1				
comp32095_c0_seq1.p1				
comp32095_c0_seq1.p2				
comp32095_c0_seq1.p4				
comp32095_c0_seq4.p1				
comp32095_c0_seq4.p4				
comp32096_c0_seq7.p1				
comp32096_c0_seq8.p1				
comp32097_c0_seq3.p1	sp|Q8RWS8|PP199_ARATH_Pentatricopeptide_repeat-containing_protein_At2g41720_OS=Arabidopsis_thaliana_GN=EMB2654_PE=2_SV=1	1.00E-33		
comp32097_c0_seq5.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	3.00E-25		
comp32097_c0_seq7.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	9.00E-25		
comp32097_c0_seq7.p2	sp|Q9SR00|PP213_ARATH_Pentatricopeptide_repeat-containing_protein_At3g04760,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g04760_PE=2_SV=1	5.00E-11	[illegible]	[illegible]
comp32098_c0_seq1.p1	sp|Q9V730|EXT1_DROME_Exostosin-1_OS=Drosophila_melanogaster_GN=ttv_PE=1_SV=1	2.00E-18	[illegible]	[illegible]
comp32098_c0_seq2.p1	sp|Q9V730|EXT1_DROME_Exostosin-1_OS=Drosophila_melanogaster_GN=ttv_PE=1_SV=1	1.00E-18	[illegible]	[illegible]
comp32100_c0_seq1.p1				
comp32101_c0_seq1.p1				
comp32101_c0_seq2.p1				
comp32101_c0_seq3.p1				
comp32101_c1_seq1.p1				
comp32101_c1_seq5.p1	sp|Q03131|ERYA1_SACER_Erythronolide_synthase,_modules_1_and_2_OS=Saccharopolyspora_erythraea_GN=eryA_PE=1_SV=1	5.00E-117	[illegible]	[illegible]
comp32101_c2_seq1.p1				
comp32102_c0_seq1.p1				
comp32102_c0_seq2.p1	sp|Q9C0J8|WDR33_HUMAN_pre-mRNA_3'_end_processing_protein_WDR33_OS=Homo_sapiens_GN=WDR33_PE=1_SV=2	4.00E-17	[illegible]	[illegible]
comp32102_c0_seq5.p1				
comp32103_c0_seq1.p1				
comp32103_c0_seq12.p1	sp|Q9FJI5|G6PD6_ARATH_Glucose-6-phosphate_1-dehydrogenase,_cytoplasmic_isoform_2_OS=Arabidopsis_thaliana_GN=ACG12_PE=1_SV=1	2.00E-169	[illegible]	[illegible]
comp32103_c0_seq12.p3				
comp32103_c0_seq16.p1				
comp32103_c0_seq17.p1				
comp32103_c0_seq18.p1				
comp32103_c0_seq20.p1				
comp32103_c0_seq21.p1	sp|A0JM23|NPHP3_XENTR_Nephrocystin-3_OS=Xenopus_tropicalis_GN=nphp3_PE=2_SV=2	9.00E-22	[illegible]	[illegible]
comp32103_c0_seq21.p2				
comp32103_c0_seq23.p1	sp|P66006|STHA_MYCTU_Probable_soluble_pyridine_nucleotide_transhydrogenase_OS=Mycobacterium_tuberculosis_GN=sthA_PE=3_SV=1	1.00E-82		
comp32103_c0_seq23.p3	sp|Q53FV1|ORML2_HUMAN_ORM1-like_protein_2_OS=Homo_sapiens_GN=ORMDL2_PE=2_SV=2	9.00E-19	[illegible]	[illegible]
comp32103_c0_seq25.p1				
comp32103_c0_seq28.p1				
comp32103_c0_seq29.p1				
comp32103_c0_seq29.p6				
comp32103_c0_seq30.p1				
comp32103_c0_seq39.p1	sp|P66006|STHA_MYCTU_Probable_soluble_pyridine_nucleotide_transhydrogenase_OS=Mycobacterium_tuberculosis_GN=sthA_PE=3_SV=1	3.00E-56		
comp32103_c0_seq39.p2	sp|P66006|STHA_MYCTU_Probable_soluble_pyridine_nucleotide_transhydrogenase_OS=Mycobacterium_tuberculosis_GN=sthA_PE=3_SV=1	1.00E-30		
comp32103_c0_seq39.p3	sp|Q53FV1|ORML2_HUMAN_ORM1-like_protein_2_OS=Homo_sapiens_GN=ORMDL2_PE=2_SV=2	1.00E-22	[illegible]	[illegible]
comp32103_c0_seq40.p1	sp|A0JM23|NPHP3_XENTR_Nephrocystin-3_OS=Xenopus_tropicalis_GN=nphp3_PE=2_SV=2	9.00E-22	[illegible]	[illegible]
comp32103_c0_seq40.p2				
comp32105_c0_seq2.p1				
comp32105_c1_seq1.p1	sp|Q40863|EMB8_PICGL_Embryogenesis-associated_protein_EMB8_OS=Picea_glauca_GN=EMB8_PE=2_SV=1	4.00E-17	[illegible]	[illegible]
comp32105_c1_seq11.p1	sp|Q91ZH7|ABHD3_MOUSE_Abhydrolase_domain-containing_protein_3_OS=Mus_musculus_GN=Abhd3_PE=2_SV=1	6.00E-49	[illegible]	[illegible]
comp32105_c1_seq6.p1	sp|Q91ZH7|ABHD3_MOUSE_Abhydrolase_domain-containing_protein_3_OS=Mus_musculus_GN=Abhd3_PE=2_SV=1	1.00E-50	[illegible]	[illegible]
comp32106_c0_seq11.p1	sp|Q9JJ66|CDC20_MOUSE_Cell_division_cycle_protein_20_homolog_OS=Mus_musculus_GN=Cdc20_PE=1_SV=2	9.00E-91	[illegible]	[illegible]
comp32106_c0_seq11.p3				
comp32106_c0_seq13.p1	sp|Q9JJ66|CDC20_MOUSE_Cell_division_cycle_protein_20_homolog_OS=Mus_musculus_GN=Cdc20_PE=1_SV=2	9.00E-91	[illegible]	[illegible]
comp32106_c0_seq4.p1				
comp32106_c0_seq4.p2	sp|Q9JJ66|CDC20_MOUSE_Cell_division_cycle_protein_20_homolog_OS=Mus_musculus_GN=Cdc20_PE=1_SV=2	9.00E-91	[illegible]	[illegible]
comp32106_c0_seq6.p1				
comp32106_c0_seq7.p1				
comp32106_c0_seq7.p2	sp|Q9JJ66|CDC20_MOUSE_Cell_division_cycle_protein_20_homolog_OS=Mus_musculus_GN=Cdc20_PE=1_SV=2	9.00E-91	[illegible]	[illegible]
comp32106_c0_seq8.p2				
comp32106_c0_seq9.p1				
comp32107_c0_seq10.p1	sp|Q5BKI6|ANKR1_XENTR_Ankyrin_repeat_domain-containing_protein_1_OS=Xenopus_tropicalis_GN=ankrd1_PE=2_SV=1	2.00E-15	[illegible]	[illegible]
comp32107_c0_seq10.p2				
comp32107_c0_seq4.p1	sp|Q5BKI6|ANKR1_XENTR_Ankyrin_repeat_domain-containing_protein_1_OS=Xenopus_tropicalis_GN=ankrd1_PE=2_SV=1	2.00E-15	[illegible]	[illegible]
comp32107_c0_seq8.p1	sp|Q5BKI6|ANKR1_XENTR_Ankyrin_repeat_domain-containing_protein_1_OS=Xenopus_tropicalis_GN=ankrd1_PE=2_SV=1	2.00E-15	[illegible]	[illegible]
comp32108_c0_seq1.p1				
comp32109_c0_seq10.p1				
comp32109_c0_seq3.p1				
comp32109_c0_seq6.p1				
comp32110_c0_seq12.p1				
comp32110_c0_seq13.p1				
comp32110_c0_seq16.p1	sp|Q9EPU4|CPSF1_MOUSE_Cleavage_and_polyadenylation_specificity_factor_subunit_1_OS=Mus_musculus_GN=Cpsf1_PE=1_SV=1	5.00E-19	[illegible]	[illegible]
comp32110_c0_seq20.p1	sp|O15439|MRP4_HUMAN_Multidrug_resistance-associated_protein_4_OS=Homo_sapiens_GN=ABCC4_PE=1_SV=3	5.00E-12	[illegible]	[illegible]
comp32110_c0_seq3.p1				
comp32110_c0_seq4.p1	sp|Q7XWP1|CPSF1_ORYSJ_Probable_cleavage_and_polyadenylation_specificity_factor_subunit_1_OS=Oryza_sativa_subsp._japonica_GN=Os04g0252200_PE=3_SV=2	9.00E-40	[illegible]	[illegible]
comp32110_c0_seq5.p1				
comp32110_c0_seq8.p1	sp|Q8VI47|MRP2_MOUSE_Canalicular_multispecific_organic_anion_transporter_1_OS=Mus_musculus_GN=Abcc2_PE=2_SV=2	5.00E-178	[illegible]	[illegible]
comp32110_c0_seq9.p1				
comp32111_c0_seq1.p1	sp|O75533|SF3B1_HUMAN_Splicing_factor_3B_subunit_1_OS=Homo_sapiens_GN=SF3B1_PE=1_SV=3	0	[illegible]	[illegible]
comp32111_c0_seq2.p1	sp|O75533|SF3B1_HUMAN_Splicing_factor_3B_subunit_1_OS=Homo_sapiens_GN=SF3B1_PE=1_SV=3	1.00E-157	[illegible]	[illegible]
comp32111_c0_seq2.p3				
comp32111_c1_seq1.p2				
comp32112_c1_seq4.p1				
comp32112_c1_seq5.p1				
comp32112_c1_seq6.p1				
comp32113_c0_seq17.p1				
comp32113_c0_seq17.p2				
comp32113_c0_seq17.p3				
comp32113_c0_seq4.p1				
comp32113_c0_seq4.p2				
comp32113_c0_seq4.p3				
comp32115_c0_seq2.p1				
comp32115_c0_seq2.p2	sp|Q09328|MGT5A_HUMAN_Alpha-1,6-mannosylglycoprotein_6-beta-N-acetylglucosaminyltransferase_A_OS=Homo_sapiens_GN=MGAT5_PE=1_SV=1	2.00E-19	[illegible]	[illegible]
comp32116_c0_seq10.p1	sp|Q6QNL9|KC1_EIMTE_Casein_kinase_I_OS=Eimeria_tenella_PE=2_SV=1	2.00E-74	[illegible]	[illegible]
comp32116_c0_seq13.p1				
comp32116_c0_seq13.p5				
comp32116_c0_seq2.p1				
comp32116_c0_seq9.p1				
comp32117_c0_seq4.p1	sp|Q9N0W2|FUT8_BOVIN_Alpha-(1,6)-fucosyltransferase_OS=Bos_taurus_GN=FUT8_PE=2_SV=1	1.00E-16	[illegible]	[illegible]
comp32117_c0_seq5.p1	sp|Q5NVB3|FUT8_PONAB_Alpha-(1,6)-fucosyltransferase_OS=Pongo_abelii_GN=FUT8_PE=2_SV=1	7.00E-11	[illegible]	[illegible]
comp32118_c0_seq12.p1				
comp32118_c0_seq19.p1				
comp32119_c0_seq11.p1	sp|A1DP85|NM111_NEOFI_Pro-apoptotic_serine_protease_nma111_OS=Neosartorya_fischeri_(strain_ATCC_1020_/_DSM_3700_/_FGSC_A1164_/_NRRL_181)_GN=nma111_PE=3_SV=2	3.00E-131	[illegible]	[illegible]
comp32119_c0_seq12.p2				
comp32119_c0_seq2.p3				
comp32119_c0_seq23.p3				
comp32119_c0_seq24.p1				
comp32119_c0_seq25.p1				
comp32119_c0_seq26.p1				
comp32119_c0_seq28.p1				
comp32119_c0_seq30.p1				
comp32119_c0_seq31.p1				
comp32119_c0_seq34.p1				
comp32119_c0_seq38.p4				
comp32119_c0_seq6.p3				
comp32119_c0_seq9.p1	sp|A1DP85|NM111_NEOFI_Pro-apoptotic_serine_protease_nma111_OS=Neosartorya_fischeri_(strain_ATCC_1020_/_DSM_3700_/_FGSC_A1164_/_NRRL_181)_GN=nma111_PE=3_SV=2	1.00E-129	[illegible]	[illegible]
comp32121_c1_seq13.p2				
comp32121_c1_seq14.p1				
comp32121_c1_seq5.p1				
comp32122_c0_seq2.p1				
comp32124_c0_seq2.p1				
comp32124_c0_seq4.p1				
comp32124_c1_seq1.p1				
comp32124_c1_seq2.p1				
comp32124_c1_seq4.p1				
comp32124_c1_seq4.p2	sp|Q8VEA8|RAB7B_MOUSE_Ras-related_protein_Rab-7b_OS=Mus_musculus_GN=Rab7b_PE=1_SV=1	6.00E-14	[illegible]	[illegible]
comp32124_c1_seq4.p4				
comp32124_c1_seq5.p1	sp|Q8VEA8|RAB7B_MOUSE_Ras-related_protein_Rab-7b_OS=Mus_musculus_GN=Rab7b_PE=1_SV=1	4.00E-13	[illegible]	[illegible]
comp32124_c1_seq5.p2				
comp32124_c2_seq13.p1	sp|Q9WVQ5|MTNB_MOUSE_Probable_methylthioribulose-1-phosphate_dehydratase_OS=Mus_musculus_GN=Apip_PE=1_SV=1	1.00E-66	[illegible]	[illegible]
comp32124_c2_seq9.p1	sp|Q8VZG8|Y4885_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At4g08850_OS=Arabidopsis_thaliana_GN=At4g08850_PE=1_SV=3	4.00E-27	[illegible]	[illegible]
comp32124_c3_seq1.p1				
comp32124_c3_seq2.p1				
comp32124_c4_seq1.p1				
comp32124_c4_seq2.p1				
comp32124_c4_seq2.p2				
comp32124_c5_seq2.p1				
comp32125_c0_seq1.p1	sp|Q9DBH0|WWP2_MOUSE_NEDD4-like_E3_ubiquitin-protein_ligase_WWP2_OS=Mus_musculus_GN=Wwp2_PE=1_SV=1	3.00E-19	[illegible]	[illegible]
comp32125_c0_seq10.p1				
comp32125_c0_seq10.p2	sp|Q8BZZ3|WWP1_MOUSE_NEDD4-like_E3_ubiquitin-protein_ligase_WWP1_OS=Mus_musculus_GN=Wwp1_PE=1_SV=2	6.00E-22	[illegible]	[illegible]
comp32125_c0_seq11.p1				
comp32125_c0_seq11.p2	sp|Q8BZZ3|WWP1_MOUSE_NEDD4-like_E3_ubiquitin-protein_ligase_WWP1_OS=Mus_musculus_GN=Wwp1_PE=1_SV=2	2.00E-23	[illegible]	[illegible]
comp32125_c0_seq12.p1	sp|Q8BZZ3|WWP1_MOUSE_NEDD4-like_E3_ubiquitin-protein_ligase_WWP1_OS=Mus_musculus_GN=Wwp1_PE=1_SV=2	6.00E-23	[illegible]	[illegible]
comp32125_c0_seq13.p1				
comp32125_c0_seq2.p1	sp|Q8BZZ3|WWP1_MOUSE_NEDD4-like_E3_ubiquitin-protein_ligase_WWP1_OS=Mus_musculus_GN=Wwp1_PE=1_SV=2	7.00E-23	[illegible]	[illegible]
comp32125_c0_seq3.p1				
comp32125_c0_seq4.p1				
comp32125_c0_seq7.p1				
comp32125_c0_seq7.p2				
comp32125_c0_seq9.p1				
comp32126_c0_seq1.p1	sp|O00625|PIR_HUMAN_Pirin_OS=Homo_sapiens_GN=PIR_PE=1_SV=1	2.00E-108	[illegible]	[illegible]
comp32127_c0_seq10.p1	sp|O60658|PDE8A_HUMAN_High_affinity_cAMP-specific_and_IBMX-insensitive_3',5'-cyclic_phosphodiesterase_8A_OS=Homo_sapiens_GN=PDE8A_PE=1_SV=2	3.00E-28	[illegible]	[illegible]
comp32127_c0_seq10.p2				
comp32127_c0_seq10.p3				
comp32127_c0_seq10.p6				
comp32127_c0_seq12.p1				
comp32127_c0_seq12.p2	sp|Q8IRU4|PDE4E_DROME_cAMP-specific_3',5'-cyclic_phosphodiesterase,_isoform_F_OS=Drosophila_melanogaster_GN=dnc_PE=2_SV=1	3.00E-11	[illegible]	[illegible]
comp32127_c0_seq21.p1				
comp32127_c0_seq21.p2				
comp32127_c0_seq21.p5				
comp32127_c0_seq21.p6				
comp32127_c0_seq24.p1	sp|O60658|PDE8A_HUMAN_High_affinity_cAMP-specific_and_IBMX-insensitive_3',5'-cyclic_phosphodiesterase_8A_OS=Homo_sapiens_GN=PDE8A_PE=1_SV=2	3.00E-27	[illegible]	[illegible]
comp32127_c0_seq24.p2				
comp32127_c0_seq24.p5				
comp32127_c0_seq39.p1				
comp32127_c0_seq39.p2				
comp32127_c0_seq39.p5				
comp32127_c0_seq39.p6				
comp32127_c0_seq39.p7				
comp32127_c0_seq44.p1				
comp32127_c0_seq44.p2	sp|Q8IRU4|PDE4E_DROME_cAMP-specific_3',5'-cyclic_phosphodiesterase,_isoform_F_OS=Drosophila_melanogaster_GN=dnc_PE=2_SV=1	3.00E-11	[illegible]	[illegible]
comp32127_c0_seq44.p4				
comp32127_c0_seq5.p1	sp|O76083|PDE9A_HUMAN_High_affinity_cGMP-specific_3',5'-cyclic_phosphodiesterase_9A_OS=Homo_sapiens_GN=PDE9A_PE=1_SV=1	5.00E-20	[illegible]	[illegible]
comp32127_c0_seq58.p1	sp|O60658|PDE8A_HUMAN_High_affinity_cAMP-specific_and_IBMX-insensitive_3',5'-cyclic_phosphodiesterase_8A_OS=Homo_sapiens_GN=PDE8A_PE=1_SV=2	4.00E-27	[illegible]	[illegible]
comp32127_c0_seq59.p1				
comp32127_c0_seq63.p1	sp|O60658|PDE8A_HUMAN_High_affinity_cAMP-specific_and_IBMX-insensitive_3',5'-cyclic_phosphodiesterase_8A_OS=Homo_sapiens_GN=PDE8A_PE=1_SV=2	1.00E-27	[illegible]	[illegible]
comp32127_c0_seq63.p2				
comp32129_c0_seq4.p1				
comp32130_c0_seq5.p1	sp|Q9SFB8|PI5K6_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_6_OS=Arabidopsis_thaliana_GN=PIP5K6_PE=2_SV=1	2.00E-33	[illegible]	[illegible]
comp32130_c0_seq8.p1	sp|Q9SLG9|PI5K5_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_5_OS=Arabidopsis_thaliana_GN=PIP5K5_PE=2_SV=1	3.00E-30	[illegible]	[illegible]
comp32131_c0_seq5.p1	sp|P0CD62|LIMKB_DICDI_Probable_LIM_domain-containing_serine/threonine-protein_kinase_DDB_G0286997_OS=Dictyostelium_discoideum_GN=DDB_G0286997_PE=3_SV=1	1.00E-25	[illegible]	[illegible]
comp32133_c0_seq1.p1				
comp32133_c0_seq3.p1				
comp32133_c0_seq6.p1	sp|Q7ZWS2|5N3LA_XENLA_Cytosolic_5'-nucleotidase_III-like_protein_A_OS=Xenopus_laevis_GN=nt5c3l-a_PE=2_SV=2	5.00E-15	[illegible]	[illegible]
comp32133_c1_seq1.p1				
comp32133_c2_seq11.p1	sp|Q60B13|DAPA_METCA_Dihydrodipicolinate_synthase_OS=Methylococcus_capsulatus_(strain_ATCC_33009_/_NCIMB_11132_/_Bath)_GN=dapA_PE=3_SV=1	3.00E-83	[illegible]	[illegible]
comp32133_c2_seq14.p1				
comp32133_c2_seq16.p1	sp|Q54VF4|Y8236_DICDI_TPR-containing_protein_DDB_G0280363_OS=Dictyostelium_discoideum_GN=DDB_G0280363_PE=4_SV=2	5.00E-85	[illegible]	[illegible]
comp32133_c2_seq18.p1				
comp32133_c2_seq20.p2				
comp32133_c2_seq4.p2				
comp32133_c2_seq6.p1	sp|Q9Y4W2|LAS1L_HUMAN_Ribosomal_biogenesis_protein_LAS1L_OS=Homo_sapiens_GN=LAS1L_PE=1_SV=2	7.00E-21	[illegible]	[illegible]
comp32133_c2_seq7.p1	sp|Q5UR67|YR617_MIMIV_Uncharacterized_protein_R617_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R617_PE=4_SV=1	5.00E-21		
comp32135_c1_seq13.p1				
comp32135_c1_seq16.p1				
comp32135_c1_seq19.p1				
comp32135_c1_seq3.p1	sp|Q86AQ7|VAM7B_DICDI_Vesicle-associated_membrane_protein_7B_OS=Dictyostelium_discoideum_GN=vamp7B_PE=3_SV=1	1.00E-62	[illegible]	[illegible]
comp32135_c1_seq8.p1	sp|P20054|PYR1_DICDI_Protein_PYR1-3_OS=Dictyostelium_discoideum_GN=pyr1-3_PE=1_SV=3	7.00E-84	[illegible]	[illegible]
comp32135_c1_seq8.p2	sp|Q93VG8|U326_ARATH_UPF0326_protein_At4g17486_OS=Arabidopsis_thaliana_GN=At4g17486_PE=2_SV=1	6.00E-28	[illegible]	[illegible]
comp32137_c0_seq10.p1				
comp32137_c0_seq17.p3				
comp32137_c0_seq22.p1				
comp32137_c0_seq26.p2				
comp32137_c0_seq26.p3				
comp32137_c0_seq3.p1				
comp32137_c0_seq3.p3				
comp32137_c0_seq32.p1				
comp32137_c0_seq4.p1				
comp32137_c0_seq6.p1				
comp32138_c1_seq12.p1				
comp32138_c1_seq14.p1	sp|P46437|GST_MUSDO_Glutathione_S-transferase_OS=Musca_domestica_PE=2_SV=1	7.00E-23	[illegible]	[illegible]
comp32138_c1_seq18.p1	sp|Q54Y76|MAF1_DICDI_Repressor_of_RNA_polymerase_III_transcription_OS=Dictyostelium_discoideum_GN=maf1_PE=3_SV=1	3.00E-39	[illegible]	[illegible]
comp32138_c1_seq19.p1				
comp32138_c1_seq20.p1	sp|Q54Y76|MAF1_DICDI_Repressor_of_RNA_polymerase_III_transcription_OS=Dictyostelium_discoideum_GN=maf1_PE=3_SV=1	3.00E-39	[illegible]	[illegible]
comp32138_c1_seq22.p1	sp|Q54Y76|MAF1_DICDI_Repressor_of_RNA_polymerase_III_transcription_OS=Dictyostelium_discoideum_GN=maf1_PE=3_SV=1	1.00E-22	[illegible]	[illegible]
comp32138_c1_seq25.p1				
comp32138_c1_seq26.p2				
comp32138_c1_seq28.p1				
comp32138_c1_seq3.p1	sp|Q54Y76|MAF1_DICDI_Repressor_of_RNA_polymerase_III_transcription_OS=Dictyostelium_discoideum_GN=maf1_PE=3_SV=1	5.00E-22	[illegible]	[illegible]
comp32138_c1_seq5.p1	sp|P46428|GST_ANOGA_Glutathione_S-transferase_OS=Anopheles_gambiae_GN=GstS1_PE=2_SV=4	6.00E-11	[illegible]	[illegible]
comp32138_c1_seq9.p1				
comp32138_c1_seq9.p2				
comp32139_c0_seq2.p1	sp|Q8IXZ2|ZC3H3_HUMAN_Zinc_finger_CCCH_domain-containing_protein_3_OS=Homo_sapiens_GN=ZC3H3_PE=1_SV=3	7.00E-28	[illegible]	[illegible]
comp32139_c0_seq2.p5				
comp32139_c0_seq6.p1	sp|Q8IXZ2|ZC3H3_HUMAN_Zinc_finger_CCCH_domain-containing_protein_3_OS=Homo_sapiens_GN=ZC3H3_PE=1_SV=3	9.00E-28	[illegible]	[illegible]
comp32139_c0_seq7.p1	sp|P37631|YHIN_ECOLI_Uncharacterized_protein_yhiN_OS=Escherichia_coli_(strain_K12)_GN=yhiN_PE=4_SV=3	2.00E-14	GO:0055114	[illegible]
comp32140_c0_seq10.p1	sp|Q54CS7|JMJCE_DICDI_JmjC_domain-containing_protein_E_OS=Dictyostelium_discoideum_GN=jcdE_PE=4_SV=2	4.00E-17	[illegible]	[illegible]
comp32140_c0_seq13.p1	sp|P84675|PFM_CHAGB_Putative_fungistatic_metabolite_OS=Chaetomium_globosum_(strain_ATCC_6205_/_CBS_148.51_/_DSM_1962_/_NBRC_6347_/_NRRL_1970)_GN=CHGG_05463_PE=1_SV=2	2.00E-15	[illegible]	[illegible]
comp32140_c0_seq5.p1	sp|P84675|PFM_CHAGB_Putative_fungistatic_metabolite_OS=Chaetomium_globosum_(strain_ATCC_6205_/_CBS_148.51_/_DSM_1962_/_NBRC_6347_/_NRRL_1970)_GN=CHGG_05463_PE=1_SV=2	1.00E-15	[illegible]	[illegible]
comp32140_c0_seq5.p2				
comp32140_c0_seq9.p1				
comp32141_c0_seq2.p1				
comp32141_c0_seq2.p2				
comp32141_c0_seq5.p1				
comp32144_c0_seq1.p1	sp|O05118|KPYK_METEA_Pyruvate_kinase_OS=Methylobacterium_extorquens_(strain_ATCC_14718_/_DSM_1338_/_AM1)_GN=pyk_PE=3_SV=2	1.00E-140	[illegible]	[illegible]
comp32144_c0_seq2.p1	sp|O05118|KPYK_METEA_Pyruvate_kinase_OS=Methylobacterium_extorquens_(strain_ATCC_14718_/_DSM_1338_/_AM1)_GN=pyk_PE=3_SV=2	1.00E-125	[illegible]	[illegible]
comp32144_c0_seq4.p1	sp|O05118|KPYK_METEA_Pyruvate_kinase_OS=Methylobacterium_extorquens_(strain_ATCC_14718_/_DSM_1338_/_AM1)_GN=pyk_PE=3_SV=2	1.00E-125	[illegible]	[illegible]
comp32144_c0_seq5.p1	sp|O05118|KPYK_METEA_Pyruvate_kinase_OS=Methylobacterium_extorquens_(strain_ATCC_14718_/_DSM_1338_/_AM1)_GN=pyk_PE=3_SV=2	1.00E-140	[illegible]	[illegible]
comp32145_c0_seq2.p1				
comp32145_c1_seq1.p1				
comp32145_c1_seq3.p1				
comp32145_c1_seq4.p1				
comp32145_c2_seq1.p1				
comp32145_c2_seq10.p1				
comp32145_c2_seq13.p1				
comp32145_c2_seq16.p1	sp|Q31QG5|RPOD3_SYNE7_RNA_polymerase_sigma_factor_rpoD3_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=rpoD3_PE=3_SV=1	4.00E-35	[illegible]	[illegible]
comp32145_c2_seq16.p2	sp|Q8H1U5|APC2_ARATH_Anaphase-promoting_complex_subunit_2_OS=Arabidopsis_thaliana_GN=APC2_PE=1_SV=1	1.00E-105	[illegible]	[illegible]
comp32145_c2_seq2.p1	sp|Q8H1U5|APC2_ARATH_Anaphase-promoting_complex_subunit_2_OS=Arabidopsis_thaliana_GN=APC2_PE=1_SV=1	1.00E-105	[illegible]	[illegible]
comp32145_c2_seq2.p2	sp|Q59996|RPSC_SYNY3_Probable_RNA_polymerase_sigma-C_factor_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sigC_PE=3_SV=1	9.00E-27	[illegible]	[illegible]
comp32145_c2_seq8.p1				
comp32145_c2_seq9.p1	sp|Q5UQX5|YR883_MIMIV_Uncharacterized_protein_R883_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R883_PE=4_SV=1	2.00E-17		
comp32145_c3_seq4.p1				
comp32145_c3_seq5.p1				
comp32145_c3_seq6.p1				
comp32145_c3_seq7.p1				
comp32145_c3_seq8.p1				
comp32145_c3_seq8.p2				
comp32145_c4_seq1.p1				
comp32145_c4_seq2.p1				
comp32145_c4_seq3.p1	sp|Q5R652|RAD17_PONAB_Cell_cycle_checkpoint_protein_RAD17_OS=Pongo_abelii_GN=RAD17_PE=2_SV=1	6.00E-11	[illegible]	[illegible]
comp32145_c4_seq5.p2				
comp32145_c4_seq5.p3				
comp32145_c4_seq6.p2				
comp32145_c5_seq1.p2				
comp32145_c5_seq1.p4				
comp32145_c6_seq2.p1	sp|Q6DEH3|KC2D1_DANRE_Calcium/calmodulin-dependent_protein_kinase_type_II_delta_1_chain_OS=Danio_rerio_GN=camk2d1_PE=2_SV=2	2.00E-88	[illegible]	[illegible]
comp32145_c7_seq1.p1				
comp32146_c0_seq1.p1				
comp32147_c1_seq3.p1				
comp32147_c1_seq4.p1				
comp32148_c0_seq1.p1				
comp32148_c0_seq2.p1				
comp32148_c0_seq3.p1				
comp32148_c0_seq4.p1				
comp32149_c0_seq2.p1				
comp32150_c0_seq1.p1				
comp32151_c0_seq4.p1				
comp32152_c0_seq4.p1				
comp32152_c0_seq6.p1				
comp32153_c0_seq1.p1	sp|P08133|ANXA6_HUMAN_Annexin_A6_OS=Homo_sapiens_GN=ANXA6_PE=1_SV=3	5.00E-15	[illegible]	[illegible]
comp32153_c0_seq3.p1	sp|P48037|ANXA6_RAT_Annexin_A6_OS=Rattus_norvegicus_GN=Anxa6_PE=1_SV=2	5.00E-63	[illegible]	[illegible]

comp32154_c0_seq14.p1	sp|Q9LYZ9|PP362_ARATH_Pentatricopeptide_repeat-containing_protein_At5g02860_OS=Arabidopsis_thaliana_GN=At5g02860_PE=2_SV=1	2.00E-36
comp32154_c0_seq14.p2		
comp32154_c0_seq4.p1	sp|Q7TSH8|K0195_MOUSE_Uncharacterized_protein_KIAA0195_OS=Mus_musculus_GN=Kiaa0195_PE=1_SV=1	6.00E-35
comp32154_c0_seq5.p1	sp|Q7TSH8|K0195_MOUSE_Uncharacterized_protein_KIAA0195_OS=Mus_musculus_GN=Kiaa0195_PE=1_SV=1	2.00E-13
comp32154_c0_seq5.p2	sp|Q7TSH8|K0195_MOUSE_Uncharacterized_protein_KIAA0195_OS=Mus_musculus_GN=Kiaa0195_PE=1_SV=1	8.00E-34
comp32156_c0_seq8.p1		
comp32157_c0_seq13.p2		
comp32157_c0_seq15.p1	sp|Q755C4|IPL1_ASHGO_Spindle_assembly_checkpoint_kinase_OS=Ashbya_gossypii_(strain_ATCC_10895_/_CBS_109.51_/_FGSC_9923_/_NRRL_Y-1056)_GN=IPL1_PE=3_SV=1	3.00E-27
comp32157_c0_seq16.p1	sp|P10242|MYB_HUMAN_Transcriptional_activator_Myb_OS=Homo_sapiens_GN=MYB_PE=1_SV=2	2.00E-43
comp32157_c0_seq18.p1	sp|Q9C5X9|HAC1_ARATH_Histone_acetyltransferase_HAC1_OS=Arabidopsis_thaliana_GN=HAC1_PE=1_SV=2	3.00E-95
comp32157_c0_seq19.p1		
comp32157_c0_seq2.p1		
comp32157_c0_seq20.p1	sp|Q9C5X9|HAC1_ARATH_Histone_acetyltransferase_HAC1_OS=Arabidopsis_thaliana_GN=HAC1_PE=1_SV=2	4.00E-36
comp32157_c0_seq5.p1	sp|Q7Z401|MYCPP_HUMAN_C-myc_promoter-binding_protein_OS=Homo_sapiens_GN=DENND4A_PE=1_SV=2	2.00E-37
comp32158_c0_seq1.p1		
comp32158_c1_seq15.p2		
comp32158_c1_seq23.p1	sp|Q6K9G1|AMT12_ORYSJ_Ammonium_transporter_1_member_2_OS=Oryza_sativa_subsp._japonica_GN=AMT1-2_PE=2_SV=1	1.00E-77
comp32158_c1_seq26.p1		
comp32158_c1_seq28.p1		
comp32159_c0_seq2.p1		
comp32159_c0_seq3.p1		
comp32160_c0_seq1.p1	sp|Q39491|PTP3_CHLMO_Dual_specificity_protein_phosphatase_OS=Chlamydomonas_moewusii_GN=VH-PTP13_PE=1_SV=1	6.00E-19
comp32160_c0_seq10.p1		
comp32160_c0_seq10.p4		
comp32160_c0_seq14.p1		
comp32160_c0_seq14.p10		
comp32160_c0_seq14.p3	sp|Q9VH90|TRBID_DROME_Ubiquitin_thioesterase_trabid_OS=Drosophila_melanogaster_GN=trbd_PE=1_SV=1	4.00E-11
comp32160_c0_seq14.p5		
comp32160_c0_seq18.p1	sp|Q9US41|URG1_SCHPO_Uracil-regulated_protein_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=urg1_PE=2_SV=1	2.00E-155
comp32160_c0_seq8.p1	sp|Q39491|PTP3_CHLMO_Dual_specificity_protein_phosphatase_OS=Chlamydomonas_moewusii_GN=VH-PTP13_PE=1_SV=1	6.00E-19
comp32160_c0_seq9.p1		
comp32160_c0_seq9.p10		
comp32160_c0_seq9.p3	sp|Q9VH90|TRBID_DROME_Ubiquitin_thioesterase_trabid_OS=Drosophila_melanogaster_GN=trbd_PE=1_SV=1	4.00E-11
comp32160_c0_seq9.p5		
comp32161_c0_seq5.p1		
comp32163_c1_seq3.p1	sp|Q54I71|AARA_DICDI_Protein_aardvark_OS=Dictyostelium_discoideum_GN=aarA_PE=2_SV=1	5.00E-19
comp32164_c0_seq1.p2		
comp32164_c0_seq2.p1		
comp32164_c0_seq3.p1		
comp32164_c0_seq4.p1		
comp32165_c0_seq1.p1		
comp32165_c0_seq10.p1		
comp32165_c1_seq1.p1	sp|Q54F05|DHX8_DICDI_ATP-dependent_RNA_helicase_dhx8_OS=Dictyostelium_discoideum_GN=dhx8_PE=3_SV=1	7.00E-99
comp32165_c1_seq1.p2		
comp32165_c1_seq10.p1		
comp32165_c1_seq2.p1		
comp32165_c1_seq2.p2		
comp32165_c1_seq3.p1		
comp32165_c1_seq5.p1		
comp32165_c1_seq7.p1		
comp32165_c1_seq8.p1		
comp32167_c0_seq1.p1		
comp32167_c0_seq11.p1		
comp32167_c0_seq18.p1		
comp32167_c0_seq19.p1		
comp32167_c0_seq20.p1		
comp32167_c0_seq21.p1	sp|Q84K71|MATE2_ARATH_MATE_efflux_family_protein_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=DTX44_PE=2_SV=1	7.00E-46
comp32167_c0_seq23.p1		
comp32167_c0_seq26.p1	sp|Q8BK63|KC1A_MOUSE_Casein_kinase_I_isoform_alpha_OS=Mus_musculus_GN=Csnk1a1_PE=2_SV=2	2.00E-103
comp32167_c0_seq28.p2		
comp32167_c0_seq3.p1	sp|Q6AYU3|DNJB6_RAT_DnaJ_homolog_subfamily_B_member_6_OS=Rattus_norvegicus_GN=Dnajb6_PE=1_SV=1	3.00E-25
comp32167_c0_seq32.p1		
comp32167_c0_seq32.p2		
comp32167_c0_seq4.p1	sp|P40235|HHP1_SCHPO_Casein_kinase_I_homolog_hhp1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=hhp1_PE=2_SV=1	4.00E-35
comp32167_c0_seq5.p1	sp|Q84K71|MATE2_ARATH_MATE_efflux_family_protein_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=DTX44_PE=2_SV=1	2.00E-42
comp32167_c1_seq2.p1	sp|P57709|AT2C1_BOVIN_Calcium-transporting_ATPase_type_2C_member_1_OS=Bos_taurus_GN=ATP2C1_PE=2_SV=1	0
comp32167_c1_seq2.p5	sp|O43108|ATC1_YARLI_Calcium-transporting_ATPase_1_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=PMR1_PE=3_SV=1	2.00E-21
comp32167_c1_seq3.p1	sp|P57709|AT2C1_BOVIN_Calcium-transporting_ATPase_type_2C_member_1_OS=Bos_taurus_GN=ATP2C1_PE=2_SV=1	0
comp32167_c1_seq5.p1	sp|P57709|AT2C1_BOVIN_Calcium-transporting_ATPase_type_2C_member_1_OS=Bos_taurus_GN=ATP2C1_PE=2_SV=1	0
comp32167_c1_seq7.p1	sp|P57709|AT2C1_BOVIN_Calcium-transporting_ATPase_type_2C_member_1_OS=Bos_taurus_GN=ATP2C1_PE=2_SV=1	0
comp32167_c1_seq7.p4	sp|O43108|ATC1_YARLI_Calcium-transporting_ATPase_1_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=PMR1_PE=3_SV=1	3.00E-21
comp32167_c2_seq1.p1		
comp32167_c3_seq4.p1		
comp32167_c4_seq1.p1	sp|Q96DH6|MSI2H_HUMAN_RNA-binding_protein_Musashi_homolog_2_OS=Homo_sapiens_GN=MSI2_PE=1_SV=1	6.00E-47
comp32167_c4_seq3.p1	sp|Q96DH6|MSI2H_HUMAN_RNA-binding_protein_Musashi_homolog_2_OS=Homo_sapiens_GN=MSI2_PE=1_SV=1	2.00E-46
comp32168_c0_seq5.p1	sp|Q17770|PDI2_CAEEL_Protein_disulfide-isomerase_2_OS=Caenorhabditis_elegans_GN=pdi-2_PE=1_SV=1	7.00E-105
comp32168_c0_seq6.p1	sp|Q942L2|PDI22_ORYSJ_Protein_disulfide_isomerase-like_2-2_OS=Oryza_sativa_subsp._japonica_GN=PDIL2-2_PE=2_SV=1	2.00E-92
comp32169_c0_seq11.p1		
comp32169_c0_seq4.p1		
comp32169_c0_seq5.p1		
comp32169_c0_seq5.p2		
comp32169_c0_seq6.p1		
comp32170_c0_seq3.p1		
comp32171_c0_seq1.p1	sp|Q96KV7|WDR90_HUMAN_WD_repeat-containing_protein_90_OS=Homo_sapiens_GN=WDR90_PE=1_SV=2	2.00E-52
comp32172_c0_seq12.p1	sp|Q09666|AHNK_HUMAN_Neuroblast_differentiation-associated_protein_AHNAK_OS=Homo_sapiens_GN=AHNAK_PE=1_SV=2	3.00E-32
comp32172_c0_seq16.p2		
comp32172_c0_seq17.p1		
comp32172_c0_seq18.p1		
comp32172_c0_seq20.p1		
comp32172_c0_seq21.p1		
comp32172_c0_seq7.p1		
comp32172_c0_seq8.p1		
comp32173_c0_seq10.p1		
comp32173_c0_seq13.p1		
comp32174_c0_seq1.p1		
comp32174_c0_seq2.p1		
comp32174_c0_seq8.p1		
comp32175_c0_seq16.p1		
comp32175_c0_seq2.p1		
comp32175_c0_seq20.p1	sp|Q5M7N9|ESYT3_XENTR_Extended_synaptotagmin-3_OS=Xenopus_tropicalis_GN=esyt3_PE=2_SV=1	1.00E-36
comp32175_c0_seq23.p2		
comp32175_c0_seq27.p1		
comp32175_c0_seq5.p1	sp|Q5M7N9|ESYT3_XENTR_Extended_synaptotagmin-3_OS=Xenopus_tropicalis_GN=esyt3_PE=2_SV=1	1.00E-36
comp32175_c0_seq8.p1		
comp32176_c0_seq1.p1		
comp32176_c1_seq13.p1		
comp32176_c1_seq25.p1		
comp32176_c1_seq4.p1	sp|O27390|DCDA_METTH_Diaminopimelate_decarboxylase_OS=Methanothermobacter_thermautotrophicus_(strain_ATCC_29096_/_DSM_1053_/_JCM_10044_/_NBRC_100330_/_Delta_H)_GN=lysA_PE=3_SV=1	2.00E-25
comp32176_c1_seq6.p1		
comp32177_c0_seq1.p1	sp|Q5ZKJ0|CLP1L_CHICK_Cleft_lip_and_palate_transmembrane_protein_1-like_protein_OS=Gallus_gallus_GN=CLPTM1L_PE=2_SV=1	2.00E-81
comp32177_c2_seq1.p1	sp|Q00955|ACAC_YEAST_Acetyl-CoA_carboxylase_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=ACC1_PE=1_SV=2	0
comp32177_c3_seq1.p1		
comp32177_c4_seq1.p1	sp|Q922K7|NOP2_MOUSE_Putative_ribosomal_RNA_methyltransferase_NOP2_OS=Mus_musculus_GN=Nop2_PE=2_SV=1	2.00E-107
comp32177_c4_seq2.p1	sp|O94268|NOP2_SCHPO_Putative_ribosomal_RNA_methyltransferase_nop2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBP8B7.20c_PE=1_SV=1	2.00E-69
comp32177_c4_seq5.p1	sp|O94268|NOP2_SCHPO_Putative_ribosomal_RNA_methyltransferase_nop2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBP8B7.20c_PE=1_SV=1	2.00E-69
comp32177_c4_seq5.p2		
comp32177_c4_seq6.p2		
comp32177_c4_seq6.p3		
comp32177_c4_seq7.p1	sp|Q922K7|NOP2_MOUSE_Putative_ribosomal_RNA_methyltransferase_NOP2_OS=Mus_musculus_GN=Nop2_PE=2_SV=1	7.00E-141
comp32177_c5_seq1.p1		
comp32177_c6_seq1.p1	sp|Q9SZ52|PP344_ARATH_Pentatricopeptide_repeat-containing_protein_At4g31850,_chloroplastic_OS=Arabidopsis_thaliana_GN=PGR3_PE=1_SV=1	6.00E-13
comp32177_c6_seq2.p1	sp|Q9S7Q2|PP124_ARATH_Pentatricopeptide_repeat-containing_protein_At1g74850,_chloroplastic_OS=Arabidopsis_thaliana_GN=PTAC2_PE=2_SV=1	2.00E-41
comp32177_c6_seq3.p1	sp|P73627|Y1770_SYNY3_Uncharacterized_protein_sll1770_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll1770_PE=3_SV=1	1.00E-111
comp32177_c6_seq5.p1		
comp32178_c0_seq5.p1	sp|Q54KM6|KAT_DICDI_Kynurenine--oxoglutarate_transaminase_OS=Dictyostelium_discoideum_GN=ccbl_PE=3_SV=1	1.00E-91
comp32178_c0_seq9.p1	sp|Q54KM6|KAT_DICDI_Kynurenine--oxoglutarate_transaminase_OS=Dictyostelium_discoideum_GN=ccbl_PE=3_SV=1	2.00E-37
comp32179_c0_seq2.p1		
comp32180_c0_seq3.p1		
comp32181_c1_seq11.p1		
comp32181_c1_seq6.p1		
comp32181_c1_seq7.p1		
comp32181_c1_seq9.p1		
comp32182_c0_seq1.p1	sp|Q9RL35|NPD1_STRCO_NAD-dependent_deacetylase_1_OS=Streptomyces_coelicolor_GN=cobB1_PE=3_SV=1	2.00E-62
comp32182_c0_seq4.p1	sp|Q89EA6|NPD2_BRAJA_NAD-dependent_deacetylase_2_OS=Bradyrhizobium_japonicum_(strain_USDA_110)_GN=cobB2_PE=3_SV=2	5.00E-63
comp32183_c0_seq1.p1		
comp32184_c0_seq1.p1		
comp32185_c1_seq3.p1		
comp32185_c1_seq4.p1		
comp32185_c1_seq5.p1		
comp32185_c1_seq6.p1		
comp32185_c1_seq7.p1		
comp32186_c0_seq2.p1		
comp32186_c0_seq4.p1	sp|Q2TAW0|CNDG2_XENLA_Condensin-2_complex_subunit_G2_OS=Xenopus_laevis_GN=ncapg2_PE=1_SV=1	3.00E-12
comp32186_c0_seq4.p2	sp|Q86XI2|CNDG2_HUMAN_Condensin-2_complex_subunit_G2_OS=Homo_sapiens_GN=NCAPG2_PE=1_SV=1	3.00E-51
comp32187_c0_seq12.p1		
comp32187_c0_seq12.p2	sp|Q86H36|RPA1_DICDI_DNA-directed_RNA_polymerase_I_subunit_rpa1_OS=Dictyostelium_discoideum_GN=polr1a_PE=3_SV=1	6.00E-32
comp32187_c0_seq12.p3		
comp32187_c0_seq14.p1	sp|P15398|RPA1_SCHPO_DNA-directed_RNA_polymerase_I_subunit_rpa1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpa1_PE=1_SV=2	0
comp32187_c0_seq14.p2	sp|P15398|RPA1_SCHPO_DNA-directed_RNA_polymerase_I_subunit_rpa1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpa1_PE=1_SV=2	1.00E-40
comp32187_c0_seq15.p1	sp|P15398|RPA1_SCHPO_DNA-directed_RNA_polymerase_I_subunit_rpa1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpa1_PE=1_SV=2	0
comp32187_c0_seq15.p2	sp|P15398|RPA1_SCHPO_DNA-directed_RNA_polymerase_I_subunit_rpa1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpa1_PE=1_SV=2	6.00E-42
comp32187_c0_seq15.p3	sp|P15398|RPA1_SCHPO_DNA-directed_RNA_polymerase_I_subunit_rpa1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpa1_PE=1_SV=2	1.00E-40
comp32187_c0_seq2.p1	sp|P15398|RPA1_SCHPO_DNA-directed_RNA_polymerase_I_subunit_rpa1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpa1_PE=1_SV=2	4.00E-44
comp32187_c0_seq24.p1		
comp32187_c0_seq24.p2	sp|Q86H36|RPA1_DICDI_DNA-directed_RNA_polymerase_I_subunit_rpa1_OS=Dictyostelium_discoideum_GN=polr1a_PE=3_SV=1	6.00E-32
comp32187_c0_seq25.p1		
comp32187_c0_seq26.p3		
comp32187_c0_seq30.p1		
comp32187_c0_seq30.p2		
comp32188_c0_seq16.p2		
comp32188_c0_seq18.p1		
comp32188_c0_seq25.p1		
comp32188_c0_seq25.p4		
comp32188_c0_seq34.p1		
comp32188_c0_seq35.p1		
comp32188_c0_seq37.p1		
comp32188_c0_seq37.p4		
comp32189_c0_seq2.p1		
comp32189_c0_seq3.p1		
comp32189_c0_seq6.p4		
comp32190_c0_seq12.p2		
comp32190_c0_seq14.p1		
comp32190_c0_seq16.p2		
comp32190_c0_seq5.p1		
comp32190_c0_seq6.p1		
comp32191_c0_seq1.p1		
comp32191_c0_seq2.p1		
comp32192_c0_seq1.p1	sp|O35409|FOLH1_MOUSE_Glutamate_carboxypeptidase_2_OS=Mus_musculus_GN=Folh1_PE=2_SV=2	5.00E-96
comp32192_c0_seq2.p1		
comp32193_c0_seq1.p1	sp|Q9C6S1|FH14_ARATH_Formin-like_protein_14_OS=Arabidopsis_thaliana_GN=FH14_PE=3_SV=3	7.00E-32
comp32193_c0_seq1.p12		
comp32193_c0_seq2.p1		
comp32193_c0_seq8.p1		
comp32194_c0_seq12.p1	sp|Q96LD8|SENP8_HUMAN_Sentrin-specific_protease_8_OS=Homo_sapiens_GN=SENP8_PE=1_SV=1	5.00E-17
comp32194_c0_seq14.p1	sp|Q96LD8|SENP8_HUMAN_Sentrin-specific_protease_8_OS=Homo_sapiens_GN=SENP8_PE=1_SV=1	1.00E-23
comp32194_c0_seq14.p2		
comp32194_c0_seq25.p1		
comp32195_c0_seq1.p1		
comp32195_c0_seq11.p1		
comp32195_c0_seq2.p1		
comp32195_c0_seq4.p1		
comp32195_c0_seq5.p2		
comp32196_c0_seq17.p1	sp|Q6IAN0|DRS7B_HUMAN_Dehydrogenase/reductase_SDR_family_member_7B_OS=Homo_sapiens_GN=DHRS7B_PE=1_SV=2	1.00E-44
comp32196_c0_seq17.p2		
comp32196_c0_seq21.p1	sp|Q55680|Y005_SYNY3_Uncharacterized_protein_sll0005_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll0005_PE=3_SV=1	1.00E-87
comp32196_c0_seq21.p2	sp|P0AF08|MRP_ECOLI_Protein_mrp_OS=Escherichia_coli_(strain_K12)_GN=mrp_PE=3_SV=1	6.00E-46
comp32196_c0_seq3.p1	sp|P0AF08|MRP_ECOLI_Protein_mrp_OS=Escherichia_coli_(strain_K12)_GN=mrp_PE=3_SV=1	6.00E-46
comp32196_c0_seq3.p2		
comp32196_c0_seq32.p1	sp|Q6IAN0|DRS7B_HUMAN_Dehydrogenase/reductase_SDR_family_member_7B_OS=Homo_sapiens_GN=DHRS7B_PE=1_SV=2	1.00E-44
comp32196_c0_seq32.p2		
comp32196_c0_seq8.p1		
comp32196_c0_seq8.p2		
comp32196_c0_seq9.p1	sp|Q01484|ANK2_HUMAN_Ankyrin-2_OS=Homo_sapiens_GN=ANK2_PE=1_SV=3	1.00E-18
comp32197_c0_seq1.p1		
comp32197_c0_seq4.p1		
comp32198_c0_seq10.p1	sp|Q9LND7|SKI16_ARATH_F-box_protein_SKIP16_OS=Arabidopsis_thaliana_GN=SKIP16_PE=1_SV=1	7.00E-20
comp32198_c0_seq12.p1	sp|Q95QN6|YQOE_CAEEL_Uncharacterized_RING_finger_protein_EEED8.16_OS=Caenorhabditis_elegans_GN=EEED8.16_PE=2_SV=1	8.00E-51
comp32198_c0_seq3.p1	sp|Q9LND7|SKI16_ARATH_F-box_protein_SKIP16_OS=Arabidopsis_thaliana_GN=SKIP16_PE=1_SV=1	1.00E-18
comp32198_c0_seq6.p1	sp|Q9LND7|SKI16_ARATH_F-box_protein_SKIP16_OS=Arabidopsis_thaliana_GN=SKIP16_PE=1_SV=1	1.00E-17
comp32198_c0_seq7.p1	sp|Q9LND7|SKI16_ARATH_F-box_protein_SKIP16_OS=Arabidopsis_thaliana_GN=SKIP16_PE=1_SV=1	1.00E-17
comp32198_c0_seq8.p1	sp|Q9LND7|SKI16_ARATH_F-box_protein_SKIP16_OS=Arabidopsis_thaliana_GN=SKIP16_PE=1_SV=1	7.00E-20
comp32199_c0_seq1.p1		
comp32199_c0_seq1.p2	sp|Q54L00|LIMKA_DICDI_Probable_LIM_domain-containing_serine/threonine-protein_kinase_DDB_G0287001_OS=Dictyostelium_discoideum_GN=DDB_G0287001_PE=3_SV=1	5.00E-13
comp32199_c0_seq1.p5		
comp32199_c0_seq1.p6		
comp32199_c0_seq2.p1		
comp32199_c0_seq3.p1		
comp32199_c0_seq4.p1	sp|Q55GU0|Y9955_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0267514_OS=Dictyostelium_discoideum_GN=DDB_G0267514_PE=3_SV=1	8.00E-28
comp32199_c0_seq6.p1		
comp32199_c1_seq3.p1	sp|Q8SSY6|SPKUL_DICDI_Bifunctional_serine/threonine-protein_kinase/NEDD4-like_E3_ubiquitin-protein_ligase_OS=Dictyostelium_discoideum_GN=DDB_G0276527_PE=3_SV=2	7.00E-25
comp32200_c0_seq1.p1		
comp32200_c0_seq1.p2	sp|O35379|MRP1_MOUSE_Multidrug_resistance-associated_protein_1_OS=Mus_musculus_GN=Abcc1_PE=1_SV=1	4.00E-81
comp32200_c0_seq13.p1		
comp32200_c0_seq13.p2	sp|O35379|MRP1_MOUSE_Multidrug_resistance-associated_protein_1_OS=Mus_musculus_GN=Abcc1_PE=1_SV=1	4.00E-81
comp32200_c0_seq3.p1	sp|Q9C8G9|AB1C_ARATH_ABC_transporter_C_family_member_1_OS=Arabidopsis_thaliana_GN=ABCC1_PE=1_SV=1	4.00E-107
comp32200_c0_seq7.p1		
comp32201_c0_seq2.p1		
comp32203_c1_seq12.p1	sp|A1A5S1|PRP6_RAT_Pre-mRNA-processing_factor_6_OS=Rattus_norvegicus_GN=Prpf6_PE=2_SV=1	0
comp32203_c1_seq13.p1		
comp32203_c1_seq14.p1	sp|Q86A79|CPSF3_DICDI_Cleavage_and_polyadenylation_specificity_factor_subunit_3_OS=Dictyostelium_discoideum_GN=cpsf3_PE=3_SV=1	0
comp32203_c1_seq17.p1		
comp32203_c1_seq2.p1		
comp32203_c1_seq3.p1		
comp32203_c1_seq6.p1		
comp32203_c1_seq8.p1		
comp32203_c1_seq9.p1	sp|Q55DZ8|SYWC_DICDI_Tryptophan--tRNA_ligase,_cytoplasmic_OS=Dictyostelium_discoideum_GN=trpS_PE=3_SV=1	9.00E-155
comp32203_c2_seq2.p1	sp|P25341|KIN82_YEAST_Serine/threonine-protein_kinase_KIN82_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=KIN82_PE=1_SV=3	8.00E-39
comp32203_c2_seq2.p2		
comp32203_c2_seq2.p3	sp|Q9D8Y8|ING5_MOUSE_Inhibitor_of_growth_protein_5_OS=Mus_musculus_GN=Ing5_PE=1_SV=1	2.00E-35
comp32204_c0_seq1.p1		
comp32204_c0_seq3.p1		
comp32206_c0_seq3.p1		
comp32206_c0_seq4.p1		
comp32206_c0_seq7.p1	sp|Q6P298|NUBP1_DANRE_Cytosolic_Fe-S_cluster_assembly_factor_nubp1_OS=Danio_rerio_GN=nubp1_PE=2_SV=2	7.00E-110
comp32206_c0_seq7.p6		
comp32207_c0_seq2.p1	sp|Q8CG45|ARK72_RAT_Aflatoxin_B1_aldehyde_reductase_member_2_OS=Rattus_norvegicus_GN=Akr7a2_PE=1_SV=2	1.00E-86
comp32207_c0_seq3.p1	sp|O95154|ARK73_HUMAN_Aflatoxin_B1_aldehyde_reductase_member_3_OS=Homo_sapiens_GN=AKR7A3_PE=1_SV=2	2.00E-50
comp32208_c3_seq17.p1		
comp32208_c3_seq29.p1		
comp32208_c3_seq3.p1		
comp32208_c3_seq6.p1		
comp32208_c3_seq8.p1		
comp32209_c0_seq1.p1		
comp32209_c0_seq10.p1		
comp32209_c0_seq3.p1		
comp32209_c2_seq2.p1		
comp32209_c2_seq3.p1		
comp32209_c2_seq3.p2		
comp32210_c0_seq1.p1		
comp32211_c0_seq4.p1		
comp32212_c0_seq1.p1		
comp32212_c0_seq2.p1	sp|Q55GU0|Y9955_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0267514_OS=Dictyostelium_discoideum_GN=DDB_G0267514_PE=3_SV=1	3.00E-47
comp32213_c0_seq1.p1		
comp32213_c0_seq2.p1		
comp32213_c0_seq3.p1		
comp32213_c0_seq5.p1		
comp32214_c1_seq11.p1		
comp32214_c1_seq11.p3		
comp32214_c1_seq11.p6		
comp32214_c1_seq13.p1		
comp32214_c1_seq3.p1	sp|Q91365|QN1_COTCO_Protein_quail_neuroretina_1_(Fragment)_OS=Coturnix_coturnix_GN=QN1_PE=1_SV=1	2.00E-12
comp32214_c1_seq3.p2		
comp32214_c1_seq3.p9		
comp32214_c1_seq7.p1	sp|Q91365|QN1_COTCO_Protein_quail_neuroretina_1_(Fragment)_OS=Coturnix_coturnix_GN=QN1_PE=1_SV=1	3.00E-12
comp32215_c0_seq4.p1		
comp32215_c0_seq7.p1		
comp32216_c0_seq10.p1	sp|P14318|MP20_DROME_Muscle-specific_protein_20_OS=Drosophila_melanogaster_GN=Mp20_PE=2_SV=2	1.00E-13
comp32216_c0_seq11.p1		
comp32216_c0_seq3.p1	sp|P14318|MP20_DROME_Muscle-specific_protein_20_OS=Drosophila_melanogaster_GN=Mp20_PE=2_SV=2	2.00E-14
comp32216_c0_seq5.p1	sp|P14318|MP20_DROME_Muscle-specific_protein_20_OS=Drosophila_melanogaster_GN=Mp20_PE=2_SV=2	6.00E-14
comp32216_c0_seq8.p1		
comp32217_c0_seq10.p1		
comp32217_c0_seq13.p1		
comp32217_c0_seq21.p2		
comp32217_c0_seq25.p1		
comp32217_c0_seq29.p2		
comp32217_c0_seq5.p1		
comp32217_c0_seq6.p1		
comp32219_c0_seq1.p1	sp|Q86C65|TOR_DICDI_Target_of_rapamycin_OS=Dictyostelium_discoideum_GN=tor_PE=1_SV=1	1.00E-137
comp32219_c0_seq1.p2	sp|O14053|YC47_SCHPO_Uncharacterized_WD_repeat-containing_protein_C1672.07_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC1672.07_PE=2_SV=1	2.00E-128
comp32219_c0_seq1.p3	sp|Q86C65|TOR_DICDI_Target_of_rapamycin_OS=Dictyostelium_discoideum_GN=tor_PE=1_SV=1	9.00E-146
comp32219_c0_seq20.p1	sp|Q86C65|TOR_DICDI_Target_of_rapamycin_OS=Dictyostelium_discoideum_GN=tor_PE=1_SV=1	1.00E-137
comp32219_c0_seq20.p2	sp|O14053|YC47_SCHPO_Uncharacterized_WD_repeat-containing_protein_C1672.07_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC1672.07_PE=2_SV=1	2.00E-128
comp32219_c0_seq20.p3	sp|Q86C65|TOR_DICDI_Target_of_rapamycin_OS=Dictyostelium_discoideum_GN=tor_PE=1_SV=1	3.00E-146
comp32219_c0_seq21.p1	sp|Q86C65|TOR_DICDI_Target_of_rapamycin_OS=Dictyostelium_discoideum_GN=tor_PE=1_SV=1	0
comp32219_c0_seq21.p2	sp|O14053|YC47_SCHPO_Uncharacterized_WD_repeat-containing_protein_C1672.07_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC1672.07_PE=2_SV=1	2.00E-128
comp32219_c0_seq4.p1	sp|Q86C65|TOR_DICDI_Target_of_rapamycin_OS=Dictyostelium_discoideum_GN=tor_PE=1_SV=1	0
comp32219_c0_seq4.p2	sp|O14053|YC47_SCHPO_Uncharacterized_WD_repeat-containing_protein_C1672.07_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC1672.07_PE=2_SV=1	2.00E-128
comp32219_c0_seq8.p1		
comp3222_c0_seq1.p2	sp|P0ADW3|YHCB_ECOLI_Putative_cytochrome_d_ubiquinol_oxidase_subunit_3_OS=Escherichia_coli_(strain_K12)_GN=yhcB_PE=1_SV=2	2.00E-64
comp32220_c0_seq11.p1		
comp32220_c0_seq12.p1	sp|Q63164|DYH1_RAT_Dynein_heavy_chain_1,_axonemal_OS=Rattus_norvegicus_GN=Dnah1_PE=2_SV=2	3.00E-73
comp32220_c0_seq3.p1		
comp32220_c0_seq3.p4		
comp32221_c1_seq6.p1		
comp32221_c1_seq6.p2		
comp32221_c1_seq7.p1		
comp32224_c0_seq1.p1		
comp32224_c0_seq16.p1		
comp32224_c0_seq18.p1		
comp32224_c0_seq19.p1		
comp32224_c0_seq3.p1		
comp32224_c0_seq8.p1		
comp32224_c0_seq9.p1		
comp32225_c0_seq3.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-14
comp32225_c0_seq4.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	8.00E-24
comp32226_c0_seq11.p1	sp|P70805|ALGG_AZOVI_Poly(beta-D-mannuronate)_C5_epimerase_OS=Azotobacter_vinelandii_GN=algG_PE=2_SV=1	3.00E-16
comp32227_c0_seq1.p1		
comp32227_c0_seq12.p1		
comp32227_c0_seq13.p1		
comp32227_c0_seq16.p1		
comp32227_c0_seq17.p1		
comp32227_c0_seq18.p1		
comp32227_c0_seq19.p1		
comp32227_c0_seq20.p2		
comp32227_c0_seq22.p2		
comp32227_c0_seq23.p2		
comp32227_c0_seq5.p1		
comp32227_c0_seq6.p1		
comp32227_c0_seq7.p1		
comp32228_c0_seq1.p1		
comp32228_c0_seq1.p2		
comp32228_c0_seq2.p1		

comp32228_c0_seq2.p2			
comp3223_c0_seq1.p1	sp|P77539|YDJL_ECOLI_Uncharacterized_zinc-type_alcohol_dehydrogenase-like_protein_YdjL_OS=Escherichia_coli_(strain_K12)_GN=ydjL_PE=3_SV=1	4.00E-71	GO:0008270,GO:0016491,GO:0016491,GO:0046872,GO:0055114,GO:0055114
comp32230_c0_seq1.p1			
comp32230_c0_seq3.p1			
comp32230_c1_seq3.p1	sp|Q5BKM3|CHMP3_XENTR_Charged_multivesicular_body_protein_3_OS=Xenopus_tropicalis_GN=chmp3_PE=2_SV=4	5.00E-35	GO:0005737,GO:0005768,GO:0005768,GO:0005829,GO:0006810,GO:0015031,GO:0015031,GO:0016020,GO:0016020,GO:0031902
comp32230_c1_seq7.p1	sp|Q6NY88|CHMP3_DANRE_Charged_multivesicular_body_protein_3_OS=Danio_rerio_GN=chmp3_PE=2_SV=3	2.00E-21	GO:0003674,GO:0005737,GO:0005768,GO:0005768,GO:0005829,GO:0006810,GO:0015031,GO:0015031,GO:0016020,GO:0016020,GO:0031902
comp32230_c1_seq8.p1	sp|Q6NY88|CHMP3_DANRE_Charged_multivesicular_body_protein_3_OS=Danio_rerio_GN=chmp3_PE=2_SV=3	2.00E-21	GO:0003674,GO:0005737,GO:0005768,GO:0005768,GO:0005829,GO:0006810,GO:0015031,GO:0015031,GO:0016020,GO:0016020,GO:0031902
comp32230_c1_seq9.p1	sp|Q5BKM3|CHMP3_XENTR_Charged_multivesicular_body_protein_3_OS=Xenopus_tropicalis_GN=chmp3_PE=2_SV=4	5.00E-35	GO:0005737,GO:0005768,GO:0005768,GO:0005829,GO:0006810,GO:0015031,GO:0015031,GO:0016020,GO:0016020,GO:0031902
comp32231_c0_seq10.p1	sp|P92935|TLC2_ARATH_ADP,ATP_carrier_protein_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=AATP2_PE=1_SV=2	7.00E-179	GO:0000166,GO:0005471,GO:0005524,GO:0005524,GO:0005737,GO:0006810,GO:0006810,GO:0009507,GO:0009507,GO:0009536,GO:0009536,GO:0009941,GO:0009941,GO:0015866,GO:0015867,GO:0016020,GO:0016021,GO:0016021,GO:0031969
comp32231_c0_seq2.p1			
comp32231_c0_seq20.p1			
comp32231_c0_seq29.p1			
comp32231_c0_seq29.p2			
comp32231_c0_seq5.p1			
comp32231_c0_seq7.p1			
comp32232_c0_seq4.p1			
comp32232_c0_seq7.p1			
comp32232_c0_seq7.p2	sp|Q55GQ6|UPP_DICDI_Uracil_phosphoribosyltransferase_OS=Dictyostelium_discoideum_GN=uprt_PE=3_SV=1	3.00E-55	GO:0000166,GO:0003824,GO:0004845,GO:0004845,GO:0005525,GO:0005575,GO:0008152,GO:0008655,GO:0016740,GO:0016757,GO:0044206,GO:0044351
comp32232_c0_seq7.p3	sp|P48276|YCF36_CYAPA_Uncharacterized_protein_ycf36_OS=Cyanophora_paradoxa_GN=ycf36_PE=3_SV=1	3.00E-20	GO:0009536,GO:0009842,GO:0009842
comp32232_c0_seq7.p8			
comp32232_c0_seq8.p1	sp|P48276|YCF36_CYAPA_Uncharacterized_protein_ycf36_OS=Cyanophora_paradoxa_GN=ycf36_PE=3_SV=1	8.00E-20	GO:0009536,GO:0009842,GO:0009842
comp32232_c0_seq8.p2			
comp32233_c0_seq1.p1			
comp32233_c0_seq2.p1			
comp32233_c0_seq3.p1			
comp32233_c1_seq1.p3	sp|Q8BHG2|CA123_MOUSE_UPF0587_protein_C1orf123_homolog_OS=Mus_musculus_PE=2_SV=1	7.00E-16	GO:0003674,GO:0008150,GO:0070062
comp32233_c1_seq1.p4			
comp32233_c1_seq2.p1			
comp32233_c1_seq2.p3			
comp32234_c0_seq10.p1			
comp32234_c0_seq2.p1	sp|Q96T52|IMP2L_HUMAN_Mitochondrial_inner_membrane_protease_subunit_2_OS=Homo_sapiens_GN=IMMP2L_PE=2_SV=1	7.00E-36	GO:0001541,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0006508,GO:0006508,GO:0006627,GO:0006627,GO:0007283,GO:0008233,GO:0008233,GO:0008236,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016787,GO:0030728,GO:0042720,GO:0042720
comp32235_c1_seq1.p1	sp|Q8CI75|DI3L2_MOUSE_DIS3-like_exonuclease_2_OS=Mus_musculus_GN=Dis3l2_PE=1_SV=1	5.00E-142	GO:0000175,GO:0000175,GO:0000175,GO:0000175,GO:0000175,GO:0000287,GO:0000291,GO:0000291,GO:0000291,GO:0000932,GO:0000932,GO:0000932,GO:0000932,GO:0003723,GO:0004518,GO:0004527,GO:0004540,GO:0004540,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0007049,GO:0007067,GO:0007067,GO:0007067,GO:0008266,GO:0008285,GO:0008285,GO:0010587,GO:0010587,GO:0010587,GO:0016787,GO:0019827,GO:0034427,GO:0046872,GO:0051301,GO:0051306,GO:0051306,GO:0090501,GO:0090503,GO:0090503,GO:0090503,GO:0090503,GO:0090503,GO:0090503,GO:1990074,GO:1990074
comp32235_c1_seq1.p2			
comp32235_c1_seq15.p1	sp|P39588|YWBE_BACSU_Uncharacterized_protein_ywbE_OS=Bacillus_subtilis_GN=ywbE_PE=4_SV=1	2.00E-12	
comp32235_c1_seq21.p1	sp|P54696|MYOH_DICDI_Myosin-H_heavy_chain_OS=Dictyostelium_discoideum_GN=myoH_PE=4_SV=3	2.00E-45	GO:0000166,GO:0003774,GO:0003779,GO:0005516,GO:0005524,GO:0005524,GO:0008152,GO:0016459,GO:0016459
comp32235_c1_seq5.p1	sp|Q8CI75|DI3L2_MOUSE_DIS3-like_exonuclease_2_OS=Mus_musculus_GN=Dis3l2_PE=1_SV=1	5.00E-142	GO:0000175,GO:0000175,GO:0000175,GO:0000175,GO:0000175,GO:0000287,GO:0000291,GO:0000291,GO:0000291,GO:0000932,GO:0000932,GO:0000932,GO:0000932,GO:0003723,GO:0004518,GO:0004527,GO:0004540,GO:0004540,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0007049,GO:0007067,GO:0007067,GO:0007067,GO:0008266,GO:0008285,GO:0008285,GO:0010587,GO:0010587,GO:0010587,GO:0016787,GO:0019827,GO:0034427,GO:0046872,GO:0051301,GO:0051306,GO:0051306,GO:0090501,GO:0090503,GO:0090503,GO:0090503,GO:0090503,GO:0090503,GO:0090503,GO:1990074,GO:1990074
comp32235_c1_seq5.p2			
comp32235_c1_seq6.p1	sp|Q9U1M8|MYOI_DICDI_Myosin-I_heavy_chain_OS=Dictyostelium_discoideum_GN=myoI_PE=1_SV=1	2.00E-120	GO:0000166,GO:0000902,GO:0001891,GO:0003774,GO:0003774,GO:0003779,GO:0003779,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005829,GO:0005856,GO:0006200,GO:0006909,GO:0006909,GO:0008152,GO:0008152,GO:0009847,GO:0016020,GO:0016459,GO:0016459,GO:0016459,GO:0030048,GO:0030175,GO:0030898,GO:0031252,GO:0031252,GO:0031589,GO:0043621,GO:0046847
comp32235_c1_seq8.p1	sp|Q9U1M8|MYOI_DICDI_Myosin-I_heavy_chain_OS=Dictyostelium_discoideum_GN=myoI_PE=1_SV=1	2.00E-129	GO:0000166,GO:0000902,GO:0001891,GO:0003774,GO:0003774,GO:0003779,GO:0003779,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005829,GO:0005856,GO:0006200,GO:0006909,GO:0006909,GO:0008152,GO:0008152,GO:0009847,GO:0016020,GO:0016459,GO:0016459,GO:0016459,GO:0030048,GO:0030175,GO:0030898,GO:0031252,GO:0031252,GO:0031589,GO:0043621,GO:0046847
comp32235_c1_seq9.p1	sp|Q9U1M8|MYOI_DICDI_Myosin-I_heavy_chain_OS=Dictyostelium_discoideum_GN=myoI_PE=1_SV=1	2.00E-120	GO:0000166,GO:0000902,GO:0001891,GO:0003774,GO:0003774,GO:0003779,GO:0003779,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005829,GO:0005856,GO:0006200,GO:0006909,GO:0006909,GO:0008152,GO:0008152,GO:0009847,GO:0016020,GO:0016459,GO:0016459,GO:0016459,GO:0030048,GO:0030175,GO:0030898,GO:0031252,GO:0031252,GO:0031589,GO:0043621,GO:0046847
comp32236_c1_seq1.p1			
comp32236_c1_seq4.p1	sp|O54825|BYST_MOUSE_Bystin_OS=Mus_musculus_GN=Bysl_PE=1_SV=3	6.00E-108	GO:0000462,GO:0001701,GO:0001825,GO:0001829,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0005730,GO:0005730,GO:0005737,GO:0005737,GO:0005737,GO:0007155,GO:0008283,GO:0016020,GO:0042254,GO:0043231,GO:0044822,GO:0045177
comp32236_c1_seq6.p1			
comp32236_c1_seq8.p2			
comp32238_c1_seq1.p1	sp|Q0JC27|NLP2_ORYSJ_Protein_NLP2_OS=Oryza_sativa_subsp._japonica_GN=NLP2_PE=2_SV=2	3.00E-12	GO:0003677,GO:0005634,GO:0005634,GO:0006351,GO:0006355
comp32238_c1_seq11.p1			
comp32238_c1_seq15.p1	sp|Q0JC27|NLP2_ORYSJ_Protein_NLP2_OS=Oryza_sativa_subsp._japonica_GN=NLP2_PE=2_SV=2	7.00E-12	GO:0003677,GO:0005634,GO:0005634,GO:0006351,GO:0006355
comp32238_c1_seq18.p1			
comp32238_c1_seq19.p1	sp|Q0JC27|NLP2_ORYSJ_Protein_NLP2_OS=Oryza_sativa_subsp._japonica_GN=NLP2_PE=2_SV=2	6.00E-12	GO:0003677,GO:0005634,GO:0005634,GO:0006351,GO:0006355
comp32238_c1_seq3.p1			
comp32238_c1_seq4.p1			
comp32238_c1_seq4.p2			
comp32238_c1_seq7.p1			
comp32238_c1_seq8.p1			
comp32238_c1_seq9.p1			
comp32239_c0_seq11.p1	sp|Q6A548|TERT_CANFA_Telomerase_reverse_transcriptase_OS=Canis_familiaris_GN=TERT_PE=2_SV=1	6.00E-17	GO:0000781,GO:0000781,GO:0003677,GO:0003677,GO:0003721,GO:0003964,GO:0003964,GO:0003964,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005694,GO:0005730,GO:0005737,GO:0005737,GO:0006278,GO:0006278,GO:0006278,GO:0006278,GO:0008152,GO:0008152,GO:0016605,GO:0016740,GO:0016779,GO:0030529,GO:0046872
comp32239_c0_seq13.p1	sp|O13339|TERT_SCHPO_Telomerase_reverse_transcriptase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=trt1_PE=1_SV=1	1.00E-15	GO:0000228,GO:0000333,GO:0000723,GO:0000781,GO:0000781,GO:0001309,GO:0003677,GO:0003677,GO:0003721,GO:0003721,GO:0003723,GO:0003964,GO:0003964,GO:0003964,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0007004,GO:0007004,GO:0016740,GO:0016779,GO:0042162,GO:0046872,GO:0070034
comp32239_c0_seq13.p2	sp|Q6A548|TERT_CANFA_Telomerase_reverse_transcriptase_OS=Canis_familiaris_GN=TERT_PE=2_SV=1	8.00E-18	GO:0000781,GO:0000781,GO:0003677,GO:0003677,GO:0003721,GO:0003964,GO:0003964,GO:0003964,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005694,GO:0005730,GO:0005737,GO:0005737,GO:0006278,GO:0006278,GO:0006278,GO:0006278,GO:0008152,GO:0008152,GO:0016605,GO:0016740,GO:0016779,GO:0030529,GO:0046872
comp32239_c0_seq13.p3	sp|P72854|SIR_SYNY3_Sulfite_reductase_[ferredoxin]_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sir_PE=1_SV=1	2.00E-14	GO:0005515,GO:0005515,GO:0016491,GO:0016491,GO:0020037,GO:0046872,GO:0050311,GO:0050311,GO:0051536,GO:0051536,GO:0051539,GO:0051539,GO:0055114,GO:0055114
comp32239_c0_seq17.p1	sp|P72854|SIR_SYNY3_Sulfite_reductase_[ferredoxin]_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sir_PE=1_SV=1	2.00E-14	GO:0005515,GO:0005515,GO:0016491,GO:0016491,GO:0020037,GO:0046872,GO:0050311,GO:0050311,GO:0051536,GO:0051536,GO:0051539,GO:0051539,GO:0055114,GO:0055114
comp32239_c0_seq20.p1	sp|O13339|TERT_SCHPO_Telomerase_reverse_transcriptase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=trt1_PE=1_SV=1	2.00E-15	GO:0000228,GO:0000333,GO:0000723,GO:0000781,GO:0000781,GO:0001309,GO:0003677,GO:0003677,GO:0003721,GO:0003721,GO:0003723,GO:0003964,GO:0003964,GO:0003964,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0007004,GO:0007004,GO:0016740,GO:0016779,GO:0042162,GO:0046872,GO:0070034
comp32239_c0_seq20.p2	sp|Q6A548|TERT_CANFA_Telomerase_reverse_transcriptase_OS=Canis_familiaris_GN=TERT_PE=2_SV=1	8.00E-18	GO:0000781,GO:0000781,GO:0003677,GO:0003677,GO:0003721,GO:0003964,GO:0003964,GO:0003964,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005694,GO:0005730,GO:0005737,GO:0005737,GO:0006278,GO:0006278,GO:0006278,GO:0006278,GO:0008152,GO:0008152,GO:0016605,GO:0016740,GO:0016779,GO:0030529,GO:0046872
comp32239_c0_seq23.p1	sp|P30008|SIR_SYNE7_Sulfite_reductase_[ferredoxin]_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=sir_PE=3_SV=2	0	GO:0016491,GO:0016491,GO:0020037,GO:0046872,GO:0050311,GO:0050311,GO:0051536,GO:0051536,GO:0051539,GO:0051539,GO:0055114,GO:0055114
comp32239_c0_seq9.p1	sp|Q6A548|TERT_CANFA_Telomerase_reverse_transcriptase_OS=Canis_familiaris_GN=TERT_PE=2_SV=1	4.00E-17	GO:0000781,GO:0000781,GO:0003677,GO:0003677,GO:0003721,GO:0003964,GO:0003964,GO:0003964,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005694,GO:0005730,GO:0005737,GO:0005737,GO:0006278,GO:0006278,GO:0006278,GO:0006278,GO:0008152,GO:0008152,GO:0016605,GO:0016740,GO:0016779,GO:0030529,GO:0046872
comp32239_c0_seq9.p2	sp|P72854|SIR_SYNY3_Sulfite_reductase_[ferredoxin]_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sir_PE=1_SV=1	2.00E-14	GO:0005515,GO:0005515,GO:0016491,GO:0016491,GO:0020037,GO:0046872,GO:0050311,GO:0050311,GO:0051536,GO:0051536,GO:0051539,GO:0051539,GO:0055114,GO:0055114
comp32240_c0_seq2.p1			
comp32240_c0_seq4.p1			
comp32240_c1_seq2.p1			
comp32240_c1_seq3.p1			
comp32240_c2_seq2.p1			
comp32241_c0_seq1.p1	sp|Q55E58|PATS1_DICDI_Probable_serine/threonine-protein_kinase_pats1_OS=Dictyostelium_discoideum_GN=pats1_PE=3_SV=1	7.00E-17	GO:0000166,GO:0000281,GO:0004672,GO:0004674,GO:0004674,GO:0004721,GO:0005524,GO:0005524,GO:0005525,GO:0005525,GO:0005622,GO:0006468,GO:0006470,GO:0007264,GO:0016301,GO:0016310,GO:0016311,GO:0016740,GO:0016772,GO:0016791,GO:0035176,GO:0042641
comp32241_c0_seq2.p1			
comp32241_c1_seq1.p1			
comp32242_c0_seq2.p1			
comp32242_c0_seq3.p1			
comp32243_c1_seq2.p1	sp|P46436|GST1_ASCSU_Glutathione_S-transferase_1_OS=Ascaris_suum_GN=GST1_PE=1_SV=3	1.00E-17	GO:0004364,GO:0004364,GO:0005575,GO:0008150,GO:0008152,GO:0008152,GO:0008152,GO:0016740
comp32243_c1_seq3.p1	sp|A8IR43|WDR12_CHLRE_Ribosome_biogenesis_protein_WDR12_homolog_OS=Chlamydomonas_reinhardtii_GN=CHLREDRAFT_128420_PE=3_SV=2	3.00E-71	GO:0000463,GO:0000466,GO:0000478,GO:0001510,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005730,GO:0005730,GO:0005730,GO:0006364,GO:0006606,GO:0006626,GO:0008150,GO:0009506,GO:0030687,GO:0042254,GO:0042254,GO:0042254,GO:0042273,GO:0043021,GO:0051604,GO:0080008
comp32243_c2_seq1.p1	sp|Q7KWX9|EXOS3_DICDI_Putative_exosome_complex_component_rrp40_OS=Dictyostelium_discoideum_GN=exosc3_PE=3_SV=1	7.00E-22	GO:0000176,GO:0000177,GO:0000178,GO:0000178,GO:0000467,GO:0003723,GO:0003723,GO:0003723,GO:0005634,GO:0005634,GO:0005730,GO:0005737,GO:0005737,GO:0006364,GO:0034427,GO:0034475,GO:0043928,GO:0071034,GO:0071035,GO:0071038,GO:0071049,GO:0071051
comp32243_c2_seq10.p1			
comp32243_c2_seq13.p1	sp|Q55DE7|ATX2_DICDI_Ataxin-2_homolog_OS=Dictyostelium_discoideum_GN=atxn2_PE=3_SV=1	1.00E-16	GO:0003674,GO:0005575,GO:0008150
comp32243_c2_seq13.p2	sp|Q7KWX9|EXOS3_DICDI_Putative_exosome_complex_component_rrp40_OS=Dictyostelium_discoideum_GN=exosc3_PE=3_SV=1	6.00E-53	GO:0000176,GO:0000177,GO:0000178,GO:0000178,GO:0000467,GO:0003723,GO:0003723,GO:0003723,GO:0005634,GO:0005634,GO:0005730,GO:0005737,GO:0005737,GO:0006364,GO:0034427,GO:0034475,GO:0043928,GO:0071034,GO:0071035,GO:0071038,GO:0071049,GO:0071051
comp32243_c2_seq14.p1			
comp32243_c2_seq15.p1			
comp32243_c2_seq21.p1			
comp32244_c0_seq4.p1			
comp32244_c0_seq6.p1			
comp32245_c0_seq13.p1	sp|Q9C821|PEK15_ARATH_Proline-rich_receptor-like_protein_kinase_PERK15_OS=Arabidopsis_thaliana_GN=PERK15_PE=1_SV=1	6.00E-37	GO:0000166,GO:0004672,GO:0004674,GO:0005524,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0006468,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0051510
comp32245_c0_seq19.p1			
comp32245_c0_seq2.p1	sp|Q99PE2|ANRA2_MOUSE_Ankyrin_repeat_family_A_protein_2_OS=Mus_musculus_GN=Ankra2_PE=1_SV=1	6.00E-15	GO:0003712,GO:0005515,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0005856,GO:0005856,GO:0006357,GO:0016020,GO:0016020,GO:0016020,GO:0016020,GO:0030169,GO:0042826
comp32245_c0_seq2.p7			
comp32245_c0_seq21.p1	sp|Q9C821|PEK15_ARATH_Proline-rich_receptor-like_protein_kinase_PERK15_OS=Arabidopsis_thaliana_GN=PERK15_PE=1_SV=1	3.00E-36	GO:0000166,GO:0004672,GO:0004674,GO:0005524,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0006468,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0051510
comp32245_c0_seq24.p1			
comp32245_c0_seq27.p1	sp|Q501Z5|GTPB3_DANRE_tRNA_modification_GTPase_GTPBP3,_mitochondrial_OS=Danio_rerio_GN=gtpbp3_PE=2_SV=1	1.00E-104	GO:0000166,GO:0003924,GO:0005525,GO:0005525,GO:0005622,GO:0005739,GO:0005739,GO:0006184,GO:0006400,GO:0008033
comp32245_c0_seq30.p4			
comp32245_c0_seq31.p2			
comp32245_c0_seq32.p1			
comp32245_c0_seq4.p1	sp|Q6NRY2|NOL6_XENLA_Nucleolar_protein_6_OS=Xenopus_laevis_GN=nol6_PE=2_SV=2	6.00E-102	GO:0003723,GO:0005634,GO:0005730
comp32245_c0_seq4.p5			
comp32245_c1_seq1.p1			
comp32246_c0_seq1.p1			
comp32246_c4_seq11.p3			
comp32246_c4_seq15.p1			
comp32246_c4_seq22.p1	sp|Q4P0K0|ATG1_USTMA_Serine/threonine-protein_kinase_ATG1_OS=Ustilago_maydis_(strain_521_/_FGSC_9021)_GN=ATG1_PE=3_SV=1	4.00E-31	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0006468,GO:0006810,GO:0006914,GO:0015031,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0034045
comp32246_c4_seq28.p1	sp|A2QIL5|ATG1_ASPNC_Serine/threonine-protein_kinase_atg1_OS=Aspergillus_niger_(strain_CBS_513.88_/_FGSC_A1513)_GN=atg1_PE=3_SV=1	4.00E-54	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005575,GO:0005737,GO:0005737,GO:0006468,GO:0006810,GO:0006914,GO:0006914,GO:0015031,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0034045,GO:0034599
comp32246_c4_seq30.p1	sp|A2QIL5|ATG1_ASPNC_Serine/threonine-protein_kinase_atg1_OS=Aspergillus_niger_(strain_CBS_513.88_/_FGSC_A1513)_GN=atg1_PE=3_SV=1	4.00E-54	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005575,GO:0005737,GO:0005737,GO:0006468,GO:0006810,GO:0006914,GO:0006914,GO:0015031,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0034045,GO:0034599
comp32247_c0_seq2.p1			
comp32247_c0_seq4.p1			
comp32247_c0_seq5.p1			
comp32247_c0_seq7.p1			
comp32247_c0_seq8.p1			
comp32248_c0_seq1.p1			
comp32248_c1_seq10.p1			
comp32248_c1_seq14.p1			
comp32248_c1_seq4.p1	sp|Q8HXX2|MPI_MACFA_Mannose-6-phosphate_isomerase_OS=Macaca_fascicularis_GN=MPI_PE=2_SV=3	3.00E-81	GO:0004476,GO:0004476,GO:0005737,GO:0005737,GO:0005975,GO:0008270,GO:0009298,GO:0009298,GO:0016853,GO:0046872
comp32248_c1_seq5.p2			
comp32248_c1_seq7.p1			
comp32248_c4_seq1.p1	sp|Q8VDR9|DOCK6_MOUSE_Dedicator_of_cytokinesis_protein_6_OS=Mus_musculus_GN=Dock6_PE=1_SV=4	1.00E-35	GO:0003674,GO:0005085,GO:0005085,GO:0005575,GO:0005737,GO:0005737,GO:0007264,GO:0008150,GO:0043547,GO:0043547,GO:0048471
comp32248_c6_seq2.p1			
comp32248_c7_seq3.p1	sp|Q6T3U4|NPCL1_MOUSE_Niemann-Pick_C1-like_protein_1_OS=Mus_musculus_GN=Npc1l1_PE=2_SV=1	2.00E-17	GO:0005886,GO:0005886,GO:0006629,GO:0007165,GO:0008158,GO:0008202,GO:0008203,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016324,GO:0030301,GO:0042632
comp32250_c0_seq10.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	7.00E-17	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305
comp32250_c0_seq11.p1			
comp32250_c0_seq7.p1			
comp32250_c0_seq8.p2			
comp32250_c0_seq8.p3			
comp32251_c0_seq10.p1			
comp32251_c0_seq11.p1			
comp32251_c0_seq14.p1			
comp32251_c0_seq16.p1			
comp32251_c0_seq4.p1			
comp32251_c0_seq5.p1			
comp32251_c0_seq7.p1			
comp32252_c0_seq3.p1			
comp32252_c0_seq5.p1			
comp32253_c0_seq12.p1			
comp32253_c0_seq13.p1	sp|P74045|COAX_SYNY3_Type_III_pantothenate_kinase_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=coaX_PE=3_SV=1	2.00E-29	GO:0000166,GO:0004594,GO:0004594,GO:0004594,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0015937,GO:0015937,GO:0015937,GO:0016301,GO:0016310,GO:0016740,GO:0043169,GO:0046872
comp32253_c0_seq14.p1	sp|Q3MC63|COAX_ANAVT_Type_III_pantothenate_kinase_OS=Anabaena_variabilis_(strain_ATCC_29413_/_PCC_7937)_GN=coaX_PE=3_SV=1	5.00E-35	GO:0000166,GO:0004594,GO:0004594,GO:0004594,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0015937,GO:0015937,GO:0015937,GO:0016301,GO:0016310,GO:0016740,GO:0043169,GO:0046872
comp32253_c0_seq15.p1			
comp32253_c0_seq16.p1	sp|P74045|COAX_SYNY3_Type_III_pantothenate_kinase_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=coaX_PE=3_SV=1	6.00E-31	GO:0000166,GO:0004594,GO:0004594,GO:0004594,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0015937,GO:0015937,GO:0015937,GO:0016301,GO:0016310,GO:0016740,GO:0043169,GO:0046872
comp32253_c0_seq7.p1	sp|Q3MC63|COAX_ANAVT_Type_III_pantothenate_kinase_OS=Anabaena_variabilis_(strain_ATCC_29413_/_PCC_7937)_GN=coaX_PE=3_SV=1	5.00E-35	GO:0000166,GO:0004594,GO:0004594,GO:0004594,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0015937,GO:0015937,GO:0015937,GO:0016301,GO:0016310,GO:0016740,GO:0043169,GO:0046872
comp32253_c0_seq8.p1			
comp32254_c0_seq2.p2			
comp32255_c0_seq1.p1			
comp32255_c0_seq10.p1			
comp32255_c0_seq11.p1			
comp32256_c0_seq11.p1			
comp32256_c0_seq13.p1			
comp32256_c0_seq15.p1			
comp32256_c0_seq15.p2			
comp32256_c0_seq16.p1			
comp32256_c0_seq16.p2			
comp32256_c0_seq17.p1			
comp32256_c0_seq2.p1	sp|Q09758|YA71_SCHPO_Putative_membrane-bound_O-acyltransferase_C24H6.01c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC24H6.01c_PE=2_SV=4	4.00E-88	GO:0005789,GO:0005829,GO:0005886,GO:0006506,GO:0008374,GO:0015793,GO:0016020,GO:0016020,GO:0016021,GO:0016740,GO:0016746
comp32256_c0_seq21.p1			
comp32256_c0_seq3.p2			
comp32256_c0_seq5.p1			
comp32256_c0_seq7.p1			
comp32257_c0_seq2.p1			
comp32258_c0_seq2.p1			
comp32259_c0_seq1.p1			
comp32260_c0_seq2.p1			
comp32260_c0_seq3.p1			
comp32261_c0_seq2.p1	sp|A2R472|CAF17_ASPNC_Putative_transferase_caf17,_mitochondrial_OS=Aspergillus_niger_(strain_CBS_513.88_/_FGSC_A1513)_GN=caf17_PE=3_SV=1	2.00E-29	GO:0004047,GO:0005737,GO:0005739,GO:0005739,GO:0006546,GO:0016740,GO:0032259
comp32261_c1_seq10.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	1.00E-43	GO:0003674,GO:0005576,GO:0005576,GO:0008150,GO:0070062,GO:0072562
comp32261_c1_seq12.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	3.00E-40	GO:0003674,GO:0005576,GO:0005576,GO:0008150,GO:0070062,GO:0072562
comp32261_c1_seq13.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	7.00E-43	GO:0003674,GO:0005576,GO:0005576,GO:0008150,GO:0070062,GO:0072562
comp32261_c1_seq18.p1	sp|Q8VZG8|Y4885_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At4g08850_OS=Arabidopsis_thaliana_GN=At4g08850_PE=1_SV=3	6.00E-31	GO:0000166,GO:0004672,GO:0004674,GO:0005524,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006468,GO:0006857,GO:0006995,GO:0009506,GO:0009627,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0031347
comp32261_c1_seq2.p1	sp|Q9DBB9|CPN2_MOUSE_Carboxypeptidase_N_subunit_2_OS=Mus_musculus_GN=Cpn2_PE=1_SV=2	2.00E-46	GO:0003674,GO:0005576,GO:0005576,GO:0008150,GO:0070062,GO:0072562
comp32262_c0_seq1.p3			
comp32262_c0_seq3.p1			
comp32262_c0_seq6.p1			
comp32262_c0_seq7.p2			
comp32262_c0_seq8.p1			
comp32263_c1_seq11.p1	sp|Q83WC3|SDMT_APHHA_Sarcosine/dimethylglycine_N-methyltransferase_OS=Aphanothece_halophytica_PE=1_SV=1	5.00E-24	GO:0008152,GO:0008168,GO:0008168,GO:0016740,GO:0019286,GO:0019286,GO:0032259,GO:0032259,GO:0052729,GO:0052729,GO:0052730
comp32263_c1_seq14.p1	sp|Q83WC3|SDMT_APHHA_Sarcosine/dimethylglycine_N-methyltransferase_OS=Aphanothece_halophytica_PE=1_SV=1	5.00E-24	GO:0008152,GO:0008168,GO:0008168,GO:0016740,GO:0019286,GO:0019286,GO:0032259,GO:0032259,GO:0052729,GO:0052729,GO:0052730
comp32263_c1_seq18.p1	sp|Q83WC3|SDMT_APHHA_Sarcosine/dimethylglycine_N-methyltransferase_OS=Aphanothece_halophytica_PE=1_SV=1	4.00E-24	GO:0008152,GO:0008168,GO:0008168,GO:0016740,GO:0019286,GO:0019286,GO:0032259,GO:0032259,GO:0052729,GO:0052729,GO:0052730
comp32263_c1_seq21.p1	sp|Q83WC3|SDMT_APHHA_Sarcosine/dimethylglycine_N-methyltransferase_OS=Aphanothece_halophytica_PE=1_SV=1	5.00E-24	GO:0008152,GO:0008168,GO:0008168,GO:0016740,GO:0019286,GO:0019286,GO:0032259,GO:0032259,GO:0052729,GO:0052729,GO:0052730
comp32263_c1_seq7.p1	sp|Q83WC3|SDMT_APHHA_Sarcosine/dimethylglycine_N-methyltransferase_OS=Aphanothece_halophytica_PE=1_SV=1	2.00E-24	GO:0008152,GO:0008168,GO:0008168,GO:0016740,GO:0019286,GO:0019286,GO:0032259,GO:0032259,GO:0052729,GO:0052729,GO:0052730
comp32263_c1_seq9.p2			
comp32264_c1_seq10.p1			
comp32264_c1_seq10.p2			
comp32264_c1_seq5.p1	sp|Q55FG3|VP13C_DICDI_Putative_vacuolar_protein_sorting-associated_protein_13C_OS=Dictyostelium_discoideum_GN=tipC_PE=3_SV=1	3.00E-11	GO:0003674,GO:0005622,GO:0005794,GO:0005794,GO:0006623,GO:0006810,GO:0015031,GO:0019898,GO:0031154,GO:0045053,GO:0045324
comp32264_c1_seq5.p4	sp|Q07878|VPS13_YEAST_Vacuolar_protein_sorting-associated_protein_13_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=VPS13_PE=1_SV=1	4.00E-19	GO:0003674,GO:0005628,GO:0005794,GO:0005794,GO:0006623,GO:0006810,GO:0015031,GO:0019898,GO:0032120,GO:0045053,GO:0045324,GO:0045324
comp32264_c1_seq7.p1	sp|Q07878|VPS13_YEAST_Vacuolar_protein_sorting-associated_protein_13_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=VPS13_PE=1_SV=1	7.00E-33	GO:0003674,GO:0005628,GO:0005794,GO:0005794,GO:0006623,GO:0006810,GO:0015031,GO:0019898,GO:0032120,GO:0045053,GO:0045324,GO:0045324
comp32264_c1_seq9.p1			
comp32264_c1_seq9.p4			
comp32265_c0_seq1.p1			
comp32265_c1_seq10.p1	sp|Q6GN58|YF1BA_XENLA_Protein_YIF1B-A_OS=Xenopus_laevis_GN=yif1b-a_PE=2_SV=1	4.00E-16	GO:0016020,GO:0016020,GO:0016021
comp32265_c1_seq2.p1	sp|P54777|PEX6_RAT_Peroxisome_assembly_factor_2_OS=Rattus_norvegicus_GN=Pex6_PE=1_SV=1	9.00E-104	GO:0000166,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005777,GO:0005777,GO:0005778,GO:0005778,GO:0005778,GO:0005829,GO:0006200,GO:0006625,GO:0007031,GO:0007031,GO:0007031,GO:0008022,GO:0016020,GO:0016561,GO:0016887,GO:0032403,GO:0042623,GO:0050821
comp32265_c1_seq2.p2	sp|Q6P301|YIF1B_XENTR_Protein_YIF1B_OS=Xenopus_tropicalis_GN=yif1b_PE=2_SV=1	1.00E-25	GO:0016020,GO:0016020,GO:0016021
comp32265_c1_seq2.p6			
comp32265_c1_seq9.p1	sp|Q13608|PEX6_HUMAN_Peroxisome_assembly_factor_2_OS=Homo_sapiens_GN=PEX6_PE=1_SV=2	8.00E-102	GO:0000166,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005777,GO:0005777,GO:0005777,GO:0005778,GO:0005778,GO:0005829,GO:0006200,GO:0006200,GO:0006625,GO:0007031,GO:0007031,GO:0007031,GO:0008022,GO:0016020,GO:0016561,GO:0016887,GO:0032403,GO:0042623,GO:0050821
comp32265_c1_seq9.p2	sp|Q6P301|YIF1B_XENTR_Protein_YIF1B_OS=Xenopus_tropicalis_GN=yif1b_PE=2_SV=1	3.00E-26	GO:0016020,GO:0016020,GO:0016021
comp32266_c0_seq2.p1			
comp32267_c0_seq14.p1			
comp32267_c0_seq2.p1			
comp32268_c0_seq2.p2			
comp32268_c0_seq3.p1			
comp32268_c0_seq5.p1			
comp32269_c3_seq19.p1			
comp32269_c3_seq24.p1	sp|A8WXF6|KCC2D_CAEBR_Calcium/calmodulin-dependent_protein_kinase_type_II_OS=Caenorhabditis_briggsae_GN=unc-43_PE=3_SV=1	9.00E-48	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004683,GO:0004683,GO:0005516,GO:0005516,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0046872
comp32269_c3_seq24.p4			
comp32269_c3_seq9.p1			
comp32269_c3_seq9.p2			
comp32270_c1_seq11.p1	sp|Q86AQ5|RPC1_DICDI_DNA-directed_RNA_polymerase_III_subunit_rpc1_OS=Dictyostelium_discoideum_GN=polr3a_PE=3_SV=1	0	GO:0003677,GO:0003899,GO:0003899,GO:0003899,GO:0003899,GO:0005634,GO:0005634,GO:0005634,GO:0005666,GO:0005666,GO:0006351,GO:0006383,GO:0008270,GO:0016740,GO:0016779,GO:0032549,GO:0044351,GO:0046872,GO:0001056
comp32270_c1_seq12.p1	sp|P24345|KN1_MAIZE_Homeotic_protein_knotted-1_OS=Zea_mays_GN=KN-1_PE=2_SV=1	2.00E-12	GO:0003677,GO:0003677,GO:0003677,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0006355,GO:0043565
comp32270_c1_seq12.p4			
comp32270_c1_seq13.p1	sp|Q86AQ5|RPC1_DICDI_DNA-directed_RNA_polymerase_III_subunit_rpc1_OS=Dictyostelium_discoideum_GN=polr3a_PE=3_SV=1	8.00E-16	GO:0003677,GO:0003899,GO:0003899,GO:0003899,GO:0003899,GO:0005634,GO:0005634,GO:0005634,GO:0005666,GO:0005666,GO:0006351,GO:0006383,GO:0008270,GO:0016740,GO:0016779,GO:0032549,GO:0044351,GO:0046872,GO:0001056
comp32270_c1_seq18.p2			
comp32270_c1_seq20.p1	sp|P24345|KN1_MAIZE_Homeotic_protein_knotted-1_OS=Zea_mays_GN=KN-1_PE=2_SV=1	2.00E-12	GO:0003677,GO:0003677,GO:0003677,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0006355,GO:0043565
comp32271_c0_seq1.p1			
comp32271_c1_seq22.p1			
comp32271_c1_seq26.p1			
comp32271_c1_seq7.p1			
comp32273_c0_seq1.p1	sp|P47990|XDH_CHICK_Xanthine_dehydrogenase/oxidase_OS=Gallus_gallus_GN=XDH_PE=1_SV=1	2.00E-113	GO:0003824,GO:0004854,GO:0004854,GO:0004854,GO:0004855,GO:0004855,GO:0004855,GO:0005506,GO:0005737,GO:0005737,GO:0005777,GO:0005777,GO:0005829,GO:0005829,GO:0006144,GO:0008762,GO:0009055,GO:0009115,GO:0009115,GO:0016491,GO:0016491,GO:0016614,GO:0030151,GO:0034418,GO:0043546,GO:0043546,GO:0043546,GO:0044281,GO:0046872,GO:0046872,GO:0050660,GO:0050660,GO:0051536,GO:0051536,GO:0051537,GO:0051537,GO:0051537,GO:0055086,GO:0055114,GO:0055114
comp32273_c0_seq3.p1	sp|P47990|XDH_CHICK_Xanthine_dehydrogenase/oxidase_OS=Gallus_gallus_GN=XDH_PE=1_SV=1	0	GO:0003824,GO:0004854,GO:0004854,GO:0004854,GO:0004855,GO:0004855,GO:0004855,GO:0005506,GO:0005737,GO:0005737,GO:0005777,GO:0005777,GO:0005829,GO:0005829,GO:0006144,GO:0008762,GO:0009055,GO:0009115,GO:0009115,GO:0016491,GO:0016491,GO:0016614,GO:0030151,GO:0034418,GO:0043546,GO:0043546,GO:0043546,GO:0044281,GO:0046872,GO:0046872,GO:0050660,GO:0050660,GO:0051536,GO:0051536,GO:0051537,GO:0051537,GO:0051537,GO:0055086,GO:0055114,GO:0055114
comp32273_c0_seq7.p1	sp|Q9MYW6|XDH_FELCA_Xanthine_dehydrogenase/oxidase_OS=Felis_catus_GN=XDH_PE=2_SV=3	6.00E-131	GO:0003824,GO:0004854,GO:0004854,GO:0004854,GO:0004855,GO:0004855,GO:0004855,GO:0005506,GO:0005576,GO:0005576,GO:0005737,GO:0005737,GO:0005777,GO:0005777,GO:0008762,GO:0009055,GO:0009115,GO:0009115,GO:0016491,GO:0016491,GO:0016614,GO:0043546,GO:0043546,GO:0046872,GO:0050660,GO:0050660,GO:0050660,GO:0051536,GO:0051536,GO:0051537,GO:0051537,GO:0051537,GO:0051537,GO:0055114,GO:0055114
comp32274_c0_seq1.p1	sp|Q7LKZ7|BPH1_SCHPO_Beige_protein_homolog_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=lvs1_PE=1_SV=2	2.00E-72	GO:0005543,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0009268,GO:0012505,GO:0016020,GO:0016020,GO:0016197,GO:0019898,GO:0035091,GO:0043234,GO:0046872,GO:0046872
comp32275_c0_seq10.p1			
comp32275_c0_seq2.p1			
comp32275_c0_seq2.p2			
comp32275_c0_seq6.p1			
comp32275_c0_seq6.p2			
comp32275_c0_seq7.p1			
comp32275_c0_seq8.p1			
comp32276_c1_seq12.p1			
comp32276_c1_seq16.p1			
comp32276_c1_seq7.p1			
comp32277_c0_seq6.p1			
comp32277_c0_seq6.p2	sp|Q55FJ0|LVSG_DICDI_Probable_inactive_serine/threonine-protein_kinase_lvsG_OS=Dictyostelium_discoideum_GN=lvsG_PE=3_SV=1	1.00E-53	GO:0003674,GO:0004672,GO:0005524,GO:0005575,GO:0006468,GO:0008150,GO:0016772,GO:0044351
comp32277_c0_seq6.p3	sp|Q8N5S9|KKCC1_HUMAN_Calcium/calmodulin-dependent_protein_kinase_kinase_1_OS=Homo_sapiens_GN=CAMKK1_PE=1_SV=2	3.00E-35	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004683,GO:0005515,GO:0005516,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0006468,GO:0007268,GO:0007268,GO:0016301,GO:0016310,GO:0016740,GO:0016772
comp32277_c0_seq9.p1	sp|Q55FJ0|LVSG_DICDI_Probable_inactive_serine/threonine-protein_kinase_lvsG_OS=Dictyostelium_discoideum_GN=lvsG_PE=3_SV=1	8.00E-52	GO:0003674,GO:0004672,GO:0005524,GO:0005575,GO:0006468,GO:0008150,GO:0016772,GO:0044351
comp32277_c0_seq9.p2	sp|Q8N5S9|KKCC1_HUMAN_Calcium/calmodulin-dependent_protein_kinase_kinase_1_OS=Homo_sapiens_GN=CAMKK1_PE=1_SV=2	3.00E-35	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004683,GO:0005515,GO:0005516,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0006468,GO:0007268,GO:0007268,GO:0016301,GO:0016310,GO:0016740,GO:0016772
comp32278_c0_seq1.p2			
comp32278_c0_seq10.p1			
comp32278_c0_seq11.p1	sp|Q9BTY7|F203A_HUMAN_Protein_FAM203A_OS=Homo_sapiens_GN=FAM203A_PE=1_SV=1	2.00E-18	GO:0003674,GO:0005575,GO:0008150
comp32278_c0_seq19.p1			
comp32278_c0_seq2.p1			
comp32278_c0_seq3.p1			
comp32278_c0_seq4.p2			
comp32278_c0_seq5.p1			
comp32278_c0_seq6.p1			
comp32279_c0_seq1.p1	sp|P41891|GAR2_SCHPO_Protein_gar2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=gar2_PE=1_SV=2	1.00E-20	GO:0000166,GO:0001651,GO:0003676,GO:0003723,GO:0005634,GO:0005730,GO:0005730,GO:0005730,GO:0005732,GO:0006364,GO:0006364,GO:0007000,GO:0042254,GO:0042254
comp32279_c2_seq12.p1			
comp32279_c2_seq13.p1			
comp32279_c2_seq14.p1	sp|Q9FT72|RQL3_ARATH_ATP-dependent_DNA_helicase_Q-like_3_OS=Arabidopsis_thaliana_GN=RECQL3_PE=1_SV=1	5.00E-84	GO:0000166,GO:0000733,GO:0003676,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006200,GO:0006200,GO:0006310,GO:0006310,GO:0008026,GO:0008026,GO:0009378,GO:0016787,GO:0032508,GO:0036310,GO:0043138,GO:0046872
comp32279_c2_seq18.p1			
comp32279_c2_seq2.p1	sp|Q9FT72|RQL3_ARATH_ATP-dependent_DNA_helicase_Q-like_3_OS=Arabidopsis_thaliana_GN=RECQL3_PE=1_SV=1	2.00E-80	GO:0000166,GO:0000733,GO:0003676,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006200,GO:0006200,GO:0006310,GO:0006310,GO:0008026,GO:0008026,GO:0009378,GO:0016787,GO:0032508,GO:0036310,GO:0043138,GO:0046872
comp32279_c2_seq20.p1			
comp32279_c2_seq4.p1			
comp32279_c2_seq5.p1	sp|Q9DE27|RUVB2_XENLA_RuvB-like_2_OS=Xenopus_laevis_GN=ruvbl2_PE=2_SV=1	0	GO:0000166,GO:0000812,GO:0003678,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0006281,GO:0006310,GO:0006351,GO:0006355,GO:0006974,GO:0016787,GO:0032508,GO:0032508,GO:0043141,GO:0071339
comp32279_c2_seq5.p2			
comp32279_c2_seq6.p1	sp|P15043|RECQ_ECOLI_ATP-dependent_DNA_helicase_recQ_OS=Escherichia_coli_(strain_K12)_GN=recQ_PE=1_SV=5	5.00E-24	GO:0000166,GO:0000166,GO:0003676,GO:0003677,GO:0003677,GO:0003824,GO:0004003,GO:0004003,GO:0004386,GO:0005515,GO:0005524,GO:0005524,GO:0005622,GO:0005737,GO:0006200,GO:0006200,GO:0006260,GO:0006281,GO:0006281,GO:0006281,GO:0006310,GO:0006310,GO:0006310,GO:0006974,GO:0006974,GO:0008026,GO:0008094,GO:0008270,GO:0009432,GO:0009432,GO:0016787,GO:0016887,GO:0017116,GO:0017117,GO:0030894,GO:0032508,GO:0032508,GO:0032508,GO:0032508,GO:0043140,GO:0043590,GO:0044237,GO:0046914
comp32279_c2_seq9.p1			
comp32280_c0_seq1.p1	sp|Q69QJ7|MGDG1_ORYSJ_Probable_monogalactosyldiacylglycerol_synthase_1,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=MGD1_PE=2_SV=1	3.00E-25	GO:0005975,GO:0005975,GO:0008194,GO:0009247,GO:0009247,GO:0009507,GO:0009507,GO:0009528,GO:0009536,GO:0009536,GO:0009611,GO:0009620,GO:0009695,GO:0009706,GO:0009753,GO:0009790,GO:0009941,GO:0010027,GO:0016020,GO:0016020,GO:0016740,GO:0016740,GO:0016757,GO:0016757,GO:0016758,GO:0016758,GO:0030246,GO:0030246,GO:0030259,GO:0030259,GO:0031969,GO:0035250,GO:0046509,GO:0046509
comp32280_c0_seq2.p1	sp|A2YTP9|MGDG2_ORYSI_Probable_monogalactosyldiacylglycerol_synthase_2,_chloroplastic_OS=Oryza_sativa_subsp._indica_GN=MGD2_PE=3_SV=2	8.00E-29	GO:0005975,GO:0009247,GO:0009507,GO:0009536,GO:0016020,GO:0016740,GO:0016757,GO:0016758,GO:0030246,GO:0030259,GO:0031969,GO:0046509
comp32280_c0_seq3.p1	sp|Q69QJ7|MGDG1_ORYSJ_Probable_monogalactosyldiacylglycerol_synthase_1,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=MGD1_PE=2_SV=1	5.00E-42	GO:0005975,GO:0005975,GO:0008194,GO:0009247,GO:0009247,GO:0009507,GO:0009507,GO:0009528,GO:0009536,GO:0009536,GO:0009611,GO:0009620,GO:0009695,GO:0009706,GO:0009753,GO:0009790,GO:0009941,GO:0010027,GO:0016020,GO:0016020,GO:0016740,GO:0016740,GO:0016757,GO:0016757,GO:0016758,GO:0016758,GO:0030246,GO:0030246,GO:0030259,GO:0030259,GO:0031969,GO:0035250,GO:0046509,GO:0046509
comp32281_c0_seq1.p1			
comp32281_c0_seq4.p1			
comp32282_c1_seq4.p1			
comp32282_c1_seq7.p1			
comp32282_c1_seq9.p1			
comp32283_c0_seq1.p1			
comp32283_c2_seq1.p1			
comp32283_c2_seq2.p1			
comp32283_c3_seq2.p2			
comp32283_c3_seq3.p1			
comp32283_c3_seq3.p3			
comp32283_c3_seq5.p1			
comp32283_c3_seq5.p3			
comp32283_c3_seq6.p1	sp|Q4KLH4|PSPC1_RAT_Paraspeckle_component_1_OS=Rattus_norvegicus_GN=Pspc1_PE=2_SV=1	2.00E-13	GO:0000166,GO:0001047,GO:0003676,GO:0003723,GO:0003723,GO:0005634,GO:0005634,GO:0005654,GO:0005730,GO:0005730,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0016363,GO:0016607,GO:0042382,GO:0042752,GO:0044822,GO:0045892,GO:0048511
comp32283_c3_seq9.p1			
comp32283_c4_seq2.p1	sp|Q84QU8|PPT2_ORYSJ_Phosphoenolpyruvate/phosphate_translocator_2,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=PPT2_PE=2_SV=1	5.00E-54	GO:0005215,GO:0006810,GO:0006810,GO:0008643,GO:0009507,GO:0009536,GO:0009670,GO:0015121,GO:0015714,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0031969,GO:0035436,GO:0089722
comp32283_c4_seq2.p3	sp|Q6DV04|MMAD_GECJA_Methylmalonic_aciduria_and_homocystinuria_type_D_homolog,_mitochondrial_OS=Gecko_japonicus_GN=GekBS024P_PE=2_SV=1	1.00E-21	GO:0005737,GO:0005737,GO:0005739,GO:0005739,GO:0009235
comp32284_c0_seq1.p1			
comp32284_c0_seq19.p1	sp|A7E2V1|CEP76_DANRE_Centrosomal_protein_of_76_kDa_OS=Danio_rerio_GN=cep76_PE=2_SV=1	1.00E-77	GO:0005737,GO:0005814,GO:0005814,GO:0005815,GO:0005856,GO:0046599
comp32284_c0_seq28.p1			
comp32284_c0_seq3.p1	sp|A7E2V1|CEP76_DANRE_Centrosomal_protein_of_76_kDa_OS=Danio_rerio_GN=cep76_PE=2_SV=1	2.00E-32	GO:0005737,GO:0005814,GO:0005814,GO:0005815,GO:0005856,GO:0046599
comp32284_c0_seq33.p1	sp|A7E2V1|CEP76_DANRE_Centrosomal_protein_of_76_kDa_OS=Danio_rerio_GN=cep76_PE=2_SV=1	2.00E-32	GO:0005737,GO:0005814,GO:0005814,GO:0005815,GO:0005856,GO:0046599
comp32284_c0_seq33.p2	sp|A7E2V1|CEP76_DANRE_Centrosomal_protein_of_76_kDa_OS=Danio_rerio_GN=cep76_PE=2_SV=1	1.00E-31	GO:0005737,GO:0005814,GO:0005814,GO:0005815,GO:0005856,GO:0046599
comp32284_c0_seq35.p1	sp|A7E2V1|CEP76_DANRE_Centrosomal_protein_of_76_kDa_OS=Danio_rerio_GN=cep76_PE=2_SV=1	2.00E-28	GO:0005737,GO:0005814,GO:0005814,GO:0005815,GO:0005856,GO:0046599
comp32284_c0_seq35.p2	sp|A7E2V1|CEP76_DANRE_Centrosomal_protein_of_76_kDa_OS=Danio_rerio_GN=cep76_PE=2_SV=1	3.00E-42	GO:0005737,GO:0005814,GO:0005814,GO:0005815,GO:0005856,GO:0046599
comp32284_c0_seq4.p1	sp|A7E2V1|CEP76_DANRE_Centrosomal_protein_of_76_kDa_OS=Danio_rerio_GN=cep76_PE=2_SV=1	3.00E-71	GO:0005737,GO:0005814,GO:0005814,GO:0005815,GO:0005856,GO:0046599
comp32284_c0_seq8.p1			
comp32286_c1_seq1.p1			
comp32286_c1_seq2.p1			
comp32286_c1_seq3.p1			
comp32287_c0_seq10.p1			
comp32287_c0_seq10.p11			
comp32287_c0_seq12.p1			
comp32287_c0_seq9.p1			
comp32287_c0_seq9.p12			
comp32288_c0_seq4.p1	sp|Q0V9N0|S14L5_XENTR_SEC14-like_protein_5_OS=Xenopus_tropicalis_GN=sec14l1_PE=2_SV=1	1.00E-17	GO:0006810,GO:0016021
comp32289_c0_seq1.p1	sp|Q949P1|ABAH1_ARATH_Abscisic_acid_8'-hydroxylase_1_OS=Arabidopsis_thaliana_GN=CYP707A1_PE=2_SV=1	2.00E-22	GO:0004497,GO:0005506,GO:0010295,GO:0016020,GO:0016020,GO:0016021,GO:0016491,GO:0016705,GO:0020037,GO:0046345,GO:0046872,GO:0055114,GO:0055114
comp32289_c0_seq2.p1			
comp32290_c0_seq2.p1			
comp32290_c0_seq4.p1			
comp32292_c0_seq1.p1	sp|P61203|CSN2_RAT_COP9_signalosome_complex_subunit_2_OS=Rattus_norvegicus_GN=Cops2_PE=2_SV=1	2.00E-117	GO:0000122,GO:0003714,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0008180,GO:0008180,GO:0008283,GO:0010388,GO:0030182,GO:0035914,GO:0045892
comp32292_c0_seq1.p2	sp|Q9ZTN2|ERD2_PETHY_ER_lumen_protein_retaining_receptor_OS=Petunia_hybrida_GN=ERD2_PE=2_SV=1	3.00E-35	GO:0005783,GO:0005789,GO:0006621,GO:0006810,GO:0015031,GO:0016020,GO:0016021,GO:0016021,GO:0016192,GO:0046923
comp32292_c0_seq12.p1			
comp32292_c0_seq12.p2	sp|Q9ZTN2|ERD2_PETHY_ER_lumen_protein_retaining_receptor_OS=Petunia_hybrida_GN=ERD2_PE=2_SV=1	3.00E-35	GO:0005783,GO:0005789,GO:0006621,GO:0006810,GO:0015031,GO:0016020,GO:0016021,GO:0016021,GO:0016192,GO:0046923
comp32292_c0_seq14.p1			
comp32292_c0_seq16.p1			
comp32292_c0_seq17.p1	sp|P61203|CSN2_RAT_COP9_signalosome_complex_subunit_2_OS=Rattus_norvegicus_GN=Cops2_PE=2_SV=1	2.00E-117	GO:0000122,GO:0003714,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0008180,GO:0008180,GO:0008283,GO:0010388,GO:0030182,GO:0035914,GO:0045892
comp32292_c0_seq18.p2			
comp32292_c0_seq2.p1			
comp32292_c0_seq2.p2			
comp32292_c0_seq4.p1			
comp32292_c0_seq5.p1			
comp32292_c0_seq6.p1			
comp32292_c0_seq6.p2			
comp32292_c1_seq5.p1			
comp32292_c1_seq8.p1	sp|Q5U2W5|TBL3_RAT_Transducin_beta-like_protein_3_OS=Rattus_norvegicus_GN=Tbl3_PE=2_SV=1	5.00E-68	GO:0000462,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0006364,GO:0030515,GO:0032040,GO:0032040,GO:0034388,GO:0044822
comp32292_c2_seq1.p1	sp|Q8C4J7|TBL3_MOUSE_Transducin_beta-like_protein_3_OS=Mus_musculus_GN=Tbl3_PE=2_SV=1	2.00E-48	GO:0000462,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0006364,GO:0008150,GO:0030515,GO:0032040,GO:0032040,GO:0034388,GO:0044822
comp32293_c0_seq2.p1			
comp32293_c0_seq3.p2			
comp32294_c1_seq11.p2	sp|O14735|CDIPT_HUMAN_CDP-diacylglycerol--inositol_3-phosphatidyltransferase_OS=Homo_sapiens_GN=CDIPT_PE=1_SV=1	4.00E-31	GO:0000139,GO:0003881,GO:0003881,GO:0003881,GO:0003881,GO:0003881,GO:0005783,GO:0005789,GO:0005789,GO:0005794,GO:0005794,GO:0005886,GO:0005886,GO:0006629,GO:0006644,GO:0006661,GO:0006661,GO:0006661,GO:0006661,GO:0008654,GO:0008654,GO:0016020,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016740,GO:0016780,GO:0019992,GO:0030145,GO:0030246,GO:0043178,GO:0044281,GO:0046341,GO:0046474
comp32294_c1_seq12.p1			
comp32294_c1_seq12.p2			
comp32294_c1_seq13.p1	sp|Q9SH88|RRS1_ARATH_Ribosome_biogenesis_regulatory_protein_homolog_OS=Arabidopsis_thaliana_GN=At2g37990_PE=2_SV=2	2.00E-31	GO:0000478,GO:0001510,GO:0005634,GO:0005634,GO:0005634,GO:0005730,GO:0006406,GO:0006606,GO:0006626,GO:0009640,GO:0009909,GO:0010388,GO:0042254,GO:0042254
comp32294_c1_seq15.p2			
comp32294_c1_seq15.p3			
comp32294_c1_seq15.p4	sp|Q8GUK6|PIS2_ARATH_Probable_CDP-diacylglycerol--inositol_3-phosphatidyltransferase_2_OS=Arabidopsis_thaliana_GN=PIS2_PE=2_SV=2	3.00E-23	GO:0003881,GO:0003881,GO:0005783,GO:0005794,GO:0006629,GO:0006661,GO:0008654,GO:0008654,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016740,GO:0016780,GO:0046872
comp32294_c1_seq5.p2	sp|Q8GUK6|PIS2_ARATH_Probable_CDP-diacylglycerol--inositol_3-phosphatidyltransferase_2_OS=Arabidopsis_thaliana_GN=PIS2_PE=2_SV=2	3.00E-23	GO:0003881,GO:0003881,GO:0005783,GO:0005794,GO:0006629,GO:0006661,GO:0008654,GO:0008654,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016740,GO:0016780,GO:0046872
comp32294_c1_seq7.p1			
comp32294_c1_seq8.p1	sp|Q8LBA6|PIS1_ARATH_CDP-diacylglycerol--inositol_3-phosphatidyltransferase_1_OS=Arabidopsis_thaliana_GN=PIS1_PE=1_SV=2	2.00E-30	GO:0003881,GO:0003881,GO:0005783,GO:0005794,GO:0006629,GO:0006661,GO:0008654,GO:0008654,GO:0008654,GO:0016020,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016740,GO:0016780,GO:0046872
comp32294_c1_seq8.p3			
comp32295_c0_seq2.p1	sp|Q9XGM8|MGAT1_ARATH_Alpha-1,3-mannosyl-glycoprotein_2-beta-N-acetylglucosaminyltransferase_OS=Arabidopsis_thaliana_GN=GNTI_PE=1_SV=1	4.00E-83	GO:0000139,GO:0003827,GO:0003827,GO:0005768,GO:0005794,GO:0005794,GO:0005794,GO:0005794,GO:0005794,GO:0005794,GO:0005802,GO:0006486,GO:0006486,GO:0006486,GO:0006487,GO:0006491,GO:0006972,GO:0008375,GO:0016020,GO:0016021,GO:0016262,GO:0016740,GO:0016757,GO:0016757,GO:0019344,GO:0046872
comp32295_c1_seq1.p1			
comp32296_c0_seq13.p1	sp|C0QGP6|DNAK_DESAH_Chaperone_protein_DnaK_OS=Desulfobacterium_autotrophicum_(strain_ATCC_43914_/_DSM_3382_/_HRM2)_GN=dnaK_PE=3_SV=1	1.00E-60	GO:0000166,GO:0005524,GO:0005524,GO:0005524,GO:0006457,GO:0051082
comp32296_c0_seq16.p1	sp|C0QGP6|DNAK_DESAH_Chaperone_protein_DnaK_OS=Desulfobacterium_autotrophicum_(strain_ATCC_43914_/_DSM_3382_/_HRM2)_GN=dnaK_PE=3_SV=1	2.00E-56	GO:0000166,GO:0005524,GO:0005524,GO:0005524,GO:0006457,GO:0051082
comp32296_c0_seq19.p1	sp|P61859|CALM_NEUCR_Calmodulin_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=cmd-1_PE=1_SV=2	3.00E-36	GO:0005509,GO:0046872
comp32296_c0_seq21.p1			
comp32296_c0_seq3.p1	sp|Q9NP78|ABCB9_HUMAN_ATP-binding_cassette_sub-family_B_member_9_OS=Homo_sapiens_GN=ABCB9_PE=1_SV=1	7.00E-159	GO:0000166,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005764,GO:0005764,GO:0005765,GO:0005765,GO:0005765,GO:0005765,GO:0005765,GO:0006200,GO:0006810,GO:0006810,GO:0015031,GO:0015440,GO:0015440,GO:0015440,GO:0015833,GO:0015833,GO:0015833,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016887,GO:0022891,GO:0030176,GO:0042626,GO:0042803,GO:0042803,GO:0055085,GO:0055085,GO:0002474,GO:0005769,GO:0005783
comp32296_c0_seq3.p6			
comp32297_c0_seq12.p1			
comp32297_c0_seq6.p1			

comp32297_c0_seq9.p1				
comp32298_c0_seq1.p1	sp|Q9C5J6|IPT9_ARATH_tRNA_dimethylallyltransferase_9_OS=Arabidopsis_thaliana_GN=IPT9_PE=2_SV=1	3.00E-55	GO:0000166,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0008033,GO:0008033,GO:0009691,GO:0016740,GO:0052381	nucleotide binding,ATP binding,ATP binding,cytoplasm,cytoplasm,tRNA processing,tRNA processing,cytokinin biosynthetic process,transferase activity,tRNA dimethylallyltransferase activity
comp32299_c3_seq13.p1				
comp32299_c3_seq15.p1	sp|A7SL20|RRP36_NEMVE_Ribosomal_RNA_processing_protein_36_homolog_OS=Nematostella_vectensis_GN=v1g245966_PE=3_SV=1	2.00E-31	GO:0005634,GO:0005730,GO:0006364,GO:0042254	nucleus,nucleolus,rRNA processing,ribosome biogenesis
comp32299_c3_seq2.p1				
comp32299_c3_seq31.p1	sp|A7SL20|RRP36_NEMVE_Ribosomal_RNA_processing_protein_36_homolog_OS=Nematostella_vectensis_GN=v1g245966_PE=3_SV=1	9.00E-37	GO:0005634,GO:0005730,GO:0006364,GO:0042254	nucleus,nucleolus,rRNA processing,ribosome biogenesis
comp32300_c0_seq14.p1				
comp32300_c0_seq22.p1				
comp32300_c0_seq23.p1				
comp32300_c0_seq25.p1				
comp32301_c0_seq2.p1				
comp32302_c1_seq10.p1				
comp32302_c1_seq15.p1	sp|Q9QXN3|TRIP4_MOUSE_Activating_signal_cointegrator_1_OS=Mus_musculus_GN=Trip4_PE=1_SV=2	4.00E-44	GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005815,GO:0005856,GO:0006351,GO:0006355,GO:0006355,GO:0008270,GO:0016922,GO:0030520,GO:0046872,GO:1901998	nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,microtubule organizing center,cytoskeleton,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,zinc ion binding,ligand-dependent nuclear receptor binding,intracellular estrogen receptor signaling pathway,metal ion binding,toxin transport
comp32302_c1_seq17.p1				
comp32302_c1_seq2.p1				
comp32302_c1_seq27.p1				
comp32302_c1_seq28.p1	sp|Q54VV7|Y0111_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0280111_OS=Dictyostelium_discoideum_GN=DDB_G0280111_PE=3_SV=1	4.00E-49	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005543,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,phospholipid binding,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp32302_c1_seq5.p1				
comp32303_c1_seq14.p1				
comp32303_c1_seq16.p1				
comp32304_c0_seq2.p1				
comp32304_c1_seq1.p1				
comp32304_c1_seq1.p2				
comp32305_c0_seq1.p1				
comp32305_c0_seq2.p2				
comp32305_c0_seq3.p1				
comp32306_c0_seq1.p2				
comp32306_c0_seq15.p1				
comp32306_c0_seq2.p1				
comp32306_c0_seq7.p2				
comp32307_c6_seq2.p1				
comp32307_c6_seq7.p1				
comp32308_c0_seq2.p1				
comp32308_c0_seq4.p1				
comp32308_c0_seq5.p1				
comp32308_c0_seq7.p3				
comp32309_c1_seq11.p1				
comp32309_c1_seq13.p1				
comp32309_c1_seq8.p1				
comp3231_c1_seq1.p1	sp|P07395|SYFB_ECOLI_Phenylalanine--tRNA_ligase_beta_subunit_OS=Escherichia_coli_(strain_K12)_GN=pheT_PE=1_SV=2	5.00E-86	GO:0000049,GO:0000049,GO:0000049,GO:0000166,GO:0000287,GO:0000287,GO:0003723,GO:0003723,GO:0003723,GO:0004812,GO:0004826,GO:0004826,GO:0004826,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006432,GO:0006432,GO:0008033,GO:0016020,GO:0016874,GO:0042802,GO:0042802,GO:0046872	tRNA binding,tRNA binding,tRNA binding,nucleotide binding,magnesium ion binding,magnesium ion binding,RNA binding,RNA binding,RNA binding,aminoacyl-tRNA ligase activity,phenylalanine-tRNA ligase activity,phenylalanine-tRNA ligase activity,phenylalanine-tRNA ligase activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,translation,phenylalanyl-tRNA aminoacylation,phenylalanyl-tRNA aminoacylation,tRNA processing,membrane,ligase activity,identical protein binding,identical protein binding,metal ion binding
comp32310_c0_seq1.p1				
comp32311_c0_seq1.p1				
comp32311_c0_seq3.p1				
comp32312_c2_seq16.p1	sp|Q54VQ7|HDA22_DICDI_Type-2_histone_deacetylase_2_OS=Dictyostelium_discoideum_GN=hdaC_PE=2_SV=1	1.00E-17	GO:0003677,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0016568,GO:0016787,GO:0031078,GO:0032041,GO:0032129,GO:0034739,GO:0044351,GO:0046872,GO:0046969,GO:0046970,GO:0061647,GO:0070932,GO:0070933,GO:0097372	DNA binding,nucleus,nucleus,cytoplasm,cytoplasm,transcription, DNA-templated,regulation of transcription, DNA-templated,chromatin modification,hydrolase activity,histone deacetylase activity (H3-K14 specific),NAD-dependent histone deacetylase activity (H3-K14 specific),histone deacetylase activity (H3-K9 specific),histone deacetylase activity (H4-K16 specific),macropinocytosis,metal ion binding,NAD-dependent histone deacetylase activity (H3-K9 specific),NAD-dependent histone deacetylase activity (H4-K16 specific),histone H3-K9 modification,histone H3 deacetylation,histone H4 deacetylation,NAD-dependent histone deacetylase activity (H3-K18 specific)
comp32312_c2_seq3.p1	sp|Q54VQ7|HDA22_DICDI_Type-2_histone_deacetylase_2_OS=Dictyostelium_discoideum_GN=hdaC_PE=2_SV=1	1.00E-17	GO:0003677,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0016568,GO:0016787,GO:0031078,GO:0032041,GO:0032129,GO:0034739,GO:0044351,GO:0046872,GO:0046969,GO:0046970,GO:0061647,GO:0070932,GO:0070933,GO:0097372	DNA binding,nucleus,nucleus,cytoplasm,cytoplasm,transcription, DNA-templated,regulation of transcription, DNA-templated,chromatin modification,hydrolase activity,histone deacetylase activity (H3-K14 specific),NAD-dependent histone deacetylase activity (H3-K14 specific),histone deacetylase activity (H3-K9 specific),histone deacetylase activity (H4-K16 specific),macropinocytosis,metal ion binding,NAD-dependent histone deacetylase activity (H3-K9 specific),NAD-dependent histone deacetylase activity (H4-K16 specific),histone H3-K9 modification,histone H3 deacetylation,histone H4 deacetylation,NAD-dependent histone deacetylase activity (H3-K18 specific)
comp32312_c2_seq4.p1	sp|Q54VQ7|HDA22_DICDI_Type-2_histone_deacetylase_2_OS=Dictyostelium_discoideum_GN=hdaC_PE=2_SV=1	1.00E-17	GO:0003677,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0016568,GO:0016787,GO:0031078,GO:0032041,GO:0032129,GO:0034739,GO:0044351,GO:0046872,GO:0046969,GO:0046970,GO:0061647,GO:0070932,GO:0070933,GO:0097372	DNA binding,nucleus,nucleus,cytoplasm,cytoplasm,transcription, DNA-templated,regulation of transcription, DNA-templated,chromatin modification,hydrolase activity,histone deacetylase activity (H3-K14 specific),NAD-dependent histone deacetylase activity (H3-K14 specific),histone deacetylase activity (H3-K9 specific),histone deacetylase activity (H4-K16 specific),macropinocytosis,metal ion binding,NAD-dependent histone deacetylase activity (H3-K9 specific),NAD-dependent histone deacetylase activity (H4-K16 specific),histone H3-K9 modification,histone H3 deacetylation,histone H4 deacetylation,NAD-dependent histone deacetylase activity (H3-K18 specific)
comp32312_c2_seq5.p1	sp|Q54VQ7|HDA22_DICDI_Type-2_histone_deacetylase_2_OS=Dictyostelium_discoideum_GN=hdaC_PE=2_SV=1	1.00E-17	GO:0003677,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0016568,GO:0016787,GO:0031078,GO:0032041,GO:0032129,GO:0034739,GO:0044351,GO:0046872,GO:0046969,GO:0046970,GO:0061647,GO:0070932,GO:0070933,GO:0097372	DNA binding,nucleus,nucleus,cytoplasm,cytoplasm,transcription, DNA-templated,regulation of transcription, DNA-templated,chromatin modification,hydrolase activity,histone deacetylase activity (H3-K14 specific),NAD-dependent histone deacetylase activity (H3-K14 specific),histone deacetylase activity (H3-K9 specific),histone deacetylase activity (H4-K16 specific),macropinocytosis,metal ion binding,NAD-dependent histone deacetylase activity (H3-K9 specific),NAD-dependent histone deacetylase activity (H4-K16 specific),histone H3-K9 modification,histone H3 deacetylation,histone H4 deacetylation,NAD-dependent histone deacetylase activity (H3-K18 specific)
comp32312_c2_seq6.p1				
comp32313_c0_seq2.p1				
comp32313_c0_seq2.p2				
comp32313_c0_seq2.p6	sp|P0C0F7|RPFC_XANC8_Sensory/regulatory_protein_RpfC_OS=Xanthomonas_campestris_pv._campestris_(strain_8004)_GN=rpfC_PE=3_SV=2	7.00E-11	GO:0000155,GO:0000160,GO:0000160,GO:0000166,GO:0004673,GO:0004871,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0006351,GO:0006355,GO:0007165,GO:0009405,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0018106,GO:0023014	phosphorelay sensor kinase activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,protein histidine kinase activity,signal transducer activity,ATP binding,plasma membrane,plasma membrane,plasma membrane,transcription, DNA-templated,regulation of transcription, DNA-templated,signal transduction,pathogenesis,membrane,membrane,integral component of membrane,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-histidine phosphorylation,signal transduction by phosphorylation
comp32313_c0_seq24.p1	sp|Q54YZ9|DHKJ_DICDI_Hybrid_signal_transduction_histidine_kinase_J_OS=Dictyostelium_discoideum_GN=dhkJ_PE=3_SV=2	4.00E-11	GO:0000155,GO:0000155,GO:0000156,GO:0000160,GO:0000160,GO:0000166,GO:0004673,GO:0004871,GO:0004871,GO:0005524,GO:0005615,GO:0007165,GO:0007165,GO:0007234,GO:0009927,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0018106,GO:0023014,GO:0023014	phosphorelay sensor kinase activity,phosphorelay sensor kinase activity,phosphorelay response regulator activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,protein histidine kinase activity,signal transducer activity,signal transducer activity,ATP binding,extracellular space,signal transduction,signal transduction,osmosensory signaling via phosphorelay pathway,histidine phosphotransfer kinase activity,membrane,integral component of membrane,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-histidine phosphorylation,signal transduction by phosphorylation,signal transduction by phosphorylation
comp32313_c0_seq29.p1				
comp32313_c0_seq29.p2	sp|Q54YZ9|DHKJ_DICDI_Hybrid_signal_transduction_histidine_kinase_J_OS=Dictyostelium_discoideum_GN=dhkJ_PE=3_SV=2	8.00E-12	GO:0000155,GO:0000155,GO:0000156,GO:0000160,GO:0000160,GO:0000166,GO:0004673,GO:0004871,GO:0004871,GO:0005524,GO:0005615,GO:0007165,GO:0007165,GO:0007234,GO:0009927,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0018106,GO:0023014,GO:0023014	phosphorelay sensor kinase activity,phosphorelay sensor kinase activity,phosphorelay response regulator activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,protein histidine kinase activity,signal transducer activity,signal transducer activity,ATP binding,extracellular space,signal transduction,signal transduction,osmosensory signaling via phosphorelay pathway,histidine phosphotransfer kinase activity,membrane,integral component of membrane,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-histidine phosphorylation,signal transduction by phosphorylation,signal transduction by phosphorylation
comp32313_c0_seq3.p1				
comp32313_c0_seq30.p1				
comp32313_c0_seq34.p1				
comp32313_c0_seq34.p5	sp|P0C0F7|RPFC_XANC8_Sensory/regulatory_protein_RpfC_OS=Xanthomonas_campestris_pv._campestris_(strain_8004)_GN=rpfC_PE=3_SV=2	7.00E-11	GO:0000155,GO:0000160,GO:0000160,GO:0000166,GO:0004673,GO:0004871,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0006351,GO:0006355,GO:0007165,GO:0009405,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0018106,GO:0023014	phosphorelay sensor kinase activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,protein histidine kinase activity,signal transducer activity,ATP binding,plasma membrane,plasma membrane,plasma membrane,transcription, DNA-templated,regulation of transcription, DNA-templated,signal transduction,pathogenesis,membrane,membrane,integral component of membrane,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-histidine phosphorylation,signal transduction by phosphorylation
comp32313_c0_seq35.p1	sp|Q54YZ9|DHKJ_DICDI_Hybrid_signal_transduction_histidine_kinase_J_OS=Dictyostelium_discoideum_GN=dhkJ_PE=3_SV=2	9.00E-13	GO:0000155,GO:0000155,GO:0000156,GO:0000160,GO:0000160,GO:0000166,GO:0004673,GO:0004871,GO:0004871,GO:0005524,GO:0005615,GO:0007165,GO:0007165,GO:0007234,GO:0009927,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0018106,GO:0023014,GO:0023014	phosphorelay sensor kinase activity,phosphorelay sensor kinase activity,phosphorelay response regulator activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,protein histidine kinase activity,signal transducer activity,signal transducer activity,ATP binding,extracellular space,signal transduction,signal transduction,osmosensory signaling via phosphorelay pathway,histidine phosphotransfer kinase activity,membrane,integral component of membrane,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-histidine phosphorylation,signal transduction by phosphorylation,signal transduction by phosphorylation
comp32313_c0_seq7.p1	sp|Q54YZ9|DHKJ_DICDI_Hybrid_signal_transduction_histidine_kinase_J_OS=Dictyostelium_discoideum_GN=dhkJ_PE=3_SV=2	6.00E-13	GO:0000155,GO:0000155,GO:0000156,GO:0000160,GO:0000160,GO:0000166,GO:0004673,GO:0004871,GO:0004871,GO:0005524,GO:0005615,GO:0007165,GO:0007165,GO:0007234,GO:0009927,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0018106,GO:0023014,GO:0023014	phosphorelay sensor kinase activity,phosphorelay sensor kinase activity,phosphorelay response regulator activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,protein histidine kinase activity,signal transducer activity,signal transducer activity,ATP binding,extracellular space,signal transduction,signal transduction,osmosensory signaling via phosphorelay pathway,histidine phosphotransfer kinase activity,membrane,integral component of membrane,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-histidine phosphorylation,signal transduction by phosphorylation,signal transduction by phosphorylation
comp32313_c0_seq7.p2				
comp32314_c0_seq4.p1				
comp32314_c0_seq5.p1	sp|Q554C9|MET16_DICDI_Methyltransferase-like_protein_16_homolog_OS=Dictyostelium_discoideum_GN=DDB_G0275203_PE=3_SV=1	3.00E-43	GO:0003676,GO:0008168,GO:0008168,GO:0016740,GO:0032259,GO:0032259	nucleic acid binding,methyltransferase activity,methyltransferase activity,transferase activity,methylation,methylation
comp32316_c0_seq2.p1				
comp32317_c0_seq1.p1				
comp32317_c0_seq2.p1				
comp32317_c0_seq3.p1				
comp32317_c0_seq4.p1				
comp32317_c0_seq6.p1				
comp32317_c0_seq7.p1				
comp32318_c1_seq1.p1	sp|O75037|KI21B_HUMAN_Kinesin-like_protein_KIF21B_OS=Homo_sapiens_GN=KIF21B_PE=1_SV=2	2.00E-94	GO:0000166,GO:0003777,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005871,GO:0005874,GO:0006200,GO:0007018,GO:0007018,GO:0008017,GO:0008152,GO:0008152,GO:0016887	nucleotide binding,microtubule motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,kinesin complex,microtubule,ATP catabolic process,microtubule-based movement,microtubule-based movement,microtubule binding,metabolic process,metabolic process,ATPase activity
comp32318_c1_seq1.p3	sp|Q9Z2Y8|PROSC_MOUSE_Proline_synthase_co-transcribed_bacterial_homolog_protein_OS=Mus_musculus_GN=Prosc_PE=1_SV=1	7.00E-51	GO:0005622,GO:0005739,GO:0030170,GO:0070062,GO:1901605	intracellular,mitochondrion,pyridoxal phosphate binding,extracellular vesicular exosome,alpha-amino acid metabolic process
comp32318_c1_seq10.p1				
comp32318_c1_seq10.p2				
comp32318_c1_seq10.p3	sp|Q9Z2Y8|PROSC_MOUSE_Proline_synthase_co-transcribed_bacterial_homolog_protein_OS=Mus_musculus_GN=Prosc_PE=1_SV=1	7.00E-51	GO:0005622,GO:0005739,GO:0030170,GO:0070062,GO:1901605	intracellular,mitochondrion,pyridoxal phosphate binding,extracellular vesicular exosome,alpha-amino acid metabolic process
comp32318_c1_seq7.p1	sp|O75037|KI21B_HUMAN_Kinesin-like_protein_KIF21B_OS=Homo_sapiens_GN=KIF21B_PE=1_SV=2	1.00E-94	GO:0000166,GO:0003777,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005871,GO:0005874,GO:0006200,GO:0007018,GO:0007018,GO:0008017,GO:0008152,GO:0008152,GO:0016887	nucleotide binding,microtubule motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,kinesin complex,microtubule,ATP catabolic process,microtubule-based movement,microtubule-based movement,microtubule binding,metabolic process,metabolic process,ATPase activity
comp32318_c1_seq7.p3	sp|Q9Z2Y8|PROSC_MOUSE_Proline_synthase_co-transcribed_bacterial_homolog_protein_OS=Mus_musculus_GN=Prosc_PE=1_SV=1	7.00E-51	GO:0005622,GO:0005739,GO:0030170,GO:0070062,GO:1901605	intracellular,mitochondrion,pyridoxal phosphate binding,extracellular vesicular exosome,alpha-amino acid metabolic process
comp32318_c1_seq8.p1	sp|O75037|KI21B_HUMAN_Kinesin-like_protein_KIF21B_OS=Homo_sapiens_GN=KIF21B_PE=1_SV=2	1.00E-95	GO:0000166,GO:0003777,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005871,GO:0005874,GO:0006200,GO:0007018,GO:0007018,GO:0008017,GO:0008152,GO:0008152,GO:0016887	nucleotide binding,microtubule motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,kinesin complex,microtubule,ATP catabolic process,microtubule-based movement,microtubule-based movement,microtubule binding,metabolic process,metabolic process,ATPase activity
comp32318_c1_seq8.p2				
comp32318_c1_seq8.p4	sp|Q9Z2Y8|PROSC_MOUSE_Proline_synthase_co-transcribed_bacterial_homolog_protein_OS=Mus_musculus_GN=Prosc_PE=1_SV=1	7.00E-51	GO:0005622,GO:0005739,GO:0030170,GO:0070062,GO:1901605	intracellular,mitochondrion,pyridoxal phosphate binding,extracellular vesicular exosome,alpha-amino acid metabolic process
comp32319_c0_seq12.p1	sp|Q8RWY3|ISW2_ARATH_Putative_chromatin-remodeling_complex_ATPase_chain_OS=Arabidopsis_thaliana_GN=At3g06400_PE=2_SV=3	2.00E-103	GO:0000166,GO:0003676,GO:0003677,GO:0003682,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006338,GO:0008152,GO:0008152,GO:0008152,GO:0016568,GO:0016787,GO:0016818,GO:0031491,GO:0043044	nucleotide binding,nucleic acid binding,DNA binding,chromatin binding,helicase activity,ATP binding,ATP binding,nucleus,nucleus,nucleus,chromatin remodeling,metabolic process,metabolic process,metabolic process,chromatin modification,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,nucleosome binding,ATP-dependent chromatin remodeling
comp32319_c0_seq16.p1	sp|Q8RWY3|ISW2_ARATH_Putative_chromatin-remodeling_complex_ATPase_chain_OS=Arabidopsis_thaliana_GN=At3g06400_PE=2_SV=3	5.00E-128	GO:0000166,GO:0003676,GO:0003677,GO:0003682,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006338,GO:0008152,GO:0008152,GO:0008152,GO:0016568,GO:0016787,GO:0016818,GO:0031491,GO:0043044	nucleotide binding,nucleic acid binding,DNA binding,chromatin binding,helicase activity,ATP binding,ATP binding,nucleus,nucleus,nucleus,chromatin remodeling,metabolic process,metabolic process,metabolic process,chromatin modification,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,nucleosome binding,ATP-dependent chromatin remodeling
comp32319_c0_seq17.p1	sp|Q7G8Y3|ISW2_ORYSJ_Probable_chromatin-remodeling_complex_ATPase_chain_OS=Oryza_sativa_subsp._japonica_GN=Os01g0367900_PE=2_SV=2	0	GO:0000166,GO:0003676,GO:0003677,GO:0003682,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006338,GO:0008152,GO:0008152,GO:0008152,GO:0016568,GO:0016787,GO:0016818,GO:0031491,GO:0043044	nucleotide binding,nucleic acid binding,DNA binding,chromatin binding,helicase activity,ATP binding,ATP binding,nucleus,nucleus,nucleus,chromatin remodeling,metabolic process,metabolic process,metabolic process,chromatin modification,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,nucleosome binding,ATP-dependent chromatin remodeling
comp32319_c0_seq18.p1	sp|Q8RWY3|ISW2_ARATH_Putative_chromatin-remodeling_complex_ATPase_chain_OS=Arabidopsis_thaliana_GN=At3g06400_PE=2_SV=3	0	GO:0000166,GO:0003676,GO:0003677,GO:0003682,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006338,GO:0008152,GO:0008152,GO:0008152,GO:0016568,GO:0016787,GO:0016818,GO:0031491,GO:0043044	nucleotide binding,nucleic acid binding,DNA binding,chromatin binding,helicase activity,ATP binding,ATP binding,nucleus,nucleus,nucleus,chromatin remodeling,metabolic process,metabolic process,metabolic process,chromatin modification,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,nucleosome binding,ATP-dependent chromatin remodeling
comp32319_c0_seq6.p1	sp|Q8RWY3|ISW2_ARATH_Putative_chromatin-remodeling_complex_ATPase_chain_OS=Arabidopsis_thaliana_GN=At3g06400_PE=2_SV=3	4.00E-153	GO:0000166,GO:0003676,GO:0003677,GO:0003682,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006338,GO:0008152,GO:0008152,GO:0008152,GO:0016568,GO:0016787,GO:0016818,GO:0031491,GO:0043044	nucleotide binding,nucleic acid binding,DNA binding,chromatin binding,helicase activity,ATP binding,ATP binding,nucleus,nucleus,nucleus,chromatin remodeling,metabolic process,metabolic process,metabolic process,chromatin modification,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,nucleosome binding,ATP-dependent chromatin remodeling
comp32319_c0_seq7.p1	sp|Q7G8Y3|ISW2_ORYSJ_Probable_chromatin-remodeling_complex_ATPase_chain_OS=Oryza_sativa_subsp._japonica_GN=Os01g0367900_PE=2_SV=2	0	GO:0000166,GO:0003676,GO:0003677,GO:0003682,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006338,GO:0008152,GO:0008152,GO:0008152,GO:0016568,GO:0016787,GO:0016818,GO:0031491,GO:0043044	nucleotide binding,nucleic acid binding,DNA binding,chromatin binding,helicase activity,ATP binding,ATP binding,nucleus,nucleus,nucleus,chromatin remodeling,metabolic process,metabolic process,metabolic process,chromatin modification,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,nucleosome binding,ATP-dependent chromatin remodeling
comp32319_c0_seq9.p1	sp|Q7G8Y3|ISW2_ORYSJ_Probable_chromatin-remodeling_complex_ATPase_chain_OS=Oryza_sativa_subsp._japonica_GN=Os01g0367900_PE=2_SV=2	0	GO:0000166,GO:0003676,GO:0003677,GO:0003682,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0006338,GO:0008152,GO:0008152,GO:0008152,GO:0016568,GO:0016787,GO:0016818,GO:0031491,GO:0043044	nucleotide binding,nucleic acid binding,DNA binding,chromatin binding,helicase activity,ATP binding,ATP binding,nucleus,nucleus,nucleus,chromatin remodeling,metabolic process,metabolic process,metabolic process,chromatin modification,hydrolase activity,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,nucleosome binding,ATP-dependent chromatin remodeling
comp32319_c1_seq1.p1	sp|Q6PGB8|SMCA1_MOUSE_Probable_global_transcription_activator_SNF2L1_OS=Mus_musculus_GN=Smarca1_PE=1_SV=1	2.00E-57	GO:0000166,GO:0000733,GO:0000790,GO:0003676,GO:0003677,GO:0003677,GO:0003682,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0006200,GO:0006338,GO:0006338,GO:0006351,GO:0006351,GO:0006351,GO:0006355,GO:0006355,GO:0006355,GO:0007420,GO:0007420,GO:0007420,GO:0008094,GO:0016568,GO:0016589,GO:0016787,GO:0016817,GO:0016818,GO:0016818,GO:0030182,GO:0031491,GO:0036310,GO:0036310,GO:0043044,GO:0045893,GO:0045893,GO:0070615,GO:0090537,GO:2000177,GO:2000177,GO:0008094	nucleotide binding,DNA strand renaturation,nuclear chromatin,nucleic acid binding,DNA binding,DNA binding,chromatin binding,helicase activity,ATP binding,ATP binding,nucleus,nucleus,nucleus,nucleus,ATP catabolic process,chromatin remodeling,chromatin remodeling,transcription, DNA-templated,transcription, DNA-templated,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,brain development,brain development,brain development,DNA-dependent ATPase activity,chromatin modification,NURF complex,hydrolase activity,hydrolase activity, acting on acid anhydrides,hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,neuron differentiation,nucleosome binding,annealing helicase activity,annealing helicase activity,ATP-dependent chromatin remodeling,positive regulation of transcription, DNA-templated,positive regulation of transcription, DNA-templated,nucleosome-dependent ATPase activity,CERF complex,regulation of neural precursor cell proliferation,regulation of neural precursor cell proliferation,DNA-dependent ATPase activity
comp32320_c0_seq1.p1				
comp32321_c0_seq1.p1	sp|A8WMY3|HKE41_CAEBR_Histidine-rich_membrane_protein_KE4_homolog_1_OS=Caenorhabditis_briggsae_GN=hke-4.1_PE=3_SV=2	1.00E-16	GO:0006810,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0030001,GO:0046873,GO:0055085	transport,membrane,membrane,membrane,integral component of membrane,metal ion transport,metal ion transmembrane transporter activity,transmembrane transport
comp32321_c0_seq2.p1				
comp32321_c0_seq4.p1				
comp32322_c0_seq1.p1				
comp32322_c0_seq12.p1	sp|C0LGF5|Y1341_ARATH_Probable_LRR_receptor-like_serine/threonine-protein_kinase_At1g34110_OS=Arabidopsis_thaliana_GN=At1g34110_PE=2_SV=2	9.00E-25	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,protein phosphorylation,membrane,membrane,integral component of membrane,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp32322_c0_seq12.p2				
comp32322_c0_seq13.p1				
comp32322_c0_seq13.p2				
comp32322_c0_seq13.p3	sp|Q94AG2|SERK1_ARATH_Somatic_embryogenesis_receptor_kinase_1_OS=Arabidopsis_thaliana_GN=SERK1_PE=1_SV=2	2.00E-24	GO:0000166,GO:0000226,GO:0000911,GO:0004672,GO:0004674,GO:0004674,GO:0004675,GO:0004713,GO:0004714,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005783,GO:0005789,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006468,GO:0006468,GO:0007030,GO:0007062,GO:0007178,GO:0009556,GO:0009556,GO:0009742,GO:0009742,GO:0009793,GO:0009793,GO:0009880,GO:0010072,GO:0010152,GO:0010227,GO:0010228,GO:0010431,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016310,GO:0016740,GO:0016772,GO:0018108,GO:0018108,GO:0033612,GO:0042742,GO:0042802,GO:0042802,GO:0043234,GO:0045595,GO:0046777,GO:0051301	nucleotide binding,microtubule cytoskeleton organization,cytokinesis by cell plate formation,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,transmembrane receptor protein serine/threonine kinase activity,protein tyrosine kinase activity,transmembrane receptor protein tyrosine kinase activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,endoplasmic reticulum,endoplasmic reticulum membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,protein phosphorylation,protein phosphorylation,Golgi organization,sister chromatid cohesion,transmembrane receptor protein serine/threonine kinase signaling pathway,microsporogenesis,microsporogenesis,brassinosteroid mediated signaling pathway,brassinosteroid mediated signaling pathway,embryo development ending in seed dormancy,embryo development ending in seed dormancy,embryonic pattern specification,primary shoot apical meristem specification,pollen maturation,floral organ abscission,vegetative to reproductive phase transition of meristem,seed maturation,membrane,integral component of membrane,kinase activity,phosphorylation,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-tyrosine phosphorylation,peptidyl-tyrosine phosphorylation,receptor serine/threonine kinase binding,defense response to bacterium,identical protein binding,identical protein binding,protein complex,regulation of cell differentiation,protein autophosphorylation,cell division
comp32322_c0_seq6.p2				
comp32322_c1_seq1.p1	sp|Q05609|CTR1_ARATH_Serine/threonine-protein_kinase_CTR1_OS=Arabidopsis_thaliana_GN=CTR1_PE=1_SV=1	2.00E-17	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004674,GO:0004712,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005789,GO:0006468,GO:0009686,GO:0009723,GO:0009744,GO:0009750,GO:0009873,GO:0010105,GO:0010105,GO:0010105,GO:0010105,GO:0010182,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0046777,GO:0048510,GO:0071281,GO:2000035,GO:2000069	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine/tyrosine kinase activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,endoplasmic reticulum membrane,protein phosphorylation,gibberellin biosynthetic process,response to ethylene,response to sucrose,response to fructose,ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,sugar mediated signaling pathway,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,protein autophosphorylation,regulation of timing of transition from vegetative to reproductive phase,cellular response to iron ion,regulation of stem cell division,regulation of post-embryonic root development
comp32322_c1_seq2.p1	sp|Q55BA0|Y9866_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0271402_OS=Dictyostelium_discoideum_GN=DDB_G0271402_PE=3_SV=1	3.00E-11	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005575,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,cellular_component,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp32322_c1_seq3.p1	sp|Q05609|CTR1_ARATH_Serine/threonine-protein_kinase_CTR1_OS=Arabidopsis_thaliana_GN=CTR1_PE=1_SV=1	3.00E-17	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004674,GO:0004712,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005789,GO:0006468,GO:0009686,GO:0009723,GO:0009744,GO:0009750,GO:0009873,GO:0010105,GO:0010105,GO:0010105,GO:0010105,GO:0010182,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0046777,GO:0048510,GO:0071281,GO:2000035,GO:2000069	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine/tyrosine kinase activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,endoplasmic reticulum membrane,protein phosphorylation,gibberellin biosynthetic process,response to ethylene,response to sucrose,response to fructose,ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,sugar mediated signaling pathway,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,protein autophosphorylation,regulation of timing of transition from vegetative to reproductive phase,cellular response to iron ion,regulation of stem cell division,regulation of post-embryonic root development
comp32322_c1_seq4.p1	sp|Q55BA0|Y9866_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0271402_OS=Dictyostelium_discoideum_GN=DDB_G0271402_PE=3_SV=1	3.00E-11	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005575,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,cellular_component,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp32323_c0_seq10.p1				
comp32323_c0_seq11.p1				
comp32323_c0_seq4.p1	sp|Q5F478|ANR44_CHICK_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_B_OS=Gallus_gallus_GN=ANKRD44_PE=2_SV=1	3.00E-28		
comp32323_c0_seq6.p1				
comp32323_c0_seq8.p1				
comp32323_c0_seq9.p2				
comp32323_c1_seq2.p1				
comp32325_c0_seq1.p1	sp|Q40832|TBA2_PELFA_Tubulin_alpha-2_chain_OS=Pelvetia_fastigiata_GN=TUBA2_PE=2_SV=1	0	GO:0000166,GO:0003924,GO:0005200,GO:0005525,GO:0005525,GO:0005737,GO:0005856,GO:0005856,GO:0005874,GO:0005874,GO:0006184,GO:0007017,GO:0043234,GO:0051258	nucleotide binding,GTPase activity,structural constituent of cytoskeleton,GTP binding,GTP binding,cytoplasm,cytoskeleton,cytoskeleton,microtubule,microtubule,GTP catabolic process,microtubule-based process,protein complex,protein polymerization
comp32325_c0_seq2.p1	sp|Q40832|TBA2_PELFA_Tubulin_alpha-2_chain_OS=Pelvetia_fastigiata_GN=TUBA2_PE=2_SV=1	0	GO:0000166,GO:0003924,GO:0005200,GO:0005525,GO:0005525,GO:0005737,GO:0005856,GO:0005856,GO:0005874,GO:0005874,GO:0006184,GO:0007017,GO:0043234,GO:0051258	nucleotide binding,GTPase activity,structural constituent of cytoskeleton,GTP binding,GTP binding,cytoplasm,cytoskeleton,cytoskeleton,microtubule,microtubule,GTP catabolic process,microtubule-based process,protein complex,protein polymerization
comp32325_c1_seq1.p2	sp|Q8R173|ZDHC3_MOUSE_Palmitoyltransferase_ZDHHC3_OS=Mus_musculus_GN=Zdhhc3_PE=1_SV=1	1.00E-12	GO:0000139,GO:0005794,GO:0005794,GO:0005794,GO:0006605,GO:0008270,GO:0016020,GO:0016020,GO:0016021,GO:0016409,GO:0016409,GO:0016740,GO:0016746,GO:0018345,GO:0018345,GO:0019706,GO:0046872	Golgi membrane,Golgi apparatus,Golgi apparatus,Golgi apparatus,protein targeting,zinc ion binding,membrane,membrane,integral component of membrane,palmitoyltransferase activity,palmitoyltransferase activity,transferase activity,transferase activity, transferring acyl groups,protein palmitoylation,protein palmitoylation,protein-cysteine S-palmitoyltransferase activity,metal ion binding
comp32325_c3_seq1.p1	sp|Q9NXF8|ZDHC7_HUMAN_Palmitoyltransferase_ZDHHC7_OS=Homo_sapiens_GN=ZDHHC7_PE=2_SV=2	6.00E-14	GO:0005634,GO:0005654,GO:0005730,GO:0005794,GO:0005794,GO:0005794,GO:0005794,GO:0008270,GO:0016020,GO:0016020,GO:0016021,GO:0016409,GO:0016409,GO:0016740,GO:0016746,GO:0018230,GO:0018345,GO:0018345,GO:0019706,GO:0043231,GO:0046872	nucleus,nucleoplasm,nucleolus,Golgi apparatus,Golgi apparatus,Golgi apparatus,Golgi apparatus,zinc ion binding,membrane,membrane,integral component of membrane,palmitoyltransferase activity,palmitoyltransferase activity,transferase activity,transferase activity, transferring acyl groups,peptidyl-L-cysteine S-palmitoylation,protein palmitoylation,protein palmitoylation,protein-cysteine S-palmitoyltransferase activity,intracellular membrane-bounded organelle,metal ion binding
comp32326_c0_seq11.p1				
comp32326_c0_seq16.p2				
comp32326_c0_seq18.p1				
comp32326_c0_seq29.p1				
comp32326_c0_seq30.p1				
comp32326_c0_seq36.p1				
comp32326_c0_seq43.p2	sp|Q9ATM2|SIP12_MAIZE_Aquaporin_SIP1-2_OS=Zea_mays_GN=SIP1-2_PE=2_SV=1	2.00E-14	GO:0005215,GO:0006810,GO:0016020,GO:0016020,GO:0016020,GO:0016021	transporter activity,transport,transport,membrane,membrane,membrane,integral component of membrane
comp32326_c0_seq50.p1	sp|P50526|SSP1_SCHPO_Serine/threonine-protein_kinase_ssp1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ssp1_PE=1_SV=1	3.00E-34	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004683,GO:0005516,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0006468,GO:0006995,GO:0007165,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0030042,GO:0030428,GO:0030950,GO:0042149,GO:0051285,GO:0051519,GO:0051519,GO:0070317,GO:0071963	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,calmodulin-dependent protein kinase activity,calmodulin binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytosol,protein phosphorylation,cellular response to nitrogen starvation,signal transduction,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,actin filament depolymerization,cell septum,establishment or maintenance of actin cytoskeleton polarity,cellular response to glucose starvation,cell cortex of cell tip,activation of bipolar cell growth,activation of bipolar cell growth,negative regulation of G0 to G1 transition,establishment or maintenance of cell polarity regulating cell shape
comp32326_c0_seq59.p1				
comp32326_c0_seq62.p1	sp|P50526|SSP1_SCHPO_Serine/threonine-protein_kinase_ssp1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ssp1_PE=1_SV=1	3.00E-34	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004683,GO:0005516,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0006468,GO:0006995,GO:0007165,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0030042,GO:0030428,GO:0030950,GO:0042149,GO:0051285,GO:0051519,GO:0051519,GO:0070317,GO:0071963	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,calmodulin-dependent protein kinase activity,calmodulin binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytosol,protein phosphorylation,cellular response to nitrogen starvation,signal transduction,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,actin filament depolymerization,cell septum,establishment or maintenance of actin cytoskeleton polarity,cellular response to glucose starvation,cell cortex of cell tip,activation of bipolar cell growth,activation of bipolar cell growth,negative regulation of G0 to G1 transition,establishment or maintenance of cell polarity regulating cell shape
comp32327_c0_seq13.p1	sp|Q1PSI9|IDND_VITVI_L-idonate_5-dehydrogenase_OS=Vitis_vinifera_GN=VIT_16s0100g00290_PE=1_SV=1	2.00E-66	GO:0003939,GO:0005737,GO:0005739,GO:0005829,GO:0005886,GO:0008270,GO:0008270,GO:0009506,GO:0016020,GO:0016491,GO:0016491,GO:0016491,GO:0031966,GO:0046183,GO:0046872,GO:0046872,GO:0055114,GO:0055114,GO:0055114	L-iditol 2-dehydrogenase activity,cytoplasm,mitochondrion,cytosol,plasma membrane,zinc ion binding,zinc ion binding,plasmodesma,membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,mitochondrial membrane,L-idonate catabolic process,metal ion binding,metal ion binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp32327_c0_seq16.p2				
comp32327_c0_seq17.p1	sp|Q9Y496|KIF3A_HUMAN_Kinesin-like_protein_KIF3A_OS=Homo_sapiens_GN=KIF3A_PE=1_SV=4	2.00E-37	GO:0000166,GO:0003777,GO:0003777,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005737,GO:0005813,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0005856,GO:0005856,GO:0005871,GO:0005874,GO:0005929,GO:0005929,GO:0006200,GO:0006996,GO:0007018,GO:0007018,GO:0007018,GO:0007596,GO:0008017,GO:0008152,GO:0008152,GO:0008574,GO:0015630,GO:0016887,GO:0016939,GO:0019886,GO:0022008,GO:0030030,GO:0030507,GO:0042384,GO:0042995,GO:0060271,GO:0061024,GO:0070062,GO:0070062,GO:0072372,GO:0072383,GO:0005876	nucleotide binding,microtubule motor activity,microtubule motor activity,protein binding,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,cytoplasm,centrosome,cytosol,cytosol,cytosol,cytosol,cytoskeleton,cytoskeleton,kinesin complex,microtubule,cilium,cilium,ATP catabolic process,organelle organization,microtubule-based movement,microtubule-based movement,microtubule-based movement,blood coagulation,microtubule binding,metabolic process,metabolic process,plus-end-directed microtubule motor activity,microtubule cytoskeleton,ATPase activity,kinesin II complex,antigen processing and presentation of exogenous peptide antigen via MHC class II,neurogenesis,cell projection organization,spectrin binding,cilium assembly,cell projection,cilium morphogenesis,membrane organization,extracellular vesicular exosome,extracellular vesicular exosome,primary cilium,plus-end-directed vesicle transport along microtubule,spindle microtubule
comp32327_c0_seq18.p1				
comp32327_c0_seq3.p1	sp|Q1PSI9|IDND_VITVI_L-idonate_5-dehydrogenase_OS=Vitis_vinifera_GN=VIT_16s0100g00290_PE=1_SV=1	4.00E-123	GO:0003939,GO:0005737,GO:0005739,GO:0005829,GO:0005886,GO:0008270,GO:0008270,GO:0009506,GO:0016020,GO:0016491,GO:0016491,GO:0016491,GO:0031966,GO:0046183,GO:0046872,GO:0046872,GO:0055114,GO:0055114,GO:0055114	L-iditol 2-dehydrogenase activity,cytoplasm,mitochondrion,cytosol,plasma membrane,zinc ion binding,zinc ion binding,plasmodesma,membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,mitochondrial membrane,L-idonate catabolic process,metal ion binding,metal ion binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp32327_c0_seq7.p1	sp|Q1PSI9|IDND_VITVI_L-idonate_5-dehydrogenase_OS=Vitis_vinifera_GN=VIT_16s0100g00290_PE=1_SV=1	4.00E-67	GO:0003939,GO:0005737,GO:0005739,GO:0005829,GO:0005886,GO:0008270,GO:0008270,GO:0009506,GO:0016020,GO:0016491,GO:0016491,GO:0016491,GO:0031966,GO:0046183,GO:0046872,GO:0046872,GO:0055114,GO:0055114,GO:0055114	L-iditol 2-dehydrogenase activity,cytoplasm,mitochondrion,cytosol,plasma membrane,zinc ion binding,zinc ion binding,plasmodesma,membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,mitochondrial membrane,L-idonate catabolic process,metal ion binding,metal ion binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp32328_c0_seq5.p1	sp|Q7TSP2|KIF15_RAT_Kinesin-like_protein_KIF15_OS=Rattus_norvegicus_GN=Kif15_PE=2_SV=1	9.00E-69	GO:0000166,GO:0003777,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005819,GO:0005856,GO:0005871,GO:0005871,GO:0005874,GO:0006200,GO:0007018,GO:0007018,GO:0008017,GO:0008152,GO:0008152,GO:0016887	nucleotide binding,microtubule motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoplasm,spindle,cytoskeleton,kinesin complex,kinesin complex,microtubule,ATP catabolic process,microtubule-based movement,microtubule-based movement,microtubule binding,metabolic process,metabolic process,ATPase activity
comp32328_c0_seq6.p1	sp|Q7TSP2|KIF15_RAT_Kinesin-like_protein_KIF15_OS=Rattus_norvegicus_GN=Kif15_PE=2_SV=1	8.00E-69	GO:0000166,GO:0003777,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005819,GO:0005856,GO:0005871,GO:0005871,GO:0005874,GO:0006200,GO:0007018,GO:0007018,GO:0008017,GO:0008152,GO:0008152,GO:0016887	nucleotide binding,microtubule motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoplasm,spindle,cytoskeleton,kinesin complex,kinesin complex,microtubule,ATP catabolic process,microtubule-based movement,microtubule-based movement,microtubule binding,metabolic process,metabolic process,ATPase activity
comp32328_c0_seq7.p1	sp|Q7TSP2|KIF15_RAT_Kinesin-like_protein_KIF15_OS=Rattus_norvegicus_GN=Kif15_PE=2_SV=1	1.00E-68	GO:0000166,GO:0003777,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005819,GO:0005856,GO:0005871,GO:0005871,GO:0005874,GO:0006200,GO:0007018,GO:0007018,GO:0008017,GO:0008152,GO:0008152,GO:0016887	nucleotide binding,microtubule motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoplasm,spindle,cytoskeleton,kinesin complex,kinesin complex,microtubule,ATP catabolic process,microtubule-based movement,microtubule-based movement,microtubule binding,metabolic process,metabolic process,ATPase activity
comp32328_c0_seq9.p1	sp|Q7TSP2|KIF15_RAT_Kinesin-like_protein_KIF15_OS=Rattus_norvegicus_GN=Kif15_PE=2_SV=1	8.00E-69	GO:0000166,GO:0003777,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005819,GO:0005856,GO:0005871,GO:0005871,GO:0005874,GO:0006200,GO:0007018,GO:0007018,GO:0008017,GO:0008152,GO:0008152,GO:0016887	nucleotide binding,microtubule motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoplasm,spindle,cytoskeleton,kinesin complex,kinesin complex,microtubule,ATP catabolic process,microtubule-based movement,microtubule-based movement,microtubule binding,metabolic process,metabolic process,ATPase activity
comp32329_c0_seq12.p2				
comp32329_c0_seq16.p1				
comp32329_c0_seq20.p2				
comp32329_c0_seq7.p1				
comp32329_c1_seq11.p1				
comp32329_c1_seq12.p1				
comp32329_c1_seq20.p1	sp|Q03649|YM60_YEAST_Putative_esterase_YMR210W_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YMR210W_PE=1_SV=1	4.00E-27	GO:0005575,GO:0016746,GO:0016787,GO:0051792,GO:0052689	cellular_component,transferase activity, transferring acyl groups,hydrolase activity,medium-chain fatty acid biosynthetic process,carboxylic ester hydrolase activity
comp32329_c1_seq20.p2				
comp32329_c1_seq24.p1				
comp32329_c1_seq25.p1				
comp32329_c1_seq4.p1				
comp32330_c0_seq1.p2				
comp32331_c2_seq10.p1				
comp32331_c2_seq10.p4				
comp32331_c2_seq16.p1				
comp32331_c2_seq16.p2				
comp32331_c2_seq16.p3				
comp32331_c2_seq18.p1				
comp32331_c2_seq18.p2				
comp32331_c2_seq24.p2				
comp32331_c2_seq27.p3				
comp32331_c2_seq8.p2				
comp32332_c0_seq1.p1	sp|P31325|PHKG2_RAT_Phosphorylase_b_kinase_gamma_catalytic_chain,_testis/liver_isoform_OS=Rattus_norvegicus_GN=Phkg2_PE=1_SV=1	3.00E-11	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004689,GO:0004689,GO:0004689,GO:0004689,GO:0004689,GO:0005516,GO:0005516,GO:0005516,GO:0005524,GO:0005524,GO:0005524,GO:0005524,GO:0005964,GO:0005964,GO:0005975,GO:0005977,GO:0005977,GO:0005977,GO:0005978,GO:0006468,GO:0006468,GO:0006468,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0019899,GO:0019899	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,phosphorylase kinase activity,phosphorylase kinase activity,phosphorylase kinase activity,phosphorylase kinase activity,phosphorylase kinase activity,calmodulin binding,calmodulin binding,calmodulin binding,ATP binding,ATP binding,ATP binding,ATP binding,phosphorylase kinase complex,phosphorylase kinase complex,carbohydrate metabolic process,glycogen metabolic process,glycogen metabolic process,glycogen metabolic process,glycogen biosynthetic process,protein phosphorylation,protein phosphorylation,protein phosphorylation,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,enzyme binding,enzyme binding
comp32332_c0_seq2.p1	sp|Q9C098|DCLK3_HUMAN_Serine/threonine-protein_kinase_DCLK3_OS=Homo_sapiens_GN=DCLK3_PE=1_SV=1	8.00E-12	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,nucleus,nucleus,cytoplasm,cytoplasm,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp32332_c0_seq3.p1				
comp32333_c0_seq1.p1				
comp32333_c1_seq1.p1				
comp32333_c2_seq1.p1	sp|O43808|PM34_HUMAN_Peroxisomal_membrane_protein_PMP34_OS=Homo_sapiens_GN=SLC25A17_PE=1_SV=1	2.00E-28	GO:0001561,GO:0005347,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0005739,GO:0005777,GO:0005777,GO:0005778,GO:0005778,GO:0005778,GO:0005778,GO:0005779,GO:0005779,GO:0006635,GO:0006810,GO:0015217,GO:0015228,GO:0015230,GO:0015866,GO:0015867,GO:0015908,GO:0016020,GO:0016020,GO:0016021,GO:0035349,GO:0035350,GO:0043132,GO:0043231,GO:0044255,GO:0044281,GO:0044610,GO:0051087,GO:0051724,GO:0055085,GO:0080121,GO:0080122,GO:1901679	fatty acid alpha-oxidation,ATP transmembrane transporter activity,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,cytoplasm,cytoplasm,mitochondrion,peroxisome,peroxisome,peroxisomal membrane,peroxisomal membrane,peroxisomal membrane,peroxisomal membrane,integral component of peroxisomal membrane,integral component of peroxisomal membrane,fatty acid beta-oxidation,transport,ADP transmembrane transporter activity,coenzyme A transmembrane transporter activity,FAD transmembrane transporter activity,ADP transport,ATP transport,fatty acid transport,membrane,membrane,integral component of membrane,coenzyme A transmembrane transport,FAD transmembrane transport,NAD transport,intracellular membrane-bounded organelle,cellular lipid metabolic process,small molecule metabolic process,FMN transmembrane transporter activity,chaperone binding,NAD transporter activity,transmembrane transport,AMP transport,AMP transmembrane transporter activity,nucleotide transmembrane transport
comp32333_c3_seq12.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	3.00E-16	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp32333_c3_seq14.p1				
comp32333_c3_seq15.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	2.00E-11	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp32333_c3_seq17.p1	sp|Q06538|YL241_YEAST_Uncharacterized_membrane_protein_YLR241W_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YLR241W_PE=1_SV=1	7.00E-25	GO:0005227,GO:0006810,GO:0006811,GO:0006812,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0098655	calcium activated cation channel activity,transport,ion transport,cation transport,membrane,membrane,membrane,integral component of membrane,cation transmembrane transport
comp32333_c3_seq17.p2				
comp32333_c3_seq18.p1	sp|Q06538|YL241_YEAST_Uncharacterized_membrane_protein_YLR241W_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YLR241W_PE=1_SV=1	7.00E-25	GO:0005227,GO:0006810,GO:0006811,GO:0006812,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0098655	calcium activated cation channel activity,transport,ion transport,cation transport,membrane,membrane,membrane,integral component of membrane,cation transmembrane transport
comp32333_c3_seq18.p2				
comp32333_c3_seq31.p1				
comp32333_c3_seq6.p2				
comp32334_c0_seq6.p1				
comp32334_c0_seq9.p2				
comp32337_c0_seq11.p1	sp|Q70G58|NTRC_ORYSJ_Thioredoxin_reductase_NTRC_OS=Oryza_sativa_subsp._japonica_GN=Os07g0657900_PE=1_SV=1	7.00E-32	GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0008047,GO:0009507,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009536,GO:0009570,GO:0010027,GO:0010380,GO:0010581,GO:0016117,GO:0016491,GO:0016491,GO:0016491,GO:0016671,GO:0016671,GO:0016671,GO:0016671,GO:0019288,GO:0019430,GO:0019430,GO:0042744,GO:0042744,GO:0042802,GO:0043085,GO:0045454,GO:0045454,GO:0046686,GO:0050660,GO:0050660,GO:0055114,GO:0055114,GO:0055114,GO:0055114	thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,protein binding,protein binding,cytoplasm,cytoplasm,enzyme activator activity,chloroplast,chloroplast,chloroplast,chloroplast,plastid,plastid,chloroplast stroma,thylakoid membrane organization,regulation of chlorophyll biosynthetic process,regulation of starch biosynthetic process,carotenoid biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway,removal of superoxide radicals,removal of superoxide radicals,hydrogen peroxide catabolic process,hydrogen peroxide catabolic process,identical protein binding,positive regulation of catalytic activity,cell redox homeostasis,cell redox homeostasis,response to cadmium ion,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp32337_c0_seq13.p2	sp|Q70G58|NTRC_ORYSJ_Thioredoxin_reductase_NTRC_OS=Oryza_sativa_subsp._japonica_GN=Os07g0657900_PE=1_SV=1	7.00E-32	GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0008047,GO:0009507,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009536,GO:0009570,GO:0010027,GO:0010380,GO:0010581,GO:0016117,GO:0016491,GO:0016491,GO:0016491,GO:0016671,GO:0016671,GO:0016671,GO:0016671,GO:0019288,GO:0019430,GO:0019430,GO:0042744,GO:0042744,GO:0042802,GO:0043085,GO:0045454,GO:0045454,GO:0046686,GO:0050660,GO:0050660,GO:0055114,GO:0055114,GO:0055114,GO:0055114	thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,protein binding,protein binding,cytoplasm,cytoplasm,enzyme activator activity,chloroplast,chloroplast,chloroplast,chloroplast,plastid,plastid,chloroplast stroma,thylakoid membrane organization,regulation of chlorophyll biosynthetic process,regulation of starch biosynthetic process,carotenoid biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway,removal of superoxide radicals,removal of superoxide radicals,hydrogen peroxide catabolic process,hydrogen peroxide catabolic process,identical protein binding,positive regulation of catalytic activity,cell redox homeostasis,cell redox homeostasis,response to cadmium ion,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp32337_c0_seq20.p1	sp|Q70G58|NTRC_ORYSJ_Thioredoxin_reductase_NTRC_OS=Oryza_sativa_subsp._japonica_GN=Os07g0657900_PE=1_SV=1	3.00E-92	GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0008047,GO:0009507,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009536,GO:0009570,GO:0010027,GO:0010380,GO:0010581,GO:0016117,GO:0016491,GO:0016491,GO:0016491,GO:0016671,GO:0016671,GO:0016671,GO:0016671,GO:0019288,GO:0019430,GO:0019430,GO:0042744,GO:0042744,GO:0042802,GO:0043085,GO:0045454,GO:0045454,GO:0046686,GO:0050660,GO:0050660,GO:0055114,GO:0055114,GO:0055114,GO:0055114	thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,protein binding,protein binding,cytoplasm,cytoplasm,enzyme activator activity,chloroplast,chloroplast,chloroplast,chloroplast,plastid,plastid,chloroplast stroma,thylakoid membrane organization,regulation of chlorophyll biosynthetic process,regulation of starch biosynthetic process,carotenoid biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway,removal of superoxide radicals,removal of superoxide radicals,hydrogen peroxide catabolic process,hydrogen peroxide catabolic process,identical protein binding,positive regulation of catalytic activity,cell redox homeostasis,cell redox homeostasis,response to cadmium ion,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp32337_c0_seq20.p3	sp|Q70G58|NTRC_ORYSJ_Thioredoxin_reductase_NTRC_OS=Oryza_sativa_subsp._japonica_GN=Os07g0657900_PE=1_SV=1	7.00E-32	GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0008047,GO:0009507,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009536,GO:0009570,GO:0010027,GO:0010380,GO:0010581,GO:0016117,GO:0016491,GO:0016491,GO:0016491,GO:0016671,GO:0016671,GO:0016671,GO:0016671,GO:0019288,GO:0019430,GO:0019430,GO:0042744,GO:0042744,GO:0042802,GO:0043085,GO:0045454,GO:0045454,GO:0046686,GO:0050660,GO:0050660,GO:0055114,GO:0055114,GO:0055114,GO:0055114	thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,protein binding,protein binding,cytoplasm,cytoplasm,enzyme activator activity,chloroplast,chloroplast,chloroplast,chloroplast,plastid,plastid,chloroplast stroma,thylakoid membrane organization,regulation of chlorophyll biosynthetic process,regulation of starch biosynthetic process,carotenoid biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway,removal of superoxide radicals,removal of superoxide radicals,hydrogen peroxide catabolic process,hydrogen peroxide catabolic process,identical protein binding,positive regulation of catalytic activity,cell redox homeostasis,cell redox homeostasis,response to cadmium ion,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp32337_c0_seq5.p2	sp|Q70G58|NTRC_ORYSJ_Thioredoxin_reductase_NTRC_OS=Oryza_sativa_subsp._japonica_GN=Os07g0657900_PE=1_SV=1	7.00E-32	GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0004791,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0008047,GO:0009507,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009536,GO:0009570,GO:0010027,GO:0010380,GO:0010581,GO:0016117,GO:0016491,GO:0016491,GO:0016491,GO:0016671,GO:0016671,GO:0016671,GO:0016671,GO:0019288,GO:0019430,GO:0019430,GO:0042744,GO:0042744,GO:0042802,GO:0043085,GO:0045454,GO:0045454,GO:0046686,GO:0050660,GO:0050660,GO:0055114,GO:0055114,GO:0055114,GO:0055114	thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,thioredoxin-disulfide reductase activity,protein binding,protein binding,cytoplasm,cytoplasm,enzyme activator activity,chloroplast,chloroplast,chloroplast,chloroplast,plastid,plastid,chloroplast stroma,thylakoid membrane organization,regulation of chlorophyll biosynthetic process,regulation of starch biosynthetic process,carotenoid biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway,removal of superoxide radicals,removal of superoxide radicals,hydrogen peroxide catabolic process,hydrogen peroxide catabolic process,identical protein binding,positive regulation of catalytic activity,cell redox homeostasis,cell redox homeostasis,response to cadmium ion,flavin adenine dinucleotide binding,flavin adenine dinucleotide binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp32338_c0_seq2.p1	sp|Q67W65|TAF1_ORYSJ_Transcription_initiation_factor_TFIID_subunit_1_OS=Oryza_sativa_subsp._japonica_GN=TAF1_PE=2_SV=1	2.00E-20	GO:0003676,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0008270,GO:0016568	nucleic acid binding,nucleus,nucleus,transcription, DNA-templated,regulation of transcription, DNA-templated,zinc ion binding,chromatin modification
comp32341_c0_seq2.p1				
comp32342_c0_seq12.p1	sp|Q9HAU5|RENT2_HUMAN_Regulator_of_nonsense_transcripts_2_OS=Homo_sapiens_GN=UPF2_PE=1_SV=1	1.00E-42	GO:0000184,GO:0000184,GO:0000184,GO:0000184,GO:0000184,GO:0001889,GO:0003723,GO:0003723,GO:0005515,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0006406,GO:0010467,GO:0016070,GO:0016071,GO:0031100,GO:0035145,GO:0048471	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,liver development,RNA binding,RNA binding,protein binding,nucleus,cytoplasm,cytoplasm,cytosol,cytosol,cytosol,cytosol,mRNA export from nucleus,gene expression,RNA metabolic process,mRNA metabolic process,organ regeneration,exon-exon junction complex,perinuclear region of cytoplasm
comp32342_c0_seq14.p1				
comp32342_c0_seq15.p1	sp|Q13107|UBP4_HUMAN_Ubiquitin_carboxyl-terminal_hydrolase_4_OS=Homo_sapiens_GN=USP4_PE=1_SV=3	2.00E-53	GO:0000244,GO:0004197,GO:0004221,GO:0004221,GO:0004843,GO:0004843,GO:0004843,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005764,GO:0005886,GO:0006508,GO:0006511,GO:0008233,GO:0008234,GO:0016579,GO:0016579,GO:0016579,GO:0016579,GO:0016787,GO:0031397,GO:0031647,GO:0031685,GO:0034394,GO:0036459,GO:0042802,GO:0043161,GO:0046872,GO:0061136	spliceosomal tri-snRNP complex assembly,cysteine-type endopeptidase activity,ubiquitin thiolesterase activity,ubiquitin thiolesterase activity,ubiquitin-specific protease activity,ubiquitin-specific protease activity,ubiquitin-specific protease activity,protein binding,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,lysosome,plasma membrane,proteolysis,ubiquitin-dependent protein catabolic process,peptidase activity,cysteine-type peptidase activity,protein deubiquitination,protein deubiquitination,protein deubiquitination,protein deubiquitination,hydrolase activity,negative regulation of protein ubiquitination,regulation of protein stability,adenosine receptor binding,protein localization to cell surface,ubiquitinyl hydrolase activity,identical protein binding,proteasome-mediated ubiquitin-dependent protein catabolic process,metal ion binding,regulation of proteasomal protein catabolic process
comp32342_c0_seq16.p1	sp|Q13107|UBP4_HUMAN_Ubiquitin_carboxyl-terminal_hydrolase_4_OS=Homo_sapiens_GN=USP4_PE=1_SV=3	3.00E-55	GO:0000244,GO:0004197,GO:0004221,GO:0004221,GO:0004843,GO:0004843,GO:0004843,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005764,GO:0005886,GO:0006508,GO:0006511,GO:0008233,GO:0008234,GO:0016579,GO:0016579,GO:0016579,GO:0016579,GO:0016787,GO:0031397,GO:0031647,GO:0031685,GO:0034394,GO:0036459,GO:0042802,GO:0043161,GO:0046872,GO:0061136	spliceosomal tri-snRNP complex assembly,cysteine-type endopeptidase activity,ubiquitin thiolesterase activity,ubiquitin thiolesterase activity,ubiquitin-specific protease activity,ubiquitin-specific protease activity,ubiquitin-specific protease activity,protein binding,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,lysosome,plasma membrane,proteolysis,ubiquitin-dependent protein catabolic process,peptidase activity,cysteine-type peptidase activity,protein deubiquitination,protein deubiquitination,protein deubiquitination,protein deubiquitination,hydrolase activity,negative regulation of protein ubiquitination,regulation of protein stability,adenosine receptor binding,protein localization to cell surface,ubiquitinyl hydrolase activity,identical protein binding,proteasome-mediated ubiquitin-dependent protein catabolic process,metal ion binding,regulation of proteasomal protein catabolic process
comp32342_c0_seq5.p1	sp|Q9HAU5|RENT2_HUMAN_Regulator_of_nonsense_transcripts_2_OS=Homo_sapiens_GN=UPF2_PE=1_SV=1	3.00E-35	GO:0000184,GO:0000184,GO:0000184,GO:0000184,GO:0000184,GO:0001889,GO:0003723,GO:0003723,GO:0005515,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0006406,GO:0010467,GO:0016070,GO:0016071,GO:0031100,GO:0035145,GO:0048471	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,liver development,RNA binding,RNA binding,protein binding,nucleus,cytoplasm,cytoplasm,cytosol,cytosol,cytosol,cytosol,mRNA export from nucleus,gene expression,RNA metabolic process,mRNA metabolic process,organ regeneration,exon-exon junction complex,perinuclear region of cytoplasm
comp32342_c0_seq6.p1	sp|Q9HAU5|RENT2_HUMAN_Regulator_of_nonsense_transcripts_2_OS=Homo_sapiens_GN=UPF2_PE=1_SV=1	2.00E-13	GO:0000184,GO:0000184,GO:0000184,GO:0000184,GO:0000184,GO:0001889,GO:0003723,GO:0003723,GO:0005515,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0006406,GO:0010467,GO:0016070,GO:0016071,GO:0031100,GO:0035145,GO:0048471	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,liver development,RNA binding,RNA binding,protein binding,nucleus,cytoplasm,cytoplasm,cytosol,cytosol,cytosol,cytosol,mRNA export from nucleus,gene expression,RNA metabolic process,mRNA metabolic process,organ regeneration,exon-exon junction complex,perinuclear region of cytoplasm
comp32342_c0_seq6.p2	sp|Q9HAU5|RENT2_HUMAN_Regulator_of_nonsense_transcripts_2_OS=Homo_sapiens_GN=UPF2_PE=1_SV=1	3.00E-12	GO:0000184,GO:0000184,GO:0000184,GO:0000184,GO:0000184,GO:0001889,GO:0003723,GO:0003723,GO:0005515,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0006406,GO:0010467,GO:0016070,GO:0016071,GO:0031100,GO:0035145,GO:0048471	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,liver development,RNA binding,RNA binding,protein binding,nucleus,cytoplasm,cytoplasm,cytosol,cytosol,cytosol,cytosol,mRNA export from nucleus,gene expression,RNA metabolic process,mRNA metabolic process,organ regeneration,exon-exon junction complex,perinuclear region of cytoplasm
comp32342_c0_seq6.p5	sp|Q9HAU5|RENT2_HUMAN_Regulator_of_nonsense_transcripts_2_OS=Homo_sapiens_GN=UPF2_PE=1_SV=1	2.00E-37	GO:0000184,GO:0000184,GO:0000184,GO:0000184,GO:0000184,GO:0001889,GO:0003723,GO:0003723,GO:0005515,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0005829,GO:0005829,GO:0006406,GO:0010467,GO:0016070,GO:0016071,GO:0031100,GO:0035145,GO:0048471	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,liver development,RNA binding,RNA binding,protein binding,nucleus,cytoplasm,cytoplasm,cytosol,cytosol,cytosol,cytosol,mRNA export from nucleus,gene expression,RNA metabolic process,mRNA metabolic process,organ regeneration,exon-exon junction complex,perinuclear region of cytoplasm
comp32342_c0_seq8.p1				
comp32343_c0_seq10.p1				
comp32343_c0_seq3.p1				
comp32343_c0_seq4.p1				
comp32343_c0_seq6.p1				
comp32343_c0_seq7.p1				
comp32344_c0_seq15.p1				
comp32344_c0_seq16.p1				
comp32344_c0_seq19.p1				
comp32344_c0_seq22.p1				
comp32344_c0_seq23.p1				
comp32344_c0_seq7.p1				
comp32344_c0_seq8.p1	sp|Q941D6|HDA14_ARATH_Histone_deacetylase_14_OS=Arabidopsis_thaliana_GN=HDA14_PE=2_SV=1	8.00E-46	GO:0000023,GO:0005634,GO:0005634,GO:0005634,GO:0005829,GO:0006098,GO:0006351,GO:0006355,GO:0009507,GO:0010027,GO:0016556,GO:0016568,GO:0016787,GO:0019252,GO:0019288,GO:0019760,GO:0031078,GO:0032041,GO:0032129,GO:0034739,GO:0042903,GO:0043014,GO:0043621,GO:0046969,GO:0046970,GO:0048487,GO:0051721,GO:0061647,GO:0070932,GO:0070933,GO:0090042,GO:0097372	maltose metabolic process,nucleus,nucleus,nucleus,cytosol,pentose-phosphate shunt,transcription, DNA-templated,regulation of transcription, DNA-templated,chloroplast,thylakoid membrane organization,mRNA modification,chromatin modification,hydrolase activity,starch biosynthetic process,isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway,glucosinolate metabolic process,histone deacetylase activity (H3-K14 specific),NAD-dependent histone deacetylase activity (H3-K14 specific),histone deacetylase activity (H3-K9 specific),histone deacetylase activity (H4-K16 specific),tubulin deacetylase activity,alpha-tubulin binding,protein self-association,NAD-dependent histone deacetylase activity (H3-K9 specific),NAD-dependent histone deacetylase activity (H4-K16 specific),beta-tubulin binding,protein phosphatase 2A binding,histone H3-K9 modification,histone H3 deacetylation,histone H4 deacetylation,tubulin deacetylation,NAD-dependent histone deacetylase activity (H3-K18 specific)
comp32345_c0_seq2.p1				
comp32345_c0_seq2.p8				
comp32345_c0_seq4.p1				
comp32345_c1_seq1.p1				
comp32345_c1_seq3.p1				
comp32345_c1_seq3.p6				
comp32345_c1_seq9.p1				
comp32345_c1_seq9.p6				
comp32346_c0_seq2.p1	sp|Q9M3G7|ATM_ARATH_Serine/threonine-protein_kinase_ATM_OS=Arabidopsis_thaliana_GN=ATM_PE=2_SV=1	6.00E-125	GO:0000166,GO:0003677,GO:0004674,GO:0005524,GO:0005634,GO:0005634,GO:0006468,GO:0006974,GO:0007049,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016773,GO:0051321	nucleotide binding,DNA binding,protein serine/threonine kinase activity,ATP binding,nucleus,nucleus,protein phosphorylation,cellular response to DNA damage stimulus,cell cycle,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,phosphotransferase activity, alcohol group as acceptor,meiotic cell cycle
comp32346_c0_seq2.p2				
comp32346_c0_seq4.p1	sp|Q9M3G7|ATM_ARATH_Serine/threonine-protein_kinase_ATM_OS=Arabidopsis_thaliana_GN=ATM_PE=2_SV=1	3.00E-124	GO:0000166,GO:0003677,GO:0004674,GO:0005524,GO:0005634,GO:0005634,GO:0006468,GO:0006974,GO:0007049,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016773,GO:0051321	nucleotide binding,DNA binding,protein serine/threonine kinase activity,ATP binding,nucleus,nucleus,protein phosphorylation,cellular response to DNA damage stimulus,cell cycle,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,phosphotransferase activity, alcohol group as acceptor,meiotic cell cycle
comp32347_c0_seq2.p1	sp|Q9FIZ3|GSO2_ARATH_LRR_receptor-like_serine/threonine-protein_kinase_GSO2_OS=Arabidopsis_thaliana_GN=GSO2_PE=2_SV=2	2.00E-16	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0007275,GO:0008544,GO:0009553,GO:0009793,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,protein phosphorylation,multicellular organismal development,epidermis development,embryo sac development,embryo development ending in seed dormancy,membrane,membrane,integral component of membrane,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp32347_c0_seq4.p1	sp|Q9LP24|Y1571_ARATH_Probable_leucine-rich_repeat_receptor-like_protein_kinase_At1g35710_OS=Arabidopsis_thaliana_GN=At1g35710_PE=2_SV=1	2.00E-16	GO:0000165,GO:0000166,GO:0004672,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0009814,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772	MAPK cascade,nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,protein phosphorylation,defense response, incompatible interaction,membrane,membrane,integral component of membrane,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp32347_c0_seq7.p1	sp|Q9LP24|Y1571_ARATH_Probable_leucine-rich_repeat_receptor-like_protein_kinase_At1g35710_OS=Arabidopsis_thaliana_GN=At1g35710_PE=2_SV=1	9.00E-43	GO:0000165,GO:0000166,GO:0004672,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0009814,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772	MAPK cascade,nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,protein phosphorylation,defense response, incompatible interaction,membrane,membrane,integral component of membrane,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp32347_c0_seq8.p1	sp|Q9LP24|Y1571_ARATH_Probable_leucine-rich_repeat_receptor-like_protein_kinase_At1g35710_OS=Arabidopsis_thaliana_GN=At1g35710_PE=2_SV=1	4.00E-44	GO:0000165,GO:0000166,GO:0004672,GO:0004674,GO:0005524,GO:0005524,GO:0006468,GO:0009814,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016772	MAPK cascade,nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,protein phosphorylation,defense response, incompatible interaction,membrane,membrane,integral component of membrane,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp32348_c0_seq3.p1				
comp32348_c0_seq3.p2				
comp32349_c1_seq102.p1				
comp32349_c1_seq103.p1				
comp32349_c1_seq103.p2				
comp32349_c1_seq104.p1				
comp32349_c1_seq104.p2				
comp32349_c1_seq106.p1				
comp32349_c1_seq106.p2				
comp32349_c1_seq108.p1				
comp32349_c1_seq108.p3				
comp32349_c1_seq111.p1				
comp32349_c1_seq111.p4				
comp32349_c1_seq12.p1				
comp32349_c1_seq18.p1				
comp32349_c1_seq18.p3				
comp32349_c1_seq19.p1				
comp32349_c1_seq19.p2				
comp32349_c1_seq19.p3				
comp32349_c1_seq21.p1				
comp32349_c1_seq21.p2				
comp32349_c1_seq23.p1				
comp32349_c1_seq23.p2				
comp32349_c1_seq26.p1				
comp32349_c1_seq27.p1				
comp32349_c1_seq28.p1				
comp32349_c1_seq29.p2				
comp32349_c1_seq3.p1				
comp32349_c1_seq3.p2				
comp32349_c1_seq3.p3				
comp32349_c1_seq30.p1				
comp32349_c1_seq30.p2				
comp32349_c1_seq32.p1				
comp32349_c1_seq37.p1				
comp32349_c1_seq4.p1				
comp32349_c1_seq42.p1				
comp32349_c1_seq42.p2				
comp32349_c1_seq43.p1				
comp32349_c1_seq43.p2				
comp32349_c1_seq57.p1				
comp32349_c1_seq59.p1				
comp32349_c1_seq60.p1				
comp32349_c1_seq60.p2				
comp32349_c1_seq60.p3				
comp32349_c1_seq61.p1				
comp32349_c1_seq61.p4				
comp32349_c1_seq62.p1				
comp32349_c1_seq62.p2				
comp32349_c1_seq64.p1				
comp32349_c1_seq64.p2				
comp32349_c1_seq69.p1				
comp32349_c1_seq71.p1				
comp32349_c1_seq71.p2				
comp32349_c1_seq71.p3				
comp32349_c1_seq73.p1				
comp32349_c1_seq73.p2				
comp32349_c1_seq73.p3				
comp32349_c1_seq74.p1				
comp32349_c1_seq75.p1				
comp32349_c1_seq75.p2				
comp32349_c1_seq75.p3				
comp32349_c1_seq78.p1				
comp32349_c1_seq78.p2				
comp32349_c1_seq78.p3				
comp32349_c1_seq80.p1				
comp32349_c1_seq83.p1				
comp32349_c1_seq83.p2				
comp32349_c1_seq85.p1				
comp32349_c1_seq85.p2				
comp32349_c1_seq85.p3				
comp32349_c1_seq85.p4				
comp32349_c1_seq92.p1				
comp32349_c1_seq94.p1				
comp32349_c1_seq95.p1				
comp32349_c1_seq95.p2				
comp32349_c1_seq96.p1				
comp32349_c1_seq98.p1				
comp32350_c0_seq1.p1				
comp32350_c0_seq1.p2				
comp32350_c0_seq1.p3				
comp32350_c0_seq2.p1				
comp32350_c0_seq4.p1				
comp32352_c0_seq1.p1				
comp32352_c0_seq3.p1				
comp32352_c0_seq6.p1				
comp32353_c1_seq1.p1				
comp32353_c1_seq2.p1				
comp32353_c2_seq1.p2				
comp32353_c2_seq18.p1	sp|O24362|PSA3_SPIOL_Proteasome_subunit_alpha_type-3_OS=Spinacia_oleracea_GN=PAG1_PE=2_SV=1	1.00E-103	GO:0000502,GO:0004175,GO:0004298,GO:0004298,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005839,GO:0006508,GO:0006511,GO:0008233,GO:0016787,GO:0019773,GO:0051603	proteasome complex,endopeptidase activity,threonine-type endopeptidase activity,threonine-type endopeptidase activity,nucleus,nucleus,cytoplasm,cytoplasm,proteasome core complex,proteolysis,ubiquitin-dependent protein catabolic process,peptidase activity,hydrolase activity,proteasome core complex, alpha-subunit complex,proteolysis involved in cellular protein catabolic process
comp32353_c2_seq19.p1	sp|Q05355|HYDL_STRHA_Putative_polyketide_hydroxylase_OS=Streptomyces_halstedii_GN=schC_PE=3_SV=1	1.00E-41	GO:0008152,GO:0016491,GO:0016491,GO:0055114	metabolic process,oxidoreductase activity,oxidoreductase activity,oxidation-reduction process
comp32353_c2_seq19.p2				
comp32353_c2_seq2.p1	sp|Q7SCY7|SYM1_NEUCR_Protein_sym-1_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=sym-1_PE=3_SV=2	2.00E-17	GO:0005739,GO:0005743,GO:0005743,GO:0016020,GO:0016021,GO:0016021	mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,membrane,integral component of membrane,integral component of membrane
comp32353_c2_seq25.p1				
comp32353_c2_seq25.p2				
comp32353_c2_seq25.p3	sp|P39888|TCMG_STRGA_Tetracenomycin_polyketide_synthesis_hydroxylase_tcmG_OS=Streptomyces_glaucescens_GN=tcmG_PE=3_SV=1	4.00E-22	GO:0008152,GO:0016491,GO:0016491,GO:0017000,GO:0055114	metabolic process,oxidoreductase activity,oxidoreductase activity,antibiotic biosynthetic process,oxidation-reduction process
comp32353_c2_seq25.p7				
comp32353_c2_seq26.p1	sp|Q8NBP0|TTC13_HUMAN_Tetratricopeptide_repeat_protein_13_OS=Homo_sapiens_GN=TTC13_PE=2_SV=3	2.00E-56		
comp32353_c2_seq3.p1	sp|Q05355|HYDL_STRHA_Putative_polyketide_hydroxylase_OS=Streptomyces_halstedii_GN=schC_PE=3_SV=1	1.00E-40	GO:0008152,GO:0016491,GO:0016491,GO:0055114	metabolic process,oxidoreductase activity,oxidoreductase activity,oxidation-reduction process
comp32353_c2_seq4.p1	sp|P39888|TCMG_STRGA_Tetracenomycin_polyketide_synthesis_hydroxylase_tcmG_OS=Streptomyces_glaucescens_GN=tcmG_PE=3_SV=1	3.00E-20	GO:0008152,GO:0016491,GO:0016491,GO:0017000,GO:0055114	metabolic process,oxidoreductase activity,oxidoreductase activity,antibiotic biosynthetic process,oxidation-reduction process
comp32353_c2_seq4.p2				
comp32353_c2_seq4.p6				
comp32353_c2_seq9.p1				
comp32353_c2_seq9.p2	sp|Q7SCY7|SYM1_NEUCR_Protein_sym-1_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=sym-1_PE=3_SV=2	2.00E-17	GO:0005739,GO:0005743,GO:0005743,GO:0016020,GO:0016021,GO:0016021	mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,membrane,integral component of membrane,integral component of membrane
comp32354_c0_seq1.p1				

comp32355_c0_seq10.p1				
comp32355_c0_seq12.p1				
comp32355_c0_seq19.p1				
comp32358_c0_seq4.p1				
comp32358_c0_seq5.p2				
comp32358_c0_seq5.p3				
comp32360_c0_seq15.p1	sp|Q14AT5|ANO7_MOUSE_Anoctamin-7_OS=Mus_musculus_GN=Ano7_PE=2_SV=2	4.00E-53	GO:0005229,GO:0005622,GO:0005634,GO:0005783,GO:0005783,GO:0005783,GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006821,GO:0006869,GO:0016020,GO:0016021,GO:0017128,GO:0061589,GO:0061590,GO:0061591,GO:1902476	intracellular calcium activated chloride channel activity,intracellular,nucleus,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,plasma membrane,plasma membrane,plasma membrane,transport,chloride transport,lipid transport,membrane,integral component of membrane,phospholipid scramblase activity,calcium activated phosphatidylserine scrambling,calcium activated phosphatidylcholine scrambling,calcium activated galactosylceramide scrambling,chloride transmembrane transport
comp32360_c0_seq8.p1	sp|Q6IWH7|ANO7_HUMAN_Anoctamin-7_OS=Homo_sapiens_GN=ANO7_PE=1_SV=2	3.00E-56	GO:0005229,GO:0005622,GO:0005622,GO:0005634,GO:0005737,GO:0005783,GO:0005783,GO:0005783,GO:0005829,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006821,GO:0006821,GO:0006869,GO:0016020,GO:0016021,GO:0017128,GO:0030054,GO:0030054,GO:0034220,GO:0055085,GO:0061589,GO:0061590,GO:0061591,GO:1902476,GO:0005229,GO:0005229	intracellular calcium activated chloride channel activity,intracellular,intracellular,nucleus,cytoplasm,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,cytosol,plasma membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,transport,chloride transport,chloride transport,lipid transport,membrane,integral component of membrane,phospholipid scramblase activity,cell junction,cell junction,ion transmembrane transport,transmembrane transport,calcium activated phosphatidylserine scrambling,calcium activated phosphatidylcholine scrambling,calcium activated galactosylceramide scrambling,chloride transmembrane transport,intracellular calcium activated chloride channel activity,intracellular calcium activated chloride channel activity
comp32360_c0_seq9.p1	sp|Q01484|ANK2_HUMAN_Ankyrin-2_OS=Homo_sapiens_GN=ANK2_PE=1_SV=3	1.00E-28	GO:0002027,GO:0002027,GO:0003283,GO:0005200,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005622,GO:0005622,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0005856,GO:0005856,GO:0005856,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005887,GO:0006874,GO:0006874,GO:0007165,GO:0007399,GO:0007411,GO:0008104,GO:0010628,GO:0010628,GO:0010881,GO:0010881,GO:0010882,GO:0010882,GO:0014704,GO:0014704,GO:0015459,GO:0016020,GO:0016020,GO:0016323,GO:0016324,GO:0019899,GO:0019901,GO:0019901,GO:0030018,GO:0030018,GO:0030054,GO:0030315,GO:0030315,GO:0030507,GO:0030674,GO:0030674,GO:0030913,GO:0031430,GO:0031430,GO:0031430,GO:0031647,GO:0031672,GO:0031672,GO:0033292,GO:0033292,GO:0033365,GO:0034394,GO:0034394,GO:0034613,GO:0034613,GO:0034613,GO:0036309,GO:0036309,GO:0036309,GO:0036371,GO:0036371,GO:0042383,GO:0042383,GO:0043005,GO:0043034,GO:0043034,GO:0043268,GO:0043268,GO:0044325,GO:0044325,GO:0044325,GO:0044325,GO:0045121,GO:0045202,GO:0045211,GO:0045211,GO:0048471,GO:0050821,GO:0050821,GO:0051117,GO:0051117,GO:0051279,GO:0051597,GO:0051924,GO:0051924,GO:0051924,GO:0051928,GO:0051928,GO:0055117,GO:0055117,GO:0060048,GO:0060307,GO:0070296,GO:0070972,GO:0070972,GO:0072659,GO:0072659,GO:0072659,GO:0072659,GO:0072659,GO:0072661,GO:0086004,GO:0086004,GO:0086005,GO:0086014,GO:0086014,GO:0086014,GO:0086014,GO:0086015,GO:0086015,GO:0086036,GO:0086046,GO:0086066,GO:0086066,GO:0086070,GO:0086070,GO:0086070,GO:0086070,GO:0086091,GO:0086091,GO:0086091,GO:0086091,GO:0086091,GO:0086091,GO:1901018,GO:1901018,GO:1901019,GO:1901019,GO:1901021,GO:1901021,GO:2001257,GO:2001259,GO:2001259	regulation of heart rate,regulation of heart rate,atrial septum development,structural constituent of cytoskeleton,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,intracellular,intracellular,cytoplasm,cytoplasm,cytosol,cytosol,cytoskeleton,cytoskeleton,cytoskeleton,plasma membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,integral component of plasma membrane,cellular calcium ion homeostasis,cellular calcium ion homeostasis,signal transduction,nervous system development,axon guidance,protein localization,positive regulation of gene expression,positive regulation of gene expression,regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion,regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion,regulation of cardiac muscle contraction by calcium ion signaling,regulation of cardiac muscle contraction by calcium ion signaling,intercalated disc,intercalated disc,potassium channel regulator activity,membrane,membrane,basolateral plasma membrane,apical plasma membrane,enzyme binding,protein kinase binding,protein kinase binding,Z disc,Z disc,cell junction,T-tubule,T-tubule,spectrin binding,protein binding, bridging,protein binding, bridging,paranodal junction assembly,M band,M band,M band,regulation of protein stability,A band,A band,T-tubule organization,T-tubule organization,protein localization to organelle,protein localization to cell surface,protein localization to cell surface,cellular protein localization,cellular protein localization,cellular protein localization,protein localization to M-band,protein localization to M-band,protein localization to M-band,protein localization to T-tubule,protein localization to T-tubule,sarcolemma,sarcolemma,neuron projection,costamere,costamere,positive regulation of potassium ion transport,positive regulation of potassium ion transport,ion channel binding,ion channel binding,ion channel binding,ion channel binding,membrane raft,synapse,postsynaptic membrane,postsynaptic membrane,perinuclear region of cytoplasm,protein stabilization,protein stabilization,ATPase binding,ATPase binding,regulation of release of sequestered calcium ion into cytosol,response to methylmercury,regulation of calcium ion transport,regulation of calcium ion transport,regulation of calcium ion transport,positive regulation of calcium ion transport,positive regulation of calcium ion transport,regulation of cardiac muscle contraction,regulation of cardiac muscle contraction,cardiac muscle contraction,cardiac muscle contraction,regulation of ventricular cardiac muscle cell membrane repolarization,sarcoplasmic reticulum calcium ion transport,protein localization to endoplasmic reticulum,protein localization to plasma membrane,protein localization to plasma membrane,protein localization to plasma membrane,protein localization to plasma membrane,protein localization to plasma membrane,protein targeting to plasma membrane,regulation of cardiac muscle cell contraction,regulation of cardiac muscle cell contraction,ventricular cardiac muscle cell action potential,atrial cardiac muscle cell action potential,atrial cardiac muscle cell action potential,atrial cardiac muscle cell action potential,atrial cardiac muscle cell action potential,SA node cell action potential,SA node cell action potential,regulation of cardiac muscle cell membrane potential,membrane depolarization during SA node cell action potential,atrial cardiac muscle cell to AV node cell communication,atrial cardiac muscle cell to AV node cell communication,SA node cell to atrial cardiac muscle cell communication,SA node cell to atrial cardiac muscle cell communication,SA node cell to atrial cardiac muscle cell communication,SA node cell to atrial cardiac muscle cell communication,regulation of heart rate by cardiac conduction,regulation of heart rate by cardiac conduction,regulation of heart rate by cardiac conduction,regulation of heart rate by cardiac conduction,regulation of heart rate by cardiac conduction,regulation of heart rate by cardiac conduction,positive regulation of potassium ion transmembrane transporter activity,positive regulation of potassium ion transmembrane transporter activity,regulation of calcium ion transmembrane transporter activity,regulation of calcium ion transmembrane transporter activity,positive regulation of calcium ion transmembrane transporter activity,positive regulation of calcium ion transmembrane transporter activity,regulation of cation channel activity,positive regulation of cation channel activity,positive regulation of cation channel activity
comp32360_c1_seq1.p1				
comp32361_c0_seq6.p1	sp|Q9C8Z4|HEAT1_ARATH_Uncharacterized_protein_At3g06530_OS=Arabidopsis_thaliana_GN=At3g06530_PE=2_SV=3	4.00E-35	GO:0005634,GO:0005730,GO:0006364,GO:0030529,GO:0042254	nucleus,nucleolus,rRNA processing,ribonucleoprotein complex,ribosome biogenesis
comp32361_c0_seq6.p2	sp|Q54ML4|HEAT1_DICDI_HEAT_repeat-containing_protein_1_homolog_OS=Dictyostelium_discoideum_GN=heatr1_PE=3_SV=1	3.00E-54	GO:0000462,GO:0005634,GO:0005730,GO:0005732,GO:0006364,GO:0006364,GO:0030515,GO:0030515,GO:0030529,GO:0030686,GO:0032040,GO:0034455,GO:0042254,GO:0045943	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),nucleus,nucleolus,small nucleolar ribonucleoprotein complex,rRNA processing,rRNA processing,snoRNA binding,snoRNA binding,ribonucleoprotein complex,90S preribosome,small-subunit processome,t-UTP complex,ribosome biogenesis,positive regulation of transcription from RNA polymerase I promoter
comp32361_c0_seq9.p1	sp|Q54ML4|HEAT1_DICDI_HEAT_repeat-containing_protein_1_homolog_OS=Dictyostelium_discoideum_GN=heatr1_PE=3_SV=1	2.00E-52	GO:0000462,GO:0005634,GO:0005730,GO:0005732,GO:0006364,GO:0006364,GO:0030515,GO:0030515,GO:0030529,GO:0030686,GO:0032040,GO:0034455,GO:0042254,GO:0045943	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),nucleus,nucleolus,small nucleolar ribonucleoprotein complex,rRNA processing,rRNA processing,snoRNA binding,snoRNA binding,ribonucleoprotein complex,90S preribosome,small-subunit processome,t-UTP complex,ribosome biogenesis,positive regulation of transcription from RNA polymerase I promoter
comp32362_c0_seq5.p1				
comp32362_c0_seq5.p3				
comp32362_c0_seq7.p1				
comp32362_c0_seq7.p4				
comp32362_c1_seq1.p1				
comp32363_c0_seq4.p1	sp|Q8IRG6|SPT16_DROME_FACT_complex_subunit_spt16_OS=Drosophila_melanogaster_GN=dre4_PE=1_SV=2	5.00E-70	GO:0001672,GO:0003682,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0006260,GO:0006281,GO:0006351,GO:0006355,GO:0006974,GO:0022008,GO:0032968,GO:0035101,GO:0035101	regulation of chromatin assembly or disassembly,chromatin binding,nucleus,nucleus,nucleus,chromosome,chromosome,DNA replication,DNA repair,transcription, DNA-templated,regulation of transcription, DNA-templated,cellular response to DNA damage stimulus,neurogenesis,positive regulation of transcription elongation from RNA polymerase II promoter,FACT complex,FACT complex
comp32363_c0_seq4.p2	sp|Q9FMA3|PEX5_ARATH_Peroxisome_biogenesis_protein_5_OS=Arabidopsis_thaliana_GN=PEX5_PE=1_SV=1	2.00E-71	GO:0005052,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0005777,GO:0005778,GO:0005778,GO:0005829,GO:0006625,GO:0006635,GO:0006810,GO:0006810,GO:0006869,GO:0006891,GO:0007031,GO:0009062,GO:0009733,GO:0010351,GO:0015031,GO:0016020,GO:0016558,GO:0016558,GO:0016560	peroxisome matrix targeting signal-1 binding,protein binding,protein binding,protein binding,protein binding,cytoplasm,cytoplasm,peroxisome,peroxisomal membrane,peroxisomal membrane,cytosol,protein targeting to peroxisome,fatty acid beta-oxidation,transport,transport,lipid transport,intra-Golgi vesicle-mediated transport,peroxisome organization,fatty acid catabolic process,response to auxin,lithium ion transport,protein transport,membrane,protein import into peroxisome matrix,protein import into peroxisome matrix,protein import into peroxisome matrix, docking
comp32363_c0_seq9.p1				
comp32364_c0_seq2.p1	sp|P24280|SEC14_YEAST_SEC14_cytosolic_factor_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=SEC14_PE=1_SV=3	7.00E-21	GO:0000139,GO:0000139,GO:0005215,GO:0005515,GO:0005515,GO:0005622,GO:0005737,GO:0005794,GO:0005794,GO:0005829,GO:0005829,GO:0006810,GO:0006810,GO:0006896,GO:0006896,GO:0008525,GO:0008525,GO:0008525,GO:0008525,GO:0008526,GO:0008526,GO:0008526,GO:0008526,GO:0008526,GO:0015031,GO:0015914,GO:0015914,GO:0015914,GO:0015914,GO:0016020,GO:0030437,GO:0043001,GO:0043001,GO:0043001,GO:0046488,GO:0046488,GO:0048194,GO:0048194,GO:1901352,GO:2001246,GO:2001246	Golgi membrane,Golgi membrane,transporter activity,protein binding,protein binding,intracellular,cytoplasm,Golgi apparatus,Golgi apparatus,cytosol,cytosol,transport,transport,Golgi to vacuole transport,Golgi to vacuole transport,phosphatidylcholine transporter activity,phosphatidylcholine transporter activity,phosphatidylcholine transporter activity,phosphatidylcholine transporter activity,phosphatidylinositol transporter activity,phosphatidylinositol transporter activity,phosphatidylinositol transporter activity,phosphatidylinositol transporter activity,phosphatidylinositol transporter activity,protein transport,phospholipid transport,phospholipid transport,phospholipid transport,phospholipid transport,membrane,ascospore formation,Golgi to plasma membrane protein transport,Golgi to plasma membrane protein transport,Golgi to plasma membrane protein transport,phosphatidylinositol metabolic process,phosphatidylinositol metabolic process,Golgi vesicle budding,Golgi vesicle budding,negative regulation of phosphatidylglycerol biosynthetic process,negative regulation of phosphatidylcholine biosynthetic process,negative regulation of phosphatidylcholine biosynthetic process
comp32364_c0_seq4.p1	sp|P24280|SEC14_YEAST_SEC14_cytosolic_factor_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=SEC14_PE=1_SV=3	7.00E-21	GO:0000139,GO:0000139,GO:0005215,GO:0005515,GO:0005515,GO:0005622,GO:0005737,GO:0005794,GO:0005794,GO:0005829,GO:0005829,GO:0006810,GO:0006810,GO:0006896,GO:0006896,GO:0008525,GO:0008525,GO:0008525,GO:0008525,GO:0008526,GO:0008526,GO:0008526,GO:0008526,GO:0008526,GO:0015031,GO:0015914,GO:0015914,GO:0015914,GO:0015914,GO:0016020,GO:0030437,GO:0043001,GO:0043001,GO:0043001,GO:0046488,GO:0046488,GO:0048194,GO:0048194,GO:1901352,GO:2001246,GO:2001246	Golgi membrane,Golgi membrane,transporter activity,protein binding,protein binding,intracellular,cytoplasm,Golgi apparatus,Golgi apparatus,cytosol,cytosol,transport,transport,Golgi to vacuole transport,Golgi to vacuole transport,phosphatidylcholine transporter activity,phosphatidylcholine transporter activity,phosphatidylcholine transporter activity,phosphatidylcholine transporter activity,phosphatidylinositol transporter activity,phosphatidylinositol transporter activity,phosphatidylinositol transporter activity,phosphatidylinositol transporter activity,phosphatidylinositol transporter activity,protein transport,phospholipid transport,phospholipid transport,phospholipid transport,phospholipid transport,membrane,ascospore formation,Golgi to plasma membrane protein transport,Golgi to plasma membrane protein transport,Golgi to plasma membrane protein transport,phosphatidylinositol metabolic process,phosphatidylinositol metabolic process,Golgi vesicle budding,Golgi vesicle budding,negative regulation of phosphatidylglycerol biosynthetic process,negative regulation of phosphatidylcholine biosynthetic process,negative regulation of phosphatidylcholine biosynthetic process
comp32365_c0_seq1.p2				
comp32365_c0_seq1.p5	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	5.00E-14	GO:0000166,GO:0003676,GO:0004190,GO:0005524,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016787,GO:0046872	nucleotide binding,nucleic acid binding,aspartic-type endopeptidase activity,ATP binding,proteolysis,peptidase activity,zinc ion binding,DNA integration,hydrolase activity,metal ion binding
comp32366_c0_seq14.p1	sp|Q8K4P0|WDR33_MOUSE_pre-mRNA_3'_end_processing_protein_WDR33_OS=Mus_musculus_GN=Wdr33_PE=2_SV=1	3.00E-23	GO:0005581,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005847,GO:0006378,GO:0006379,GO:0006397,GO:0008150,GO:0044822	collagen trimer,nucleus,nucleus,nucleus,nucleus,mRNA cleavage and polyadenylation specificity factor complex,mRNA polyadenylation,mRNA cleavage,mRNA processing,biological_process,poly(A) RNA binding
comp32366_c0_seq18.p1				
comp32366_c0_seq3.p1	sp|Q6NLV4|FY_ARATH_Flowering_time_control_protein_FY_OS=Arabidopsis_thaliana_GN=FY_PE=1_SV=1	3.00E-127	GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0007275,GO:0009908,GO:0030154	protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,multicellular organismal development,flower development,cell differentiation
comp32366_c0_seq6.p1				

comp32436_c1_seq5.p1	sp|Q38931|FKB62_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP62_OS=Arabidopsis_thaliana_GN=FKBP62_PE=1_SV=2	5.00E-16	[illegible]	[illegible]
comp32437_c0_seq3.p1	sp|P0CI65|NPHP3_DANRE_Nephrocystin-3_OS=Danio_rerio_GN=nphp3_PE=3_SV=1	5.00E-21	GO:0005929,GO:0005929,GO:0016055,GO:0042995,GO:0060271,GO:0072372	[illegible]
comp32438_c0_seq1.p4				
comp32438_c0_seq3.p2	sp|Q9UR07|RTF23_SCHPO_Retrotransposable_element_Tf2_155_kDa_protein_type_3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=Tf2-11_PE=4_SV=1	8.00E-12	[illegible]	[illegible]
comp32438_c0_seq6.p2				
comp32438_c0_seq9.p2				
comp32438_c0_seq9.p5				
comp32439_c0_seq10.p1				
comp32439_c0_seq12.p1				
comp32439_c0_seq13.p1				
comp32439_c0_seq13.p3				
comp32439_c0_seq14.p1				
comp32439_c0_seq18.p1				
comp32439_c0_seq22.p1				
comp32439_c0_seq3.p1				
comp32439_c0_seq5.p1				
comp32439_c0_seq6.p1				
comp32439_c0_seq7.p1				
comp32439_c0_seq8.p1				
comp32440_c0_seq16.p2				
comp32440_c0_seq18.p1				
comp32440_c0_seq20.p2				
comp32440_c0_seq22.p1				
comp32440_c0_seq7.p2				
comp32440_c0_seq8.p1				
comp32441_c0_seq1.p1				
comp32442_c0_seq12.p1				
comp32442_c0_seq13.p1				
comp32442_c0_seq16.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-16	[illegible]	[illegible]
comp32442_c0_seq2.p1				
comp32442_c0_seq2.p3				
comp32442_c0_seq5.p1				
comp32442_c0_seq9.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-17	[illegible]	[illegible]
comp32442_c0_seq9.p2				
comp32443_c0_seq1.p1				
comp32443_c0_seq5.p1	sp|Q90ZC7|KCMA1_XENLA_Calcium-activated_potassium_channel_subunit_alpha-1_OS=Xenopus_laevis_GN=kcnma1_PE=2_SV=1	2.00E-19	[illegible]	[illegible]
comp32444_c0_seq2.p1				
comp32444_c0_seq2.p2				
comp32444_c0_seq4.p1				
comp32444_c0_seq5.p1				
comp32445_c0_seq1.p1	sp|Q09172|PP2C2_SCHPO_Protein_phosphatase_2C_homolog_2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ptc2_PE=2_SV=1	6.00E-33	[illegible]	[illegible]
comp32445_c0_seq10.p1				
comp32445_c0_seq12.p1				
comp32445_c0_seq12.p2				
comp32445_c0_seq2.p1	sp|Q09172|PP2C2_SCHPO_Protein_phosphatase_2C_homolog_2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ptc2_PE=2_SV=1	7.00E-48	[illegible]	[illegible]
comp32445_c0_seq3.p1				
comp32446_c0_seq2.p1	sp|Q9P959|AOX_EMENI_Alternative_oxidase,_mitochondrial_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=alxA_PE=3_SV=2	2.00E-71	[illegible]	[illegible]
comp32446_c0_seq3.p1	sp|O74180|AOX_ASPNG_Alternative_oxidase,_mitochondrial_OS=Aspergillus_niger_GN=aox1_PE=2_SV=2	2.00E-20	[illegible]	[illegible]
comp32446_c0_seq4.p1	sp|O74180|AOX_ASPNG_Alternative_oxidase,_mitochondrial_OS=Aspergillus_niger_GN=aox1_PE=2_SV=2	2.00E-61	[illegible]	[illegible]
comp32447_c1_seq5.p1				
comp32447_c1_seq6.p1	sp|O14735|CDIPT_HUMAN_CDP-diacylglycerol--inositol_3-phosphatidyltransferase_OS=Homo_sapiens_GN=CDIPT_PE=1_SV=1	1.00E-33	[illegible]	[illegible]
comp32447_c1_seq8.p1				
comp32448_c0_seq1.p1	sp|P08640|MUC1_YEAST_Flocculation_protein_FLO11_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=MUC1_PE=1_SV=2	7.00E-12	[illegible]	[illegible]
comp32448_c0_seq12.p1	sp|Q4U2R1|HERC2_MOUSE_E3_ubiquitin-protein_ligase_HERC2_OS=Mus_musculus_GN=Herc2_PE=1_SV=3	4.00E-65	[illegible]	[illegible]
comp32448_c0_seq12.p4				
comp32448_c0_seq2.p1				
comp32448_c0_seq4.p1	sp|Q4U2R1|HERC2_MOUSE_E3_ubiquitin-protein_ligase_HERC2_OS=Mus_musculus_GN=Herc2_PE=1_SV=3	4.00E-65	[illegible]	[illegible]
comp32448_c0_seq4.p4				
comp32448_c0_seq6.p1				
comp32448_c0_seq9.p1	sp|Q4U2R1|HERC2_MOUSE_E3_ubiquitin-protein_ligase_HERC2_OS=Mus_musculus_GN=Herc2_PE=1_SV=3	7.00E-60	[illegible]	[illegible]
comp32448_c0_seq9.p4				
comp32448_c1_seq1.p1				
comp32448_c1_seq6.p1				
comp32449_c0_seq2.p1				
comp32450_c1_seq1.p1				
comp32450_c1_seq4.p2				
comp32451_c0_seq1.p1	sp|Q0EEE2|PTHD3_MOUSE_Patched_domain-containing_protein_3_OS=Mus_musculus_GN=Ptchd3_PE=1_SV=1	3.00E-62	[illegible]	[illegible]
comp32451_c0_seq2.p1	sp|Q0EEE2|PTHD3_MOUSE_Patched_domain-containing_protein_3_OS=Mus_musculus_GN=Ptchd3_PE=1_SV=1	8.00E-16	[illegible]	[illegible]
comp32451_c0_seq2.p3	sp|Q6T3U4|NPCL1_MOUSE_Niemann-Pick_C1-like_protein_1_OS=Mus_musculus_GN=Npc1l1_PE=2_SV=1	1.00E-30	[illegible]	[illegible]
comp32451_c0_seq3.p1	sp|Q0EEE2|PTHD3_MOUSE_Patched_domain-containing_protein_3_OS=Mus_musculus_GN=Ptchd3_PE=1_SV=1	8.00E-16	[illegible]	[illegible]
comp32451_c0_seq3.p3	sp|Q6T3U4|NPCL1_MOUSE_Niemann-Pick_C1-like_protein_1_OS=Mus_musculus_GN=Npc1l1_PE=2_SV=1	1.00E-30	[illegible]	[illegible]
comp32451_c0_seq4.p1	sp|Q0EEE2|PTHD3_MOUSE_Patched_domain-containing_protein_3_OS=Mus_musculus_GN=Ptchd3_PE=1_SV=1	4.00E-53	[illegible]	[illegible]
comp32451_c0_seq5.p1	sp|Q0EEE2|PTHD3_MOUSE_Patched_domain-containing_protein_3_OS=Mus_musculus_GN=Ptchd3_PE=1_SV=1	5.00E-53	[illegible]	[illegible]
comp32451_c0_seq6.p1	sp|Q0EEE2|PTHD3_MOUSE_Patched_domain-containing_protein_3_OS=Mus_musculus_GN=Ptchd3_PE=1_SV=1	3.00E-62	[illegible]	[illegible]
comp32452_c0_seq1.p1				
comp32452_c0_seq2.p1				
comp32453_c0_seq2.p3				
comp32453_c0_seq5.p2				
comp32453_c0_seq8.p1				
comp32456_c0_seq12.p1				
comp32456_c0_seq13.p1				
comp32456_c0_seq17.p1				
comp32456_c0_seq18.p1				
comp32456_c0_seq3.p1				
comp32457_c0_seq10.p1	sp|P80193|BODG_PSESK_Gamma-butyrobetaine_dioxygenase_OS=Pseudomonas_sp._(strain_AK-1)_PE=1_SV=1	1.00E-17	[illegible]	[illegible]
comp32457_c0_seq14.p1	sp|P80193|BODG_PSESK_Gamma-butyrobetaine_dioxygenase_OS=Pseudomonas_sp._(strain_AK-1)_PE=1_SV=1	3.00E-11	[illegible]	[illegible]
comp32457_c0_seq17.p1				
comp32457_c0_seq23.p1	sp|Q9P3U1|YKX5_SCHPO_Uncharacterized_RNA-binding_protein_C328.05_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC328.05_PE=2_SV=2	1.00E-28	[illegible]	[illegible]
comp32457_c0_seq23.p4				
comp32457_c0_seq27.p1	sp|Q9P3U1|YKX5_SCHPO_Uncharacterized_RNA-binding_protein_C328.05_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC328.05_PE=2_SV=2	2.00E-28	[illegible]	[illegible]
comp32458_c0_seq1.p1				
comp32458_c0_seq10.p1				
comp32458_c0_seq11.p1				
comp32458_c0_seq12.p1				
comp32458_c0_seq16.p1				
comp32458_c0_seq17.p1				
comp32458_c0_seq19.p2	sp|O49627|ISU1_ARATH_Iron-sulfur_cluster_assembly_protein_1_OS=Arabidopsis_thaliana_GN=ISU1_PE=2_SV=1	5.00E-62	[illegible]	[illegible]
comp32458_c0_seq19.p4				
comp32458_c0_seq20.p1				
comp32459_c0_seq1.p1				
comp32460_c0_seq4.p1				
comp32461_c0_seq13.p2				
comp32461_c0_seq18.p2				
comp32461_c0_seq6.p2				
comp32461_c0_seq6.p3				
comp32463_c0_seq1.p1				
comp32463_c1_seq1.p1				
comp32463_c2_seq10.p1				
comp32463_c2_seq12.p1				
comp32463_c2_seq3.p1				
comp32463_c2_seq4.p1				
comp32463_c2_seq5.p1				
comp32463_c3_seq2.p1	sp|P22612|KAPCG_HUMAN_cAMP-dependent_protein_kinase_catalytic_subunit_gamma_OS=Homo_sapiens_GN=PRKACG_PE=1_SV=3	3.00E-34	[illegible]	[illegible]
comp32463_c4_seq1.p1				
comp32464_c0_seq1.p1				
comp32465_c0_seq10.p1				
comp32465_c0_seq11.p1				
comp32465_c0_seq7.p1				
comp32465_c0_seq7.p2				
comp32465_c0_seq8.p1				
comp32466_c0_seq2.p1				
comp32468_c3_seq1.p1	sp|Q8XCG6|CYSQ_ECO57_3'(2'),5'-bisphosphate_nucleotidase_CysQ_OS=Escherichia_coli_O157:H7_GN=cysQ_PE=3_SV=1	5.00E-43	[illegible]	[illegible]
comp32468_c3_seq10.p1				
comp32468_c3_seq12.p1				
comp32468_c3_seq16.p1				
comp32468_c3_seq4.p1				
comp32468_c3_seq6.p1				
comp32468_c3_seq7.p1	sp|Q8XCG6|CYSQ_ECO57_3'(2'),5'-bisphosphate_nucleotidase_CysQ_OS=Escherichia_coli_O157:H7_GN=cysQ_PE=3_SV=1	5.00E-40	[illegible]	[illegible]
comp32469_c0_seq1.p1	sp|Q91XS1|MTMR4_MOUSE_Myotubularin-related_protein_4_OS=Mus_musculus_GN=Mtmr4_PE=1_SV=1	2.00E-44	[illegible]	[illegible]
comp32469_c0_seq6.p1	sp|Q8VE11|MTMR6_MOUSE_Myotubularin-related_protein_6_OS=Mus_musculus_GN=Mtmr6_PE=1_SV=1	4.00E-39	[illegible]	[illegible]
comp32469_c0_seq7.p1				
comp32469_c1_seq2.p1				
comp32469_c2_seq1.p2				
comp32469_c2_seq10.p1				
comp32469_c2_seq12.p2				
comp32469_c2_seq5.p2				
comp32469_c2_seq5.p3				
comp32469_c2_seq6.p2				
comp32469_c2_seq6.p3				
comp32469_c2_seq8.p2				
comp32469_c2_seq8.p4				
comp32469_c2_seq9.p2				
comp32470_c0_seq8.p1				
comp32470_c0_seq9.p1				
comp32471_c0_seq1.p1				
comp32471_c1_seq2.p1				
comp32471_c1_seq5.p1				
comp32472_c0_seq1.p1	sp|Q55DM1|LVSA_DICDI_BEACH_domain-containing_protein_lvsA_OS=Dictyostelium_discoideum_GN=lvsA_PE=4_SV=2	1.00E-118	[illegible]	[illegible]
comp32472_c0_seq1.p2				
comp32473_c0_seq11.p1				
comp32473_c0_seq11.p2				
comp32473_c3_seq1.p1	sp|P23903|E13B_BACCI_Glucan_endo-1,3-beta-glucosidase_A1_OS=Bacillus_circulans_GN=glcA_PE=1_SV=1	2.00E-44	[illegible]	[illegible]
comp32474_c0_seq1.p1				
comp32474_c0_seq6.p1				
comp32474_c1_seq1.p1	sp|Q5UQR2|YL320_MIMIV_Uncharacterized_protein_L320_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L320_PE=4_SV=1	8.00E-15	GO:0001510,GO:0003676,GO:0008168,GO:0009452,GO:0032259	[illegible]
comp32474_c1_seq3.p3				
comp32477_c0_seq10.p1				
comp32477_c0_seq7.p1				
comp32478_c0_seq1.p1				
comp32479_c0_seq1.p1				
comp32479_c0_seq10.p1				
comp32479_c0_seq5.p1				
comp32479_c0_seq6.p1				
comp3248_c0_seq1.p1				
comp32480_c0_seq10.p1	sp|P21951|DPOE_YEAST_DNA_polymerase_epsilon_catalytic_subunit_A_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=POL2_PE=1_SV=1	5.00E-116	[illegible]	[illegible]
comp32480_c0_seq10.p2	sp|Q07864|DPOE1_HUMAN_DNA_polymerase_epsilon_catalytic_subunit_A_OS=Homo_sapiens_GN=POLE_PE=1_SV=5	0	[illegible]	[illegible]
comp32480_c0_seq13.p1	sp|Q6CUS7|DPOE_KLULA_DNA_polymerase_epsilon_catalytic_subunit_A_OS=Kluyveromyces_lactis_(strain_ATCC_8585_/_CBS_2359_/_DSM_70799_/_NBRC_1267_/_NRRL_Y-1140_/_WM37)_GN=POL2_PE=3_SV=1	9.00E-140	[illegible]	[illegible]
comp32480_c0_seq13.p2	sp|Q07864|DPOE1_HUMAN_DNA_polymerase_epsilon_catalytic_subunit_A_OS=Homo_sapiens_GN=POLE_PE=1_SV=5	0	[illegible]	[illegible]
comp32480_c0_seq23.p1	sp|Q07864|DPOE1_HUMAN_DNA_polymerase_epsilon_catalytic_subunit_A_OS=Homo_sapiens_GN=POLE_PE=1_SV=5	0	[illegible]	[illegible]
comp32480_c0_seq24.p1	sp|Q07864|DPOE1_HUMAN_DNA_polymerase_epsilon_catalytic_subunit_A_OS=Homo_sapiens_GN=POLE_PE=1_SV=5	0	[illegible]	[illegible]
comp32480_c0_seq25.p1				
comp32481_c0_seq2.p1	sp|A1Z9E2|LIN54_DROME_Protein_lin-54_homolog_OS=Drosophila_melanogaster_GN=mip120_PE=1_SV=1	6.00E-13	[illegible]	[illegible]
comp32481_c0_seq4.p2				
comp32482_c0_seq2.p1				
comp32482_c0_seq2.p2				
comp32483_c0_seq4.p1				
comp32484_c0_seq2.p1	sp|Q9SJF3|DCP1_ARATH_mRNA-decapping_enzyme-like_protein_OS=Arabidopsis_thaliana_GN=At1g08370_PE=2_SV=2	3.00E-21	[illegible]	[illegible]
comp32484_c1_seq1.p1				
comp32484_c3_seq10.p1	sp|P55861|MCM2_XENLA_DNA_replication_licensing_factor_mcm2_OS=Xenopus_laevis_GN=mcm2_PE=1_SV=2	0	[illegible]	[illegible]
comp32484_c3_seq10.p2				
comp32484_c3_seq10.p5				
comp32484_c3_seq12.p1	sp|Q9SL42|PIN1_ARATH_Peptidyl-prolyl_cis-trans_isomerase_Pin1_OS=Arabidopsis_thaliana_GN=PIN1_PE=1_SV=1	9.00E-34	[illegible]	[illegible]
comp32484_c3_seq13.p2				
comp32484_c3_seq16.p1				
comp32484_c3_seq2.p1				
comp32484_c3_seq6.p1				
comp32485_c0_seq1.p1				
comp32485_c0_seq2.p1				
comp32485_c0_seq5.p1	sp|B1AY13|UBP24_MOUSE_Ubiquitin_carboxyl-terminal_hydrolase_24_OS=Mus_musculus_GN=Usp24_PE=1_SV=1	6.00E-38	[illegible]	[illegible]
comp32485_c0_seq5.p2				
comp32485_c0_seq5.p3	sp|Q4G056|TYDP1_RAT_Tyrosyl-DNA_phosphodiesterase_1_OS=Rattus_norvegicus_GN=Tdp1_PE=2_SV=1	2.00E-33	[illegible]	[illegible]
comp32485_c0_seq6.p1				
comp32486_c0_seq11.p1				
comp32486_c0_seq6.p1				
comp32486_c1_seq1.p2				
comp32487_c0_seq1.p1	sp|B0CE36|RS21_ACAM1_30S_ribosomal_protein_S21_OS=Acaryochloris_marina_(strain_MBIC_11017)_GN=rpsU_PE=3_SV=1	1.00E-13	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0006412,GO:0030529	[illegible]
comp32487_c0_seq2.p2				
comp32487_c0_seq3.p2				
comp32487_c0_seq6.p1	sp|Q9SSF9|PP123_ARATH_Pentatricopeptide_repeat-containing_protein_At1g74750_OS=Arabidopsis_thaliana_GN=At1g74750_PE=2_SV=1	2.00E-12		
comp32487_c0_seq7.p1	sp|B0CE36|RS21_ACAM1_30S_ribosomal_protein_S21_OS=Acaryochloris_marina_(strain_MBIC_11017)_GN=rpsU_PE=3_SV=1	1.00E-13	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0006412,GO:0030529	[illegible]
comp32488_c0_seq4.p1				
comp32488_c0_seq5.p3				
comp32488_c0_seq7.p1				
comp32488_c0_seq8.p1				
comp32489_c0_seq1.p1	sp|Q40784|AAPC_CENCI_Putative_glucose-6-phosphate_1-epimerase_OS=Cenchrus_ciliaris_PE=2_SV=1	2.00E-49	GO:0003824,GO:0005975,GO:0016853,GO:0016853,GO:0030246,GO:0047938	[illegible]
comp32489_c0_seq11.p1				
comp32489_c0_seq15.p1	sp|Q40784|AAPC_CENCI_Putative_glucose-6-phosphate_1-epimerase_OS=Cenchrus_ciliaris_PE=2_SV=1	7.00E-15	GO:0003824,GO:0005975,GO:0016853,GO:0016853,GO:0030246,GO:0047938	[illegible]
comp32489_c0_seq22.p1				
comp32489_c0_seq37.p1				
comp32489_c0_seq8.p1				
comp32489_c1_seq3.p1				
comp32489_c1_seq5.p1				
comp32489_c1_seq5.p3				
comp32493_c0_seq1.p1				
comp32493_c0_seq4.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	1.00E-14	[illegible]	[illegible]
comp32493_c0_seq7.p1				
comp32494_c0_seq10.p1				
comp32494_c0_seq2.p1				
comp32494_c0_seq3.p1				
comp32494_c0_seq6.p1				
comp32494_c0_seq8.p1				
comp32495_c1_seq18.p2				
comp32495_c1_seq2.p1				
comp32495_c1_seq2.p3				
comp32495_c1_seq9.p3				
comp32496_c0_seq1.p1				
comp32497_c0_seq1.p1				
comp32497_c0_seq2.p1				
comp32497_c0_seq3.p1				
comp32498_c1_seq1.p1				
comp32498_c1_seq3.p1				
comp32499_c2_seq11.p1				
comp32499_c3_seq1.p1				
comp32499_c3_seq3.p1				
comp32499_c3_seq4.p1	sp|Q9FMV1|UMP7_ARATH_Uncharacterized_protein_At5g63510,_mitochondrial_OS=Arabidopsis_thaliana_GN=At5g63510_PE=1_SV=1	2.00E-23	GO:0005515,GO:0005515,GO:0005515,GO:0005739,GO:0016020,GO:0031966,GO:0046872	[illegible]
comp32500_c1_seq24.p1				
comp32501_c0_seq2.p1				
comp32501_c0_seq5.p2				
comp32501_c1_seq1.p1				
comp32501_c1_seq2.p1				
comp32501_c1_seq2.p4				
comp32502_c0_seq1.p1				
comp32503_c0_seq2.p1				
comp32503_c0_seq2.p2				
comp32503_c0_seq8.p1				
comp32503_c0_seq8.p2				
comp32504_c1_seq12.p1	sp|Q5ZIY4|SBDS_CHICK_Ribosome_maturation_protein_SBDS_OS=Gallus_gallus_GN=SBDS_PE=2_SV=1	5.00E-82	[illegible]	[illegible]
comp32504_c1_seq15.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	6.00E-33		
comp32504_c1_seq19.p1				
comp32504_c1_seq24.p1	sp|Q5UR85|YR636_MIMIV_Putative_FNIP_repeat-containing_protein_R636_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R636_PE=4_SV=1	4.00E-14		
comp32504_c1_seq25.p1				
comp32504_c1_seq26.p1				
comp32504_c1_seq29.p1				
comp32504_c1_seq4.p1	sp|P13234|KCC4_RAT_Calcium/calmodulin-dependent_protein_kinase_type_IV_OS=Rattus_norvegicus_GN=Camk4_PE=1_SV=3	5.00E-59	[illegible]	[illegible]
comp32504_c1_seq5.p1				
comp32504_c1_seq6.p1	sp|Q9VPH2|PRI2_DROME_DNA_primase_large_subunit_OS=Drosophila_melanogaster_GN=DNApol-alpha60_PE=1_SV=2	2.00E-16	[illegible]	[illegible]
comp32504_c1_seq8.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	8.00E-38		
comp32505_c0_seq1.p1	sp|Q67XX3|FB252_ARATH_F-box_protein_At5g06550_OS=Arabidopsis_thaliana_GN=At5g06550_PE=2_SV=1	6.00E-122	GO:0000987,GO:0005634,GO:0006355,GO:0006626,GO:0009909,GO:0010030,GO:0043985	[illegible]
comp32505_c3_seq1.p1				
comp32505_c3_seq3.p1				
comp32507_c0_seq3.p1	sp|Q15149|PLEC_HUMAN_Plectin_OS=Homo_sapiens_GN=PLEC_PE=1_SV=3	3.00E-25	[illegible]	[illegible]
comp32510_c0_seq1.p1				
comp32510_c0_seq13.p1				
comp32510_c0_seq16.p4				
comp32510_c0_seq2.p1				
comp32510_c0_seq20.p1				
comp32510_c0_seq6.p5				
comp32510_c0_seq6.p6				
comp32510_c0_seq9.p1				
comp32511_c0_seq10.p1				
comp32511_c0_seq4.p1				
comp32511_c0_seq8.p2				
comp32511_c1_seq3.p2				
comp32512_c0_seq1.p1				
comp32512_c0_seq10.p2				
comp32512_c0_seq11.p1				
comp32512_c0_seq2.p1				
comp32513_c0_seq2.p1				
comp32513_c0_seq3.p1				
comp32514_c0_seq1.p1				
comp32514_c0_seq1.p2				
comp32514_c0_seq1.p8	sp|P40984|UBC9_SCHPO_SUMO-conjugating_enzyme_ubc9_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=hus5_PE=1_SV=1	7.00E-76	[illegible]	[illegible]
comp32515_c0_seq3.p1				
comp32515_c0_seq4.p1				
comp32515_c0_seq6.p1				
comp32515_c0_seq8.p1	sp|Q9FLV9|SLAH3_ARATH_S-type_anion_channel_SLAH3_OS=Arabidopsis_thaliana_GN=SLAH3_PE=1_SV=1	2.00E-19	[illegible]	[illegible]
comp32516_c0_seq6.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	1.00E-20	[illegible]	[illegible]
comp32516_c0_seq6.p2				
comp32516_c0_seq6.p3				
comp32516_c0_seq9.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	2.00E-14	[illegible]	[illegible]
comp32516_c1_seq1.p1				
comp32517_c0_seq6.p1				
comp32517_c0_seq8.p1				
comp32518_c0_seq1.p1				
comp32518_c0_seq11.p1	sp|A8WXF6|KCC2D_CAEBR_Calcium/calmodulin-dependent_protein_kinase_type_II_OS=Caenorhabditis_briggsae_GN=unc-43_PE=3_SV=1	2.00E-65	[illegible]	[illegible]
comp32518_c0_seq15.p1				
comp32518_c0_seq17.p1				
comp32518_c0_seq18.p1	sp|A8WXF6|KCC2D_CAEBR_Calcium/calmodulin-dependent_protein_kinase_type_II_OS=Caenorhabditis_briggsae_GN=unc-43_PE=3_SV=1	2.00E-65	[illegible]	[illegible]
comp32518_c0_seq20.p1	sp|Q9TXJ0|CMK1_CAEEL_Calcium/calmodulin-dependent_protein_kinase_type_1_OS=Caenorhabditis_elegans_GN=cmk-1_PE=1_SV=1	7.00E-43	[illegible]	[illegible]
comp32518_c0_seq4.p1	sp|Q9TXJ0|CMK1_CAEEL_Calcium/calmodulin-dependent_protein_kinase_type_1_OS=Caenorhabditis_elegans_GN=cmk-1_PE=1_SV=1	3.00E-70	[illegible]	[illegible]
comp32520_c1_seq2.p1	sp|P46293|RS16_GOSHI_40S_ribosomal_protein_S16_OS=Gossypium_hirsutum_GN=RPS16_PE=2_SV=1	4.00E-75	GO:0003735,GO:0005737,GO:0005737,GO:0005840,GO:0005840,GO:0006412,GO:0030529	[illegible]
comp32520_c2_seq1.p1				
comp32520_c2_seq10.p1	sp|Q12344|GYP5_YEAST_GTPase-activating_protein_GYP5_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=GYP5_PE=1_SV=1	4.00E-15	[illegible]	[illegible]
comp32520_c2_seq11.p1				
comp32520_c2_seq14.p1	sp|Q9WVK7|HCDH_RAT_Hydroxyacyl-coenzyme_A_dehydrogenase,_mitochondrial_OS=Rattus_norvegicus_GN=Hadh_PE=2_SV=1	3.00E-73	[illegible]	[illegible]
comp32520_c3_seq5.p1	sp|Q99LZ3|SLD5_MOUSE_DNA_replication_complex_GINS_protein_SLD5_OS=Mus_musculus_GN=Gins4_PE=1_SV=1	8.00E-24	[illegible]	[illegible]
comp32520_c3_seq6.p1	sp|Q99LZ3|SLD5_MOUSE_DNA_replication_complex_GINS_protein_SLD5_OS=Mus_musculus_GN=Gins4_PE=1_SV=1	2.00E-30	[illegible]	[illegible]
comp32521_c0_seq2.p1				
comp32522_c0_seq1.p1	sp|Q5PQX0|UXS1_RAT_UDP-glucuronic_acid_decarboxylase_1_OS=Rattus_norvegicus_GN=Uxs1_PE=1_SV=1	2.00E-162	[illegible]	[illegible]
comp32522_c0_seq1.p2	sp|P51173|APEA_DICDI_DNA-(apurinic_or_apyrimidinic_site)_lyase_OS=Dictyostelium_discoideum_GN=apeA_PE=2_SV=2	2.00E-37	[illegible]	[illegible]
comp32522_c0_seq1.p3				
comp32522_c1_seq1.p1				
comp32522_c3_seq1.p1				
comp32522_c3_seq1.p2	sp|Q54VQ7|HDA22_DICDI_Type-2_histone_deacetylase_2_OS=Dictyostelium_discoideum_GN=hdaC_PE=2_SV=1	3.00E-45	[illegible]	[illegible]
comp32522_c3_seq2.p1				
comp32522_c3_seq2.p2	sp|Q5RAQ2|SH3Y1_PONAB_SH3_domain-containing_YSC84-like_protein_1_OS=Pongo_abelii_GN=SH3YL1_PE=2_SV=1	3.00E-33		
comp32522_c3_seq3.p1				
comp32522_c3_seq6.p1	sp|Q5RAQ2|SH3Y1_PONAB_SH3_domain-containing_YSC84-like_protein_1_OS=Pongo_abelii_GN=SH3YL1_PE=2_SV=1	3.00E-33		
comp32522_c3_seq7.p1				
comp32522_c3_seq7.p2	sp|Q5RAQ2|SH3Y1_PONAB_SH3_domain-containing_YSC84-like_protein_1_OS=Pongo_abelii_GN=SH3YL1_PE=2_SV=1	3.00E-33		
comp32522_c3_seq9.p1				
comp32523_c0_seq1.p1				
comp32523_c0_seq13.p3				
comp32523_c0_seq18.p1	sp|Q8I0F4|LIS1_DICDI_Lissencephaly-1_homolog_OS=Dictyostelium_discoideum_GN=lis1_PE=1_SV=1	2.00E-25	[illegible]	[illegible]
comp32523_c0_seq19.p2				
comp32523_c0_seq2.p1	sp|B5X3Z6|LIS1A_SALSA_Lissencephaly-1_homolog_A_OS=Salmo_salar_GN=pafah1b1-1_PE=2_SV=1	5.00E-108	[illegible]	[illegible]
comp32523_c0_seq21.p1	sp|Q8I0F4|LIS1_DICDI_Lissencephaly-1_homolog_OS=Dictyostelium_discoideum_GN=lis1_PE=1_SV=1	4.00E-26	[illegible]	[illegible]
comp32523_c0_seq24.p1	sp|Q8I0F4|LIS1_DICDI_Lissencephaly-1_homolog_OS=Dictyostelium_discoideum_GN=lis1_PE=1_SV=1	2.00E-25	[illegible]	[illegible]
comp32523_c0_seq25.p1	sp|Q8I0F4|LIS1_DICDI_Lissencephaly-1_homolog_OS=Dictyostelium_discoideum_GN=lis1_PE=1_SV=1	2.00E-25	[illegible]	[illegible]
comp32523_c0_seq27.p1				
comp32523_c0_seq28.p1	sp|Q21CM1|MNMG_RHOPB_tRNA_uridine_5-carboxymethylaminomethyl_modification_enzyme_MnmG_OS=Rhodopseudomonas_palustris_(strain_BisB18)_GN=mnmG_PE=3_SV=1	1.00E-163	[illegible]	[illegible]
comp32523_c0_seq31.p1				
comp32523_c0_seq32.p1	sp|Q14692|BMS1_HUMAN_Ribosome_biogenesis_protein_BMS1_homolog_OS=Homo_sapiens_GN=BMS1_PE=1_SV=1	3.00E-113	[illegible]	[illegible]
comp32523_c0_seq4.p1	sp|Q8I0F4|LIS1_DICDI_Lissencephaly-1_homolog_OS=Dictyostelium_discoideum_GN=lis1_PE=1_SV=1	4.00E-26	[illegible]	[illegible]
comp32523_c0_seq40.p1				
comp32523_c0_seq7.p2				
comp32523_c0_seq7.p4	sp|O23920|HPPD_DAUCA_4-hydroxyphenylpyruvate_dioxygenase_OS=Daucus_carota_PE=2_SV=1	4.00E-12	[illegible]	[illegible]
comp32524_c0_seq5.p1				
comp32524_c1_seq1.p1	sp|Q62967|MVD1_RAT_Diphosphomevalonate_decarboxylase_OS=Rattus_norvegicus_GN=Mvd_PE=2_SV=1	6.00E-119	[illegible]	[illegible]
comp32524_c2_seq1.p1				
comp32524_c2_seq5.p1				
comp32524_c2_seq8.p1				
comp32525_c0_seq3.p1				
comp32526_c0_seq5.p1	sp|Q8BMG7|RBGPR_MOUSE_Rab3_GTPase-activating_protein_non-catalytic_subunit_OS=Mus_musculus_GN=Rab3gap2_PE=1_SV=2	2.00E-13	[illegible]	[illegible]
comp32526_c0_seq7.p1				
comp32527_c0_seq100.p1				
comp32527_c0_seq100.p2				
comp32527_c0_seq102.p1				
comp32527_c0_seq102.p2				
comp32527_c0_seq105.p1				
comp32527_c0_seq105.p2				
comp32527_c0_seq108.p1				
comp32527_c0_seq108.p2				
comp32527_c0_seq110.p1				

comp32527_c0_seq110.p2				
comp32527_c0_seq110.p3				
comp32527_c0_seq18.p1				
comp32527_c0_seq20.p2				
comp32527_c0_seq20.p5				
comp32527_c0_seq22.p1				
comp32527_c0_seq23.p1				
comp32527_c0_seq23.p2				
comp32527_c0_seq3.p2				
comp32527_c0_seq3.p6				
comp32527_c0_seq30.p1				
comp32527_c0_seq32.p1	sp|Q9NUP7|TRM13_HUMAN_tRNA_guanosine-2'-O-methyltransferase_TRM13_homolog_OS=Homo_sapiens_GN=CCDC76_PE=1_SV=2	8.00E-37	GO:0008033,GO:0008033,GO:0008168,GO:0008168,GO:0008175,GO:0016740,GO:0030488,GO:0032259,GO:0046872	tRNA processing,tRNA processing,methyltransferase activity,methyltransferase activity,tRNA methyltransferase activity,transferase activity,tRNA methylation,methylation,metal ion binding
comp32527_c0_seq33.p1				
comp32527_c0_seq33.p2				
comp32527_c0_seq35.p1				
comp32527_c0_seq35.p2				
comp32527_c0_seq38.p1				
comp32527_c0_seq38.p2				
comp32527_c0_seq40.p1				
comp32527_c0_seq40.p2				
comp32527_c0_seq42.p1				
comp32527_c0_seq43.p1				
comp32527_c0_seq43.p2				
comp32527_c0_seq51.p1				
comp32527_c0_seq51.p2				
comp32527_c0_seq53.p1				
comp32527_c0_seq66.p1				
comp32527_c0_seq69.p1				
comp32527_c0_seq7.p1				
comp32527_c0_seq7.p2				
comp32527_c0_seq75.p1				
comp32527_c0_seq75.p2				
comp32527_c0_seq80.p1				
comp32527_c0_seq81.p1				
comp32527_c0_seq81.p2				
comp32527_c0_seq82.p1				
comp32527_c0_seq88.p1				
comp32527_c0_seq9.p1				
comp32527_c0_seq96.p1				
comp32527_c0_seq98.p1				
comp32527_c0_seq99.p1				
comp32527_c0_seq99.p2				
comp32528_c0_seq1.p1				
comp32528_c0_seq4.p1				
comp32529_c0_seq1.p1				
comp32529_c0_seq10.p1				
comp32529_c0_seq12.p1	sp|P39101|CAJ1_YEAST_Protein_CAJ1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=CAJ1_PE=1_SV=1	5.00E-12	GO:0005634,GO:0006457,GO:0051087	nucleus,protein folding,chaperone binding
comp32529_c0_seq12.p2				
comp32529_c0_seq13.p1				
comp32529_c0_seq16.p1				
comp32529_c0_seq3.p1				
comp32529_c0_seq4.p1				
comp32529_c0_seq4.p2				
comp32529_c0_seq4.p3				
comp32529_c0_seq8.p2				
comp32530_c0_seq13.p1	sp|P46865|KINL_LEICH_Kinesin-like_protein_K39_(Fragment)_OS=Leishmania_chagasi_GN=KIN_PE=2_SV=1	6.00E-20	GO:0000166,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005874,GO:0007018,GO:0008017,GO:0008152	nucleotide binding,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,microtubule,microtubule-based movement,microtubule binding,metabolic process
comp32530_c0_seq13.p2	sp|Q8NCG7|DGLB_HUMAN_Sn1-specific_diacylglycerol_lipase_beta_OS=Homo_sapiens_GN=DAGLB_PE=1_SV=2	7.00E-19	GO:0005765,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006629,GO:0006629,GO:0007405,GO:0007596,GO:0016020,GO:0016021,GO:0016042,GO:0016298,GO:0016787,GO:0019369,GO:0019369,GO:0022008,GO:0030168,GO:0042136,GO:0046872	lysosomal membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,lipid metabolic process,lipid metabolic process,neuroblast proliferation,blood coagulation,membrane,integral component of membrane,lipid catabolic process,lipase activity,hydrolase activity,arachidonic acid metabolic process,arachidonic acid metabolic process,neurogenesis,platelet activation,neurotransmitter biosynthetic process,metal ion binding
comp32530_c0_seq13.p5				
comp32530_c0_seq18.p1				
comp32530_c0_seq18.p2	sp|Q8NCG7|DGLB_HUMAN_Sn1-specific_diacylglycerol_lipase_beta_OS=Homo_sapiens_GN=DAGLB_PE=1_SV=2	7.00E-19	GO:0005765,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006629,GO:0006629,GO:0007405,GO:0007596,GO:0016020,GO:0016021,GO:0016042,GO:0016298,GO:0016787,GO:0019369,GO:0019369,GO:0022008,GO:0030168,GO:0042136,GO:0046872	lysosomal membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,lipid metabolic process,lipid metabolic process,neuroblast proliferation,blood coagulation,membrane,integral component of membrane,lipid catabolic process,lipase activity,hydrolase activity,arachidonic acid metabolic process,arachidonic acid metabolic process,neurogenesis,platelet activation,neurotransmitter biosynthetic process,metal ion binding
comp32530_c0_seq18.p3	sp|P46865|KINL_LEICH_Kinesin-like_protein_K39_(Fragment)_OS=Leishmania_chagasi_GN=KIN_PE=2_SV=1	1.00E-20	GO:0000166,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005874,GO:0007018,GO:0008017,GO:0008152	nucleotide binding,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,microtubule,microtubule-based movement,microtubule binding,metabolic process
comp32530_c0_seq18.p6				
comp32530_c0_seq26.p1	sp|P46865|KINL_LEICH_Kinesin-like_protein_K39_(Fragment)_OS=Leishmania_chagasi_GN=KIN_PE=2_SV=1	1.00E-30	GO:0000166,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005874,GO:0007018,GO:0008017,GO:0008152	nucleotide binding,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,microtubule,microtubule-based movement,microtubule binding,metabolic process
comp32530_c0_seq26.p2	sp|Q8NCG7|DGLB_HUMAN_Sn1-specific_diacylglycerol_lipase_beta_OS=Homo_sapiens_GN=DAGLB_PE=1_SV=2	7.00E-19	GO:0005765,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006629,GO:0006629,GO:0007405,GO:0007596,GO:0016020,GO:0016021,GO:0016042,GO:0016298,GO:0016787,GO:0019369,GO:0019369,GO:0022008,GO:0030168,GO:0042136,GO:0046872	lysosomal membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,lipid metabolic process,lipid metabolic process,neuroblast proliferation,blood coagulation,membrane,integral component of membrane,lipid catabolic process,lipase activity,hydrolase activity,arachidonic acid metabolic process,arachidonic acid metabolic process,neurogenesis,platelet activation,neurotransmitter biosynthetic process,metal ion binding
comp32530_c0_seq26.p6				
comp32530_c0_seq3.p1				
comp32530_c0_seq36.p1				
comp32530_c0_seq48.p1				
comp32530_c0_seq50.p1				
comp32530_c0_seq50.p2	sp|P46865|KINL_LEICH_Kinesin-like_protein_K39_(Fragment)_OS=Leishmania_chagasi_GN=KIN_PE=2_SV=1	1.00E-31	GO:0000166,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005874,GO:0007018,GO:0008017,GO:0008152	nucleotide binding,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,microtubule,microtubule-based movement,microtubule binding,metabolic process
comp32530_c0_seq50.p3	sp|Q8NCG7|DGLB_HUMAN_Sn1-specific_diacylglycerol_lipase_beta_OS=Homo_sapiens_GN=DAGLB_PE=1_SV=2	7.00E-19	GO:0005765,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006629,GO:0006629,GO:0007405,GO:0007596,GO:0016020,GO:0016021,GO:0016042,GO:0016298,GO:0016787,GO:0019369,GO:0019369,GO:0022008,GO:0030168,GO:0042136,GO:0046872	lysosomal membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,lipid metabolic process,lipid metabolic process,neuroblast proliferation,blood coagulation,membrane,integral component of membrane,lipid catabolic process,lipase activity,hydrolase activity,arachidonic acid metabolic process,arachidonic acid metabolic process,neurogenesis,platelet activation,neurotransmitter biosynthetic process,metal ion binding
comp32530_c0_seq50.p7				
comp32530_c0_seq7.p1				
comp32531_c1_seq1.p1				
comp32531_c1_seq1.p2	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	7.00E-31	GO:0000281,GO:0000281,GO:0005200,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005764,GO:0005764,GO:0005783,GO:0005794,GO:0005794,GO:0005794,GO:0005856,GO:0005856,GO:0005886,GO:0005886,GO:0005886,GO:0007009,GO:0007016,GO:0007165,GO:0007409,GO:0007409,GO:0007411,GO:0007528,GO:0008092,GO:0009986,GO:0010628,GO:0010650,GO:0010765,GO:0014704,GO:0014704,GO:0014704,GO:0014731,GO:0016020,GO:0016020,GO:0016323,GO:0016328,GO:0016529,GO:0019228,GO:0019228,GO:0030018,GO:0030054,GO:0030315,GO:0030424,GO:0030424,GO:0030425,GO:0030507,GO:0030674,GO:0031594,GO:0033268,GO:0033268,GO:0033268,GO:0033270,GO:0034112,GO:0042383,GO:0042383,GO:0042995,GO:0043001,GO:0043005,GO:0043034,GO:0043194,GO:0043194,GO:0043194,GO:0043266,GO:0044325,GO:0045184,GO:0045202,GO:0045202,GO:0045211,GO:0045211,GO:0045211,GO:0045296,GO:0045838,GO:0050808,GO:0071709,GO:0071709,GO:0072659,GO:0072659,GO:0072659,GO:0072660,GO:0072661,GO:0072661,GO:0090314,GO:1900827,GO:2000651,GO:0005923,GO:0009925	mitotic cytokinesis,mitotic cytokinesis,structural constituent of cytoskeleton,protein binding,protein binding,protein binding,cytoplasm,lysosome,lysosome,endoplasmic reticulum,Golgi apparatus,Golgi apparatus,Golgi apparatus,cytoskeleton,cytoskeleton,plasma membrane,plasma membrane,plasma membrane,plasma membrane organization,cytoskeletal anchoring at plasma membrane,signal transduction,axonogenesis,axonogenesis,axon guidance,neuromuscular junction development,cytoskeletal protein binding,cell surface,positive regulation of gene expression,positive regulation of cell communication by electrical coupling,positive regulation of sodium ion transport,intercalated disc,intercalated disc,intercalated disc,spectrin-associated cytoskeleton,membrane,membrane,basolateral plasma membrane,lateral plasma membrane,sarcoplasmic reticulum,neuronal action potential,neuronal action potential,Z disc,cell junction,T-tubule,axon,axon,dendrite,spectrin binding,protein binding, bridging,neuromuscular junction,node of Ranvier,node of Ranvier,paranode region of axon,positive regulation of homotypic cell-cell adhesion,sarcolemma,sarcolemma,cell projection,Golgi to plasma membrane protein transport,neuron projection,costamere,axon initial segment,axon initial segment,axon initial segment,regulation of potassium ion transport,ion channel binding,establishment of protein localization,synapse,synapse,postsynaptic membrane,postsynaptic membrane,postsynaptic membrane,cadherin binding,positive regulation of membrane potential,synapse organization,membrane assembly,membrane assembly,protein localization to plasma membrane,protein localization to plasma membrane,protein localization to plasma membrane,maintenance of protein location in plasma membrane,protein targeting to plasma membrane,protein targeting to plasma membrane,positive regulation of protein targeting to membrane,positive regulation of membrane depolarization during cardiac muscle cell action potential,positive regulation of sodium ion transmembrane transporter activity,tight junction,basal plasma membrane
comp32531_c1_seq1.p7				
comp32531_c1_seq10.p1				
comp32531_c1_seq10.p4				
comp32531_c1_seq10.p6				
comp32531_c1_seq8.p1	sp|Q12955|ANK3_HUMAN_Ankyrin-3_OS=Homo_sapiens_GN=ANK3_PE=1_SV=3	7.00E-31	GO:0000281,GO:0000281,GO:0005200,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005764,GO:0005764,GO:0005783,GO:0005794,GO:0005794,GO:0005794,GO:0005856,GO:0005856,GO:0005886,GO:0005886,GO:0005886,GO:0007009,GO:0007016,GO:0007165,GO:0007409,GO:0007409,GO:0007411,GO:0007528,GO:0008092,GO:0009986,GO:0010628,GO:0010650,GO:0010765,GO:0014704,GO:0014704,GO:0014704,GO:0014731,GO:0016020,GO:0016020,GO:0016323,GO:0016328,GO:0016529,GO:0019228,GO:0019228,GO:0030018,GO:0030054,GO:0030315,GO:0030424,GO:0030424,GO:0030425,GO:0030507,GO:0030674,GO:0031594,GO:0033268,GO:0033268,GO:0033268,GO:0033270,GO:0034112,GO:0042383,GO:0042383,GO:0042995,GO:0043001,GO:0043005,GO:0043034,GO:0043194,GO:0043194,GO:0043194,GO:0043266,GO:0044325,GO:0045184,GO:0045202,GO:0045202,GO:0045211,GO:0045211,GO:0045211,GO:0045296,GO:0045838,GO:0050808,GO:0071709,GO:0071709,GO:0072659,GO:0072659,GO:0072659,GO:0072660,GO:0072661,GO:0072661,GO:0090314,GO:1900827,GO:2000651,GO:0005923,GO:0009925	mitotic cytokinesis,mitotic cytokinesis,structural constituent of cytoskeleton,protein binding,protein binding,protein binding,cytoplasm,lysosome,lysosome,endoplasmic reticulum,Golgi apparatus,Golgi apparatus,Golgi apparatus,cytoskeleton,cytoskeleton,plasma membrane,plasma membrane,plasma membrane,plasma membrane organization,cytoskeletal anchoring at plasma membrane,signal transduction,axonogenesis,axonogenesis,axon guidance,neuromuscular junction development,cytoskeletal protein binding,cell surface,positive regulation of gene expression,positive regulation of cell communication by electrical coupling,positive regulation of sodium ion transport,intercalated disc,intercalated disc,intercalated disc,spectrin-associated cytoskeleton,membrane,membrane,basolateral plasma membrane,lateral plasma membrane,sarcoplasmic reticulum,neuronal action potential,neuronal action potential,Z disc,cell junction,T-tubule,axon,axon,dendrite,spectrin binding,protein binding, bridging,neuromuscular junction,node of Ranvier,node of Ranvier,paranode region of axon,positive regulation of homotypic cell-cell adhesion,sarcolemma,sarcolemma,cell projection,Golgi to plasma membrane protein transport,neuron projection,costamere,axon initial segment,axon initial segment,axon initial segment,regulation of potassium ion transport,ion channel binding,establishment of protein localization,synapse,synapse,postsynaptic membrane,postsynaptic membrane,postsynaptic membrane,cadherin binding,positive regulation of membrane potential,synapse organization,membrane assembly,membrane assembly,protein localization to plasma membrane,protein localization to plasma membrane,protein localization to plasma membrane,maintenance of protein location in plasma membrane,protein targeting to plasma membrane,protein targeting to plasma membrane,positive regulation of protein targeting to membrane,positive regulation of membrane depolarization during cardiac muscle cell action potential,positive regulation of sodium ion transmembrane transporter activity,tight junction,basal plasma membrane
comp32531_c1_seq8.p2				
comp32531_c1_seq8.p6				
comp32531_c1_seq8.p8				
comp32532_c0_seq2.p1				
comp32532_c0_seq4.p2				
comp32533_c0_seq2.p4				
comp32533_c1_seq10.p1				
comp32533_c1_seq6.p1				
comp32533_c1_seq9.p2				
comp32533_c1_seq9.p3				
comp32534_c0_seq3.p1				
comp32534_c1_seq4.p1	sp|B2FQP3|ASPN_STRMK_Peptidyl-Asp_metalloendopeptidase_OS=Stenotrophomonas_maltophilia_(strain_K279a)_GN=Smlt0970_PE=3_SV=1	2.00E-13	GO:0006508,GO:0008233,GO:0008237,GO:0008237,GO:0016787,GO:0046872	proteolysis,peptidase activity,metallopeptidase activity,metallopeptidase activity,hydrolase activity,metal ion binding
comp32534_c1_seq4.p3				
comp32536_c0_seq1.p1				
comp32537_c0_seq10.p1	sp|Q2RZX7|KATG_SALRD_Catalase-peroxidase_OS=Salinibacter_ruber_(strain_DSM_13855_/_M31)_GN=katG_PE=3_SV=1	8.00E-37	GO:0004096,GO:0004096,GO:0004601,GO:0004601,GO:0004601,GO:0006979,GO:0016491,GO:0020037,GO:0042744,GO:0046872,GO:0055114,GO:0055114	catalase activity,catalase activity,peroxidase activity,peroxidase activity,peroxidase activity,response to oxidative stress,oxidoreductase activity,heme binding,hydrogen peroxide catabolic process,metal ion binding,oxidation-reduction process,oxidation-reduction process
comp32537_c0_seq2.p1	sp|Q2RZX7|KATG_SALRD_Catalase-peroxidase_OS=Salinibacter_ruber_(strain_DSM_13855_/_M31)_GN=katG_PE=3_SV=1	1.00E-52	GO:0004096,GO:0004096,GO:0004601,GO:0004601,GO:0004601,GO:0006979,GO:0016491,GO:0020037,GO:0042744,GO:0046872,GO:0055114,GO:0055114	catalase activity,catalase activity,peroxidase activity,peroxidase activity,peroxidase activity,response to oxidative stress,oxidoreductase activity,heme binding,hydrogen peroxide catabolic process,metal ion binding,oxidation-reduction process,oxidation-reduction process
comp32537_c0_seq3.p1	sp|B4RW28|KATG_ALTMD_Catalase-peroxidase_OS=Alteromonas_macleodii_(strain_DSM_17117_/_Deep_ecotype)_GN=katG_PE=3_SV=2	4.00E-106	GO:0004096,GO:0004096,GO:0004601,GO:0004601,GO:0004601,GO:0006979,GO:0016491,GO:0020037,GO:0042744,GO:0046872,GO:0055114,GO:0055114	catalase activity,catalase activity,peroxidase activity,peroxidase activity,peroxidase activity,response to oxidative stress,oxidoreductase activity,heme binding,hydrogen peroxide catabolic process,metal ion binding,oxidation-reduction process,oxidation-reduction process
comp32537_c0_seq4.p1	sp|A4INM5|KATG_GEOTN_Catalase-peroxidase_OS=Geobacillus_thermodenitrificans_(strain_NG80-2)_GN=katG_PE=3_SV=1	1.00E-120	GO:0004096,GO:0004096,GO:0004601,GO:0004601,GO:0004601,GO:0006979,GO:0016491,GO:0020037,GO:0042744,GO:0046872,GO:0055114,GO:0055114	catalase activity,catalase activity,peroxidase activity,peroxidase activity,peroxidase activity,response to oxidative stress,oxidoreductase activity,heme binding,hydrogen peroxide catabolic process,metal ion binding,oxidation-reduction process,oxidation-reduction process
comp32537_c0_seq8.p1	sp|A4TA35|KATG_MYCGI_Catalase-peroxidase_OS=Mycobacterium_gilvum_(strain_PYR-GCK)_GN=katG_PE=3_SV=1	1.00E-13	GO:0004096,GO:0004096,GO:0004601,GO:0004601,GO:0004601,GO:0006979,GO:0016491,GO:0020037,GO:0042744,GO:0046872,GO:0055114,GO:0055114	catalase activity,catalase activity,peroxidase activity,peroxidase activity,peroxidase activity,response to oxidative stress,oxidoreductase activity,heme binding,hydrogen peroxide catabolic process,metal ion binding,oxidation-reduction process,oxidation-reduction process
comp32538_c0_seq11.p1				
comp32538_c0_seq13.p1				
comp32538_c0_seq3.p3				
comp32538_c0_seq8.p2				
comp32538_c0_seq8.p3				
comp32539_c0_seq1.p1	sp|Q9Z812|PMP20_CHLPN_Probable_outer_membrane_protein_pmp20_OS=Chlamydia_pneumoniae_GN=pmp20_PE=3_SV=2	1.00E-11	GO:0005576,GO:0005618,GO:0005618,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0019867	extracellular region,cell wall,cell wall,cell outer membrane,cell outer membrane,membrane,integral component of membrane,outer membrane
comp32539_c0_seq3.p1				
comp32539_c0_seq5.p1				
comp32540_c0_seq2.p1				
comp32540_c0_seq4.p1				
comp32542_c0_seq1.p1				
comp32542_c0_seq10.p1				
comp32542_c0_seq2.p2				
comp32542_c0_seq5.p1				
comp32542_c0_seq6.p1				
comp32542_c0_seq8.p1				
comp32543_c1_seq2.p1				
comp32543_c1_seq3.p1				
comp32543_c2_seq1.p2				
comp32543_c2_seq2.p1				
comp32544_c0_seq14.p1				
comp32544_c0_seq2.p1				
comp32544_c0_seq21.p1				
comp32544_c0_seq22.p1				
comp32544_c0_seq23.p1				
comp32544_c0_seq24.p1	sp|Q5PQL4|CLP1_RAT_Polyribonucleotide_5'-hydroxyl-kinase_Clp1_OS=Rattus_norvegicus_GN=Clp1_PE=2_SV=1	7.00E-96	GO:0000166,GO:0000214,GO:0000214,GO:0000214,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005849,GO:0005849,GO:0006378,GO:0006379,GO:0006388,GO:0006388,GO:0006388,GO:0006397,GO:0008033,GO:0016301,GO:0016310,GO:0016740,GO:0021695,GO:0021695,GO:0030423,GO:0031124,GO:0031124,GO:0035087,GO:0035087,GO:0035087,GO:0046404,GO:0051731,GO:0051733,GO:0051733,GO:0051736,GO:0051736	nucleotide binding,tRNA-intron endonuclease complex,tRNA-intron endonuclease complex,tRNA-intron endonuclease complex,ATP binding,ATP binding,nucleus,nucleus,nucleus,nucleus,mRNA cleavage factor complex,mRNA cleavage factor complex,mRNA polyadenylation,mRNA cleavage,tRNA splicing, via endonucleolytic cleavage and ligation,tRNA splicing, via endonucleolytic cleavage and ligation,tRNA splicing, via endonucleolytic cleavage and ligation,mRNA processing,tRNA processing,kinase activity,phosphorylation,transferase activity,cerebellar cortex development,cerebellar cortex development,targeting of mRNA for destruction involved in RNA interference,mRNA 3'-end processing,mRNA 3'-end processing,siRNA loading onto RISC involved in RNA interference,siRNA loading onto RISC involved in RNA interference,siRNA loading onto RISC involved in RNA interference,ATP-dependent polydeoxyribonucleotide 5'-hydroxyl-kinase activity,polynucleotide 5'-hydroxyl-kinase activity,polydeoxyribonucleotide kinase activity,polydeoxyribonucleotide kinase activity,ATP-dependent polyribonucleotide 5'-hydroxyl-kinase activity,ATP-dependent polyribonucleotide 5'-hydroxyl-kinase activity
comp32544_c0_seq5.p1	sp|P30838|AL3A1_HUMAN_Aldehyde_dehydrogenase,_dimeric_NADP-preferring_OS=Homo_sapiens_GN=ALDH3A1_PE=1_SV=3	4.00E-111	GO:0001666,GO:0004028,GO:0004028,GO:0004028,GO:0004029,GO:0004030,GO:0004030,GO:0005615,GO:0005654,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005783,GO:0005829,GO:0005829,GO:0005886,GO:0006081,GO:0006081,GO:0007568,GO:0007584,GO:0008106,GO:0008152,GO:0008284,GO:0014070,GO:0016491,GO:0016491,GO:0016620,GO:0016620,GO:0042493,GO:0043231,GO:0051384,GO:0051591,GO:0055114,GO:0055114,GO:0055114	response to hypoxia,3-chloroallyl aldehyde dehydrogenase activity,3-chloroallyl aldehyde dehydrogenase activity,3-chloroallyl aldehyde dehydrogenase activity,aldehyde dehydrogenase (NAD) activity,aldehyde dehydrogenase [NAD(P)+] activity,aldehyde dehydrogenase [NAD(P)+] activity,extracellular space,nucleoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,endoplasmic reticulum,cytosol,cytosol,plasma membrane,cellular aldehyde metabolic process,cellular aldehyde metabolic process,aging,response to nutrient,alcohol dehydrogenase (NADP+) activity,metabolic process,positive regulation of cell proliferation,response to organic cyclic compound,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor,oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor,response to drug,intracellular membrane-bounded organelle,response to glucocorticoid,response to cAMP,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp32544_c0_seq6.p1	sp|P30839|AL3A2_RAT_Fatty_aldehyde_dehydrogenase_OS=Rattus_norvegicus_GN=Aldh3a2_PE=1_SV=1	7.00E-93	GO:0000302,GO:0004028,GO:0004029,GO:0004029,GO:0004030,GO:0005634,GO:0005783,GO:0005783,GO:0005789,GO:0005829,GO:0006081,GO:0008152,GO:0016020,GO:0016021,GO:0016491,GO:0016491,GO:0016620,GO:0042406,GO:0046292,GO:0055114,GO:0055114	response to reactive oxygen species,3-chloroallyl aldehyde dehydrogenase activity,aldehyde dehydrogenase (NAD) activity,aldehyde dehydrogenase (NAD) activity,aldehyde dehydrogenase [NAD(P)+] activity,nucleus,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,cytosol,cellular aldehyde metabolic process,metabolic process,membrane,integral component of membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor,extrinsic component of endoplasmic reticulum membrane,formaldehyde metabolic process,oxidation-reduction process,oxidation-reduction process
comp32544_c0_seq6.p2				
comp32544_c0_seq7.p1	sp|P30839|AL3A2_RAT_Fatty_aldehyde_dehydrogenase_OS=Rattus_norvegicus_GN=Aldh3a2_PE=1_SV=1	7.00E-93	GO:0000302,GO:0004028,GO:0004029,GO:0004029,GO:0004030,GO:0005634,GO:0005783,GO:0005783,GO:0005789,GO:0005829,GO:0006081,GO:0008152,GO:0016020,GO:0016021,GO:0016491,GO:0016491,GO:0016620,GO:0042406,GO:0046292,GO:0055114,GO:0055114	response to reactive oxygen species,3-chloroallyl aldehyde dehydrogenase activity,aldehyde dehydrogenase (NAD) activity,aldehyde dehydrogenase (NAD) activity,aldehyde dehydrogenase [NAD(P)+] activity,nucleus,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,cytosol,cellular aldehyde metabolic process,metabolic process,membrane,integral component of membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor,extrinsic component of endoplasmic reticulum membrane,formaldehyde metabolic process,oxidation-reduction process,oxidation-reduction process
comp32544_c0_seq7.p2				
comp32544_c0_seq9.p1	sp|P30838|AL3A1_HUMAN_Aldehyde_dehydrogenase,_dimeric_NADP-preferring_OS=Homo_sapiens_GN=ALDH3A1_PE=1_SV=3	6.00E-111	GO:0001666,GO:0004028,GO:0004028,GO:0004028,GO:0004029,GO:0004030,GO:0004030,GO:0005615,GO:0005654,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005783,GO:0005829,GO:0005829,GO:0005886,GO:0006081,GO:0006081,GO:0007568,GO:0007584,GO:0008106,GO:0008152,GO:0008284,GO:0014070,GO:0016491,GO:0016491,GO:0016620,GO:0016620,GO:0042493,GO:0043231,GO:0051384,GO:0051591,GO:0055114,GO:0055114,GO:0055114	response to hypoxia,3-chloroallyl aldehyde dehydrogenase activity,3-chloroallyl aldehyde dehydrogenase activity,3-chloroallyl aldehyde dehydrogenase activity,aldehyde dehydrogenase (NAD) activity,aldehyde dehydrogenase [NAD(P)+] activity,aldehyde dehydrogenase [NAD(P)+] activity,extracellular space,nucleoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,endoplasmic reticulum,cytosol,cytosol,plasma membrane,cellular aldehyde metabolic process,cellular aldehyde metabolic process,aging,response to nutrient,alcohol dehydrogenase (NADP+) activity,metabolic process,positive regulation of cell proliferation,response to organic cyclic compound,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor,oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor,response to drug,intracellular membrane-bounded organelle,response to glucocorticoid,response to cAMP,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp32544_c1_seq3.p1	sp|P47739|AL3A1_MOUSE_Aldehyde_dehydrogenase,_dimeric_NADP-preferring_OS=Mus_musculus_GN=Aldh3a1_PE=2_SV=1	7.00E-50	GO:0001666,GO:0004028,GO:0004028,GO:0004028,GO:0004029,GO:0004029,GO:0004030,GO:0004030,GO:0005615,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005783,GO:0005829,GO:0005829,GO:0005886,GO:0006081,GO:0006081,GO:0007568,GO:0007584,GO:0008106,GO:0008106,GO:0008152,GO:0008284,GO:0014070,GO:0016491,GO:0016491,GO:0016620,GO:0016620,GO:0042493,GO:0051384,GO:0051591,GO:0055114,GO:0055114,GO:0055114	response to hypoxia,3-chloroallyl aldehyde dehydrogenase activity,3-chloroallyl aldehyde dehydrogenase activity,3-chloroallyl aldehyde dehydrogenase activity,aldehyde dehydrogenase (NAD) activity,aldehyde dehydrogenase (NAD) activity,aldehyde dehydrogenase [NAD(P)+] activity,aldehyde dehydrogenase [NAD(P)+] activity,extracellular space,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytoplasm,endoplasmic reticulum,cytosol,cytosol,plasma membrane,cellular aldehyde metabolic process,cellular aldehyde metabolic process,aging,response to nutrient,alcohol dehydrogenase (NADP+) activity,alcohol dehydrogenase (NADP+) activity,metabolic process,positive regulation of cell proliferation,response to organic cyclic compound,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor,oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor,response to drug,response to glucocorticoid,response to cAMP,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp32545_c0_seq2.p1				
comp32545_c1_seq1.p2				
comp32545_c1_seq5.p1				
comp32546_c0_seq1.p1	sp|Q3V6T2|GRDN_HUMAN_Girdin_OS=Homo_sapiens_GN=CCDC88A_PE=1_SV=2	3.00E-13	GO:0001932,GO:0001932,GO:0003779,GO:0003779,GO:0005737,GO:0005783,GO:0005794,GO:0005829,GO:0005829,GO:0005886,GO:0005886,GO:0005886,GO:0006260,GO:0006275,GO:0006275,GO:0007399,GO:0008017,GO:0008017,GO:0010975,GO:0010975,GO:0016020,GO:0016020,GO:0016020,GO:0016020,GO:0016023,GO:0016477,GO:0016477,GO:0030027,GO:0030027,GO:0030032,GO:0031124,GO:0031410,GO:0031410,GO:0031929,GO:0031929,GO:0032148,GO:0032148,GO:0032956,GO:0032956,GO:0035091,GO:0042127,GO:0042127,GO:0042803,GO:0042995,GO:0043422,GO:0043422,GO:0061024	regulation of protein phosphorylation,regulation of protein phosphorylation,actin binding,actin binding,cytoplasm,endoplasmic reticulum,Golgi apparatus,cytosol,cytosol,plasma membrane,plasma membrane,plasma membrane,DNA replication,regulation of DNA replication,regulation of DNA replication,nervous system development,microtubule binding,microtubule binding,regulation of neuron projection development,regulation of neuron projection development,membrane,membrane,membrane,membrane,cytoplasmic membrane-bounded vesicle,cell migration,cell migration,lamellipodium,lamellipodium,lamellipodium assembly,cytoplasmic vesicle,cytoplasmic vesicle,TOR signaling,TOR signaling,activation of protein kinase B activity,activation of protein kinase B activity,regulation of actin cytoskeleton organization,regulation of actin cytoskeleton organization,phosphatidylinositol binding,regulation of cell proliferation,regulation of cell proliferation,protein homodimerization activity,cell projection,protein kinase B binding,protein kinase B binding,membrane organization
comp32546_c0_seq2.p1				
comp32547_c0_seq1.p1				
comp32547_c0_seq12.p1				
comp32547_c0_seq3.p1				
comp32547_c0_seq9.p1				
comp32548_c0_seq10.p1				
comp32548_c0_seq2.p1				
comp32548_c0_seq7.p1				
comp32548_c1_seq1.p1				
comp32549_c0_seq3.p1				
comp32549_c0_seq5.p1				
comp32549_c0_seq5.p2				
comp3255_c0_seq1.p1				
comp32550_c0_seq11.p1				
comp32550_c0_seq12.p1				
comp32550_c0_seq2.p1				
comp32550_c0_seq3.p1				
comp32550_c0_seq8.p1				
comp32551_c0_seq1.p1				
comp32551_c0_seq3.p1				
comp32551_c0_seq3.p2				
comp32552_c0_seq1.p1				
comp32552_c0_seq1.p2				
comp32552_c0_seq10.p1				
comp32552_c0_seq10.p4				
comp32552_c0_seq11.p1				
comp32552_c0_seq11.p4				
comp32552_c0_seq11.p5				
comp32552_c0_seq13.p1				
comp32552_c0_seq13.p2				
comp32552_c0_seq5.p2				
comp32552_c0_seq5.p4				
comp32552_c0_seq5.p5				
comp32552_c0_seq7.p1				
comp32552_c0_seq7.p5				
comp32552_c0_seq7.p8				
comp32553_c0_seq3.p1				
comp32554_c0_seq1.p1				
comp32554_c0_seq2.p1				
comp32554_c0_seq2.p3				
comp32554_c0_seq2.p8				
comp32554_c0_seq2.p9				
comp32555_c0_seq2.p2				
comp32556_c0_seq13.p1				
comp32556_c0_seq16.p1				
comp32556_c0_seq24.p1				
comp32556_c0_seq6.p1				
comp32557_c0_seq1.p2				
comp32557_c0_seq1.p3				
comp32557_c0_seq10.p2				
comp32557_c0_seq12.p2				
comp32557_c0_seq12.p3				
comp32557_c0_seq12.p6				
comp32557_c0_seq16.p1				
comp32557_c0_seq18.p1	sp|C9ZUU9|DRE2_TRYB9_Anamorsin_homolog_OS=Trypanosoma_brucei_gambiense_(strain_MHOM/CI/86/DAL972)_GN=TbgDal_VIII1370_PE=3_SV=1	7.00E-17	GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0005758,GO:0006915,GO:0016226,GO:0046872,GO:0051536,GO:0051536,GO:0051537	cytoplasm,cytoplasm,cytoplasm,mitochondrion,mitochondrial intermembrane space,apoptotic process,iron-sulfur cluster assembly,metal ion binding,iron-sulfur cluster binding,iron-sulfur cluster binding,2 iron, 2 sulfur cluster binding
comp32557_c0_seq19.p1				
comp32557_c0_seq5.p1				
comp32557_c0_seq5.p3				
comp32557_c0_seq6.p1				
comp32557_c0_seq9.p1				
comp32557_c1_seq3.p1				
comp32558_c0_seq1.p1				
comp32558_c0_seq4.p1				
comp32558_c0_seq5.p1				
comp32559_c1_seq16.p1				
comp32559_c1_seq19.p1				
comp32559_c1_seq21.p1				
comp32559_c1_seq24.p2				
comp32559_c1_seq5.p1				
comp32560_c0_seq2.p2				
comp32560_c0_seq6.p1				
comp32560_c0_seq9.p1				
comp32561_c0_seq4.p1				
comp32561_c0_seq9.p1				
comp32562_c0_seq1.p1	sp|Q07463|PUR7_VIGAC_Phosphoribosylaminoimidazole-succinocarboxamide_synthase,_chloroplastic_(Fragment)_OS=Vigna_aconitifolia_GN=PUR7_PE=2_SV=1	3.00E-53	GO:0000166,GO:0004639,GO:0004639,GO:0005524,GO:0005524,GO:0006164,GO:0006164,GO:0006189,GO:0009507,GO:0009507,GO:0009536,GO:0016874	nucleotide binding,phosphoribosylaminoimidazolesuccinocarboxamide synthase activity,phosphoribosylaminoimidazolesuccinocarboxamide synthase activity,ATP binding,ATP binding,purine nucleotide biosynthetic process,purine nucleotide biosynthetic process,'de novo' IMP biosynthetic process,chloroplast,chloroplast,plastid,ligase activity
comp32562_c0_seq2.p1	sp|Q5WW20|PUR7_LEGPL_Phosphoribosylaminoimidazole-succinocarboxamide_synthase_OS=Legionella_pneumophila_(strain_Lens)_GN=purC_PE=3_SV=1	2.00E-120	GO:0000166,GO:0004639,GO:0004639,GO:0004639,GO:0005524,GO:0005524,GO:0006164,GO:0006164,GO:0006189,GO:0006189,GO:0016874	nucleotide binding,phosphoribosylaminoimidazolesuccinocarboxamide synthase activity,phosphoribosylaminoimidazolesuccinocarboxamide synthase activity,phosphoribosylaminoimidazolesuccinocarboxamide synthase activity,ATP binding,ATP binding,purine nucleotide biosynthetic process,purine nucleotide biosynthetic process,'de novo' IMP biosynthetic process,'de novo' IMP biosynthetic process,ligase activity
comp32562_c1_seq1.p1				
comp32562_c1_seq18.p2				
comp32562_c1_seq2.p1	sp|Q9H3Q3|G3ST2_HUMAN_Galactose-3-O-sulfotransferase_2_OS=Homo_sapiens_GN=GAL3ST2_PE=1_SV=2	1.00E-12	GO:0001733,GO:0005794,GO:0005794,GO:0008146,GO:0008150,GO:0009058,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016740,GO:0032580	galactosylceramide sulfotransferase activity,Golgi apparatus,Golgi apparatus,sulfotransferase activity,biological_process,biosynthetic process,membrane,membrane,integral component of membrane,integral component of membrane,transferase activity,Golgi cisterna membrane
comp32562_c1_seq23.p1				
comp32562_c1_seq5.p1				
comp32562_c1_seq9.p1	sp|Q02357|ANK1_MOUSE_Ankyrin-1_OS=Mus_musculus_GN=Ank1_PE=1_SV=2	8.00E-15	GO:0005634,GO:0005737,GO:0005856,GO:0005856,GO:0005886,GO:0005886,GO:0006779,GO:0006888,GO:0007165,GO:0010638,GO:0014731,GO:0014731,GO:0015672,GO:0016020,GO:0016020,GO:0016020,GO:0016529,GO:0016529,GO:0016529,GO:0030018,GO:0030507,GO:0030673,GO:0030863,GO:0031430,GO:0031672,GO:0042383,GO:0043005,GO:0045211,GO:0048821,GO:0048821,GO:0051117,GO:0055072,GO:0072661	nucleus,cytoplasm,cytoskeleton,cytoskeleton,plasma membrane,plasma membrane,porphyrin-containing compound biosynthetic process,ER to Golgi vesicle-mediated transport,signal transduction,positive regulation of organelle organization,spectrin-associated cytoskeleton,spectrin-associated cytoskeleton,monovalent inorganic cation transport,membrane,membrane,membrane,sarcoplasmic reticulum,sarcoplasmic reticulum,sarcoplasmic reticulum,Z disc,spectrin binding,axolemma,cortical cytoskeleton,M band,A band,sarcolemma,neuron projection,postsynaptic membrane,erythrocyte development,erythrocyte development,ATPase binding,iron ion homeostasis,protein targeting to plasma membrane
comp32562_c2_seq2.p1	sp|P34046|GPA8_DICDI_Guanine_nucleotide-binding_protein_alpha-8_subunit_OS=Dictyostelium_discoideum_GN=gpaH_PE=2_SV=2	2.00E-94	GO:0000166,GO:0001664,GO:0003924,GO:0003924,GO:0004871,GO:0004871,GO:0004871,GO:0005515,GO:0005525,GO:0005834,GO:0006184,GO:0006184,GO:0007165,GO:0007165,GO:0007186,GO:0007188,GO:0019001,GO:0031683,GO:0031683,GO:0044351,GO:0046872	nucleotide binding,G-protein coupled receptor binding,GTPase activity,GTPase activity,signal transducer activity,signal transducer activity,signal transducer activity,protein binding,GTP binding,heterotrimeric G-protein complex,GTP catabolic process,GTP catabolic process,signal transduction,signal transduction,G-protein coupled receptor signaling pathway,adenylate cyclase-modulating G-protein coupled receptor signaling pathway,guanyl nucleotide binding,G-protein beta/gamma-subunit complex binding,G-protein beta/gamma-subunit complex binding,macropinocytosis,metal ion binding
comp32563_c0_seq1.p1				
comp32564_c0_seq1.p1				
comp32565_c0_seq2.p1	sp|Q3UN02|LCLT1_MOUSE_Lysocardiolipin_acyltransferase_1_OS=Mus_musculus_GN=Lclat1_PE=2_SV=2	7.00E-64	GO:0003841,GO:0005783,GO:0005783,GO:0005789,GO:0006629,GO:0007275,GO:0008152,GO:0008654,GO:0016020,GO:0016020,GO:0016021,GO:0016024,GO:0016740,GO:0016746,GO:0016746,GO:0016746	1-acylglycerol-3-phosphate O-acyltransferase activity,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,lipid metabolic process,multicellular organismal development,metabolic process,phospholipid biosynthetic process,membrane,membrane,integral component of membrane,CDP-diacylglycerol biosynthetic process,transferase activity,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups,transferase activity, transferring acyl groups
comp32566_c1_seq11.p1				
comp32566_c1_seq12.p1				
comp32566_c1_seq13.p1				
comp32566_c1_seq17.p1	sp|P65843|Y1738_MYCBO_Uncharacterized_RNA_pseudouridine_synthase_Mb1738_OS=Mycobacterium_bovis_GN=Mb1738_PE=3_SV=1	8.00E-26	GO:0001522,GO:0003723,GO:0003723,GO:0009451,GO:0009982,GO:0016853,GO:0016866	pseudouridine synthesis,RNA binding,RNA binding,RNA modification,pseudouridine synthase activity,isomerase activity,intramolecular transferase activity
comp32566_c1_seq24.p1				
comp32566_c1_seq3.p1	sp|Q0P5B7|AAAD_BOVIN_Arylacetamide_deacetylase_OS=Bos_taurus_GN=AADAC_PE=2_SV=1	8.00E-21	GO:0004806,GO:0005783,GO:0005789,GO:0008152,GO:0016020,GO:0016021,GO:0016021,GO:0016787,GO:0016787,GO:0031090,GO:0043231,GO:0052689	triglyceride lipase activity,endoplasmic reticulum,endoplasmic reticulum membrane,metabolic process,membrane,integral component of membrane,integral component of membrane,hydrolase activity,hydrolase activity,organelle membrane,intracellular membrane-bounded organelle,carboxylic ester hydrolase activity
comp32566_c1_seq4.p1				
comp32567_c0_seq3.p1	sp|Q6P3R8|NEK5_HUMAN_Serine/threonine-protein_kinase_Nek5_OS=Homo_sapiens_GN=NEK5_PE=1_SV=1	5.00E-81	GO:0000166,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005634,GO:0006468,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0046872,GO:0051155,GO:2001056	nucleotide binding,protein kinase activity,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,nucleus,protein phosphorylation,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,metal ion binding,positive regulation of striated muscle cell differentiation,positive regulation of cysteine-type endopeptidase activity
comp32567_c0_seq4.p1				
comp32568_c0_seq11.p1				
comp32568_c0_seq15.p1				
comp32568_c0_seq16.p1				
comp32568_c0_seq2.p1	sp|Q5I0R4|CK070_XENTR_Uncharacterized_protein_C11orf70_homolog_OS=Xenopus_tropicalis_PE=2_SV=1	4.00E-28		
comp32568_c0_seq21.p1				
comp32568_c1_seq1.p1				
comp32568_c1_seq2.p2				
comp32569_c0_seq5.p1	sp|Q8BSL4|HS3S5_MOUSE_Heparan_sulfate_glucosamine_3-O-sulfotransferase_5_OS=Mus_musculus_GN=Hs3st5_PE=2_SV=1	1.00E-12	GO:0000139,GO:0005575,GO:0005794,GO:0006477,GO:0008146,GO:0008467,GO:0008467,GO:0008467,GO:0015015,GO:0015015,GO:0016020,GO:0016021,GO:0016740,GO:0046596,GO:0046596,GO:0050819	Golgi membrane,cellular_component,Golgi apparatus,protein sulfation,sulfotransferase activity,[heparan sulfate]-glucosamine 3-sulfotransferase 1 activity,[heparan sulfate]-glucosamine 3-sulfotransferase 1 activity,[heparan sulfate]-glucosamine 3-sulfotransferase 1 activity,heparan sulfate proteoglycan biosynthetic process, enzymatic modification,heparan sulfate proteoglycan biosynthetic process, enzymatic modification,membrane,integral component of membrane,transferase activity,regulation of viral entry into host cell,regulation of viral entry into host cell,negative regulation of coagulation
comp32570_c0_seq2.p1				
comp32570_c0_seq5.p2				
comp32572_c1_seq10.p1	sp|Q96558|UGDH_SOYBN_UDP-glucose_6-dehydrogenase_OS=Glycine_max_PE=2_SV=1	0	GO:0003979,GO:0003979,GO:0006065,GO:0016491,GO:0016616,GO:0051287,GO:0055114,GO:0055114	UDP-glucose 6-dehydrogenase activity,UDP-glucose 6-dehydrogenase activity,UDP-glucuronate biosynthetic process,oxidoreductase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,NAD binding,oxidation-reduction process,oxidation-reduction process
comp32572_c1_seq11.p1	sp|Q0GZS3|USP_CUCME_UDP-sugar_pyrophospharylase_OS=Cucumis_melo_GN=USP_PE=1_SV=1	4.00E-167	GO:0008152,GO:0016740,GO:0016779,GO:0051748,GO:0070569	metabolic process,transferase activity,nucleotidyltransferase activity,UTP-monosaccharide-1-phosphate uridylyltransferase activity,uridylyltransferase activity
comp32572_c1_seq12.p1	sp|Q0GZS3|USP_CUCME_UDP-sugar_pyrophospharylase_OS=Cucumis_melo_GN=USP_PE=1_SV=1	2.00E-101	GO:0008152,GO:0016740,GO:0016779,GO:0051748,GO:0070569	metabolic process,transferase activity,nucleotidyltransferase activity,UTP-monosaccharide-1-phosphate uridylyltransferase activity,uridylyltransferase activity
comp32572_c1_seq13.p1	sp|Q0GZS3|USP_CUCME_UDP-sugar_pyrophospharylase_OS=Cucumis_melo_GN=USP_PE=1_SV=1	2.00E-55	GO:0008152,GO:0016740,GO:0016779,GO:0051748,GO:0070569	metabolic process,transferase activity,nucleotidyltransferase activity,UTP-monosaccharide-1-phosphate uridylyltransferase activity,uridylyltransferase activity
comp32572_c1_seq14.p1	sp|Q0GZS3|USP_CUCME_UDP-sugar_pyrophospharylase_OS=Cucumis_melo_GN=USP_PE=1_SV=1	9.00E-76	GO:0008152,GO:0016740,GO:0016779,GO:0051748,GO:0070569	metabolic process,transferase activity,nucleotidyltransferase activity,UTP-monosaccharide-1-phosphate uridylyltransferase activity,uridylyltransferase activity
comp32572_c1_seq2.p1	sp|Q0GZS3|USP_CUCME_UDP-sugar_pyrophospharylase_OS=Cucumis_melo_GN=USP_PE=1_SV=1	3.00E-69	GO:0008152,GO:0016740,GO:0016779,GO:0051748,GO:0070569	metabolic process,transferase activity,nucleotidyltransferase activity,UTP-monosaccharide-1-phosphate uridylyltransferase activity,uridylyltransferase activity
comp32572_c1_seq5.p1	sp|Q0GZS3|USP_CUCME_UDP-sugar_pyrophospharylase_OS=Cucumis_melo_GN=USP_PE=1_SV=1	4.00E-49	GO:0008152,GO:0016740,GO:0016779,GO:0051748,GO:0070569	metabolic process,transferase activity,nucleotidyltransferase activity,UTP-monosaccharide-1-phosphate uridylyltransferase activity,uridylyltransferase activity
comp32572_c1_seq6.p1	sp|Q0GZS3|USP_CUCME_UDP-sugar_pyrophospharylase_OS=Cucumis_melo_GN=USP_PE=1_SV=1	7.00E-146	GO:0008152,GO:0016740,GO:0016779,GO:0051748,GO:0070569	metabolic process,transferase activity,nucleotidyltransferase activity,UTP-monosaccharide-1-phosphate uridylyltransferase activity,uridylyltransferase activity
comp32572_c1_seq8.p1	sp|Q0GZS3|USP_CUCME_UDP-sugar_pyrophospharylase_OS=Cucumis_melo_GN=USP_PE=1_SV=1	2.00E-122	GO:0008152,GO:0016740,GO:0016779,GO:0051748,GO:0070569	metabolic process,transferase activity,nucleotidyltransferase activity,UTP-monosaccharide-1-phosphate uridylyltransferase activity,uridylyltransferase activity
comp32572_c1_seq9.p1	sp|Q9FM01|UGDH2_ARATH_Probable_UDP-glucose_6-dehydrogenase_2_OS=Arabidopsis_thaliana_GN=UGD2_PE=2_SV=1	0	GO:0003979,GO:0003979,GO:0005634,GO:0005829,GO:0006065,GO:0006065,GO:0009744,GO:0009749,GO:0009750,GO:0016491,GO:0016616,GO:0048046,GO:0051287,GO:0055114,GO:0055114	UDP-glucose 6-dehydrogenase activity,UDP-glucose 6-dehydrogenase activity,nucleus,cytosol,UDP-glucuronate biosynthetic process,UDP-glucuronate biosynthetic process,response to sucrose,response to glucose,response to fructose,oxidoreductase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,apoplast,NAD binding,oxidation-reduction process,oxidation-reduction process
comp32573_c0_seq1.p1	sp|Q6P798|RCBT2_RAT_RCC1_and_BTB_domain-containing_protein_2_OS=Rattus_norvegicus_GN=Rcbtb2_PE=2_SV=1	3.00E-19	GO:0001669	acrosomal vesicle
comp32573_c0_seq2.p1	sp|Q6P798|RCBT2_RAT_RCC1_and_BTB_domain-containing_protein_2_OS=Rattus_norvegicus_GN=Rcbtb2_PE=2_SV=1	3.00E-19	GO:0001669	acrosomal vesicle
comp32573_c0_seq3.p1	sp|Q5RCZ7|RCBT2_PONAB_RCC1_and_BTB_domain-containing_protein_2_OS=Pongo_abelii_GN=RCBTB2_PE=2_SV=1	2.00E-18	GO:0001669	acrosomal vesicle
comp32573_c0_seq5.p1	sp|Q52KW8|RCC2_XENLA_Protein_RCC2_homolog_OS=Xenopus_laevis_GN=rcc2_PE=2_SV=1	2.00E-11	GO:0000278,GO:0005634,GO:0005730,GO:0007032,GO:0007049,GO:0007067,GO:0051301,GO:0051301	mitotic cell cycle,nucleus,nucleolus,endosome organization,cell cycle,mitotic nuclear division,cell division,cell division
comp32573_c0_seq6.p1	sp|Q5RCZ7|RCBT2_PONAB_RCC1_and_BTB_domain-containing_protein_2_OS=Pongo_abelii_GN=RCBTB2_PE=2_SV=1	3.00E-18	GO:0001669	acrosomal vesicle
comp32575_c0_seq4.p1				
comp32575_c0_seq6.p1				
comp32575_c0_seq6.p2	sp|Q9ZVN4|Y1500_ARATH_Probable_tyrosine-protein_phosphatase_At1g05000_OS=Arabidopsis_thaliana_GN=At1g05000_PE=1_SV=1	2.00E-53	GO:0004721,GO:0004725,GO:0004725,GO:0016311,GO:0016787,GO:0016791,GO:0035335,GO:0035335	phosphoprotein phosphatase activity,protein tyrosine phosphatase activity,protein tyrosine phosphatase activity,dephosphorylation,hydrolase activity,phosphatase activity,peptidyl-tyrosine dephosphorylation,peptidyl-tyrosine dephosphorylation
comp32576_c0_seq1.p1	sp|O14981|BTAF1_HUMAN_TATA-binding_protein-associated_factor_172_OS=Homo_sapiens_GN=BTAF1_PE=1_SV=2	4.00E-39	GO:0000166,GO:0003677,GO:0003677,GO:0003700,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0008152,GO:0008152,GO:0016787,GO:0035562,GO:0045892	nucleotide binding,DNA binding,DNA binding,sequence-specific DNA binding transcription factor activity,helicase activity,ATP binding,ATP binding,nucleus,nucleus,metabolic process,metabolic process,hydrolase activity,negative regulation of chromatin binding,negative regulation of transcription, DNA-templated
comp32576_c0_seq1.p2	sp|O14981|BTAF1_HUMAN_TATA-binding_protein-associated_factor_172_OS=Homo_sapiens_GN=BTAF1_PE=1_SV=2	2.00E-14	GO:0000166,GO:0003677,GO:0003677,GO:0003700,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0008152,GO:0008152,GO:0016787,GO:0035562,GO:0045892	nucleotide binding,DNA binding,DNA binding,sequence-specific DNA binding transcription factor activity,helicase activity,ATP binding,ATP binding,nucleus,nucleus,metabolic process,metabolic process,hydrolase activity,negative regulation of chromatin binding,negative regulation of transcription, DNA-templated
comp32576_c0_seq1.p7				
comp32576_c0_seq6.p1	sp|Q92698|RAD54_HUMAN_DNA_repair_and_recombination_protein_RAD54-like_OS=Homo_sapiens_GN=RAD54L_PE=1_SV=2	4.00E-158	GO:0000166,GO:0000724,GO:0000733,GO:0003677,GO:0003677,GO:0004386,GO:0005515,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0006281,GO:0006281,GO:0006302,GO:0006310,GO:0006974,GO:0006974,GO:0007126,GO:0010212,GO:0016787,GO:0016817,GO:0036310,GO:0042493,GO:0051276	nucleotide binding,double-strand break repair via homologous recombination,DNA strand renaturation,DNA binding,DNA binding,helicase activity,protein binding,ATP binding,ATP binding,nucleus,nucleus,nucleus,nucleoplasm,DNA repair,DNA repair,double-strand break repair,DNA recombination,cellular response to DNA damage stimulus,cellular response to DNA damage stimulus,meiotic nuclear division,response to ionizing radiation,hydrolase activity,hydrolase activity, acting on acid anhydrides,annealing helicase activity,response to drug,chromosome organization
comp32576_c0_seq8.p1	sp|O14981|BTAF1_HUMAN_TATA-binding_protein-associated_factor_172_OS=Homo_sapiens_GN=BTAF1_PE=1_SV=2	1.00E-38	GO:0000166,GO:0003677,GO:0003677,GO:0003700,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0008152,GO:0008152,GO:0016787,GO:0035562,GO:0045892	nucleotide binding,DNA binding,DNA binding,sequence-specific DNA binding transcription factor activity,helicase activity,ATP binding,ATP binding,nucleus,nucleus,metabolic process,metabolic process,hydrolase activity,negative regulation of chromatin binding,negative regulation of transcription, DNA-templated
comp32577_c0_seq10.p1				
comp32577_c0_seq16.p1				
comp32577_c0_seq17.p2				
comp32577_c0_seq17.p6				
comp32577_c0_seq17.p7				
comp32577_c0_seq21.p2				
comp32577_c0_seq21.p3				
comp32577_c0_seq28.p1				
comp32577_c0_seq3.p1				
comp32577_c0_seq32.p3				
comp32577_c0_seq32.p4				
comp32577_c0_seq32.p5				
comp32577_c0_seq33.p1				
comp32577_c0_seq35.p1				
comp32577_c0_seq45.p1				
comp32577_c0_seq7.p3				
comp32577_c0_seq7.p6				
comp32577_c0_seq8.p1				
comp32578_c0_seq12.p1				
comp32578_c0_seq5.p1				
comp32579_c0_seq1.p1				
comp32579_c0_seq25.p2				
comp32579_c0_seq30.p1				
comp32579_c0_seq32.p1	sp|Q9EPI1|XYLT1_RAT_Xylosyltransferase_1_(Fragment)_OS=Rattus_norvegicus_GN=Xylt1_PE=2_SV=1	4.00E-20	GO:0000139,GO:0000139,GO:0003674,GO:0005575,GO:0005783,GO:0005789,GO:0005794,GO:0006024,GO:0008375,GO:0015012,GO:0016020,GO:0016020,GO:0016740,GO:0016757,GO:0030158,GO:0030158,GO:0030166,GO:0030206,GO:0048681,GO:0070555	Golgi membrane,Golgi membrane,molecular_function,cellular_component,endoplasmic reticulum,endoplasmic reticulum membrane,Golgi apparatus,glycosaminoglycan biosynthetic process,acetylglucosaminyltransferase activity,heparan sulfate proteoglycan biosynthetic process,membrane,membrane,transferase activity,transferase activity, transferring glycosyl groups,protein xylosyltransferase activity,protein xylosyltransferase activity,proteoglycan biosynthetic process,chondroitin sulfate biosynthetic process,negative regulation of axon regeneration,response to interleukin-1
comp32579_c0_seq32.p2	sp|P46351|YTH1_PANTH_Uncharacterized_45.4_kDa_protein_in_thiaminase_I_5'region_OS=Paenibacillus_thiaminolyticus_PE=4_SV=1	2.00E-11	GO:0008152,GO:0008152,GO:0016787,GO:0016787	metabolic process,metabolic process,hydrolase activity,hydrolase activity
comp32579_c0_seq35.p1	sp|Q9EPI1|XYLT1_RAT_Xylosyltransferase_1_(Fragment)_OS=Rattus_norvegicus_GN=Xylt1_PE=2_SV=1	4.00E-20	GO:0000139,GO:0000139,GO:0003674,GO:0005575,GO:0005783,GO:0005789,GO:0005794,GO:0006024,GO:0008375,GO:0015012,GO:0016020,GO:0016020,GO:0016740,GO:0016757,GO:0030158,GO:0030158,GO:0030166,GO:0030206,GO:0048681,GO:0070555	Golgi membrane,Golgi membrane,molecular_function,cellular_component,endoplasmic reticulum,endoplasmic reticulum membrane,Golgi apparatus,glycosaminoglycan biosynthetic process,acetylglucosaminyltransferase activity,heparan sulfate proteoglycan biosynthetic process,membrane,membrane,transferase activity,transferase activity, transferring glycosyl groups,protein xylosyltransferase activity,protein xylosyltransferase activity,proteoglycan biosynthetic process,chondroitin sulfate biosynthetic process,negative regulation of axon regeneration,response to interleukin-1
comp32579_c0_seq35.p3				
comp32579_c0_seq35.p4				
comp32579_c0_seq40.p1				
comp32579_c0_seq41.p1				
comp32579_c0_seq9.p1				
comp32580_c0_seq13.p1	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	5.00E-28	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq13.p2	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	7.00E-28	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq13.p5	sp|Q9N2V9|PDE6_CAEEL_Probable_3',5'-cyclic_phosphodiesterase_pde-6_OS=Caenorhabditis_elegans_GN=pde-6_PE=2_SV=1	8.00E-12	GO:0004114,GO:0004114,GO:0004115,GO:0004871,GO:0007165,GO:0008081,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0016787,GO:0046872,GO:1900194	3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,signal transducer activity,signal transduction,phosphoric diester hydrolase activity,metabolic process,metabolic process,metabolic process,metabolic process,metabolic process,hydrolase activity,metal ion binding,negative regulation of oocyte maturation
comp32580_c0_seq15.p1				
comp32580_c0_seq23.p1	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	7.00E-13	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq23.p2				
comp32580_c0_seq23.p3	sp|Q9N2V9|PDE6_CAEEL_Probable_3',5'-cyclic_phosphodiesterase_pde-6_OS=Caenorhabditis_elegans_GN=pde-6_PE=2_SV=1	4.00E-11	GO:0004114,GO:0004114,GO:0004115,GO:0004871,GO:0007165,GO:0008081,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0016787,GO:0046872,GO:1900194	3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,signal transducer activity,signal transduction,phosphoric diester hydrolase activity,metabolic process,metabolic process,metabolic process,metabolic process,metabolic process,hydrolase activity,metal ion binding,negative regulation of oocyte maturation
comp32580_c0_seq28.p1	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	5.00E-28	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq28.p2	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	5.00E-28	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq40.p1	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	7.00E-28	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq40.p2	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	7.00E-28	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq40.p5	sp|Q9N2V9|PDE6_CAEEL_Probable_3',5'-cyclic_phosphodiesterase_pde-6_OS=Caenorhabditis_elegans_GN=pde-6_PE=2_SV=1	8.00E-12	GO:0004114,GO:0004114,GO:0004115,GO:0004871,GO:0007165,GO:0008081,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0016787,GO:0046872,GO:1900194	3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,signal transducer activity,signal transduction,phosphoric diester hydrolase activity,metabolic process,metabolic process,metabolic process,metabolic process,metabolic process,hydrolase activity,metal ion binding,negative regulation of oocyte maturation
comp32580_c0_seq40.p6	sp|Q9N2V9|PDE6_CAEEL_Probable_3',5'-cyclic_phosphodiesterase_pde-6_OS=Caenorhabditis_elegans_GN=pde-6_PE=2_SV=1	8.00E-12	GO:0004114,GO:0004114,GO:0004115,GO:0004871,GO:0007165,GO:0008081,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0016787,GO:0046872,GO:1900194	3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,signal transducer activity,signal transduction,phosphoric diester hydrolase activity,metabolic process,metabolic process,metabolic process,metabolic process,metabolic process,hydrolase activity,metal ion binding,negative regulation of oocyte maturation
comp32580_c0_seq47.p1	sp|Q9Z286|ADCYA_RAT_Adenylate_cyclase_type_10_OS=Rattus_norvegicus_GN=Adcy10_PE=1_SV=1	6.00E-41	GO:0000166,GO:0000287,GO:0004016,GO:0004016,GO:0004016,GO:0004016,GO:0004016,GO:0004016,GO:0005524,GO:0005737,GO:0005737,GO:0005739,GO:0005739,GO:0005814,GO:0005829,GO:0005856,GO:0005856,GO:0005886,GO:0005886,GO:0006171,GO:0006171,GO:0006171,GO:0006171,GO:0006171,GO:0007283,GO:0009190,GO:0016020,GO:0016020,GO:0016829,GO:0016849,GO:0030145,GO:0030424,GO:0030425,GO:0030426,GO:0035556,GO:0043025,GO:0043065,GO:0045177,GO:0045178,GO:0046872,GO:0048471,GO:0051117	nucleotide binding,magnesium ion binding,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,ATP binding,cytoplasm,cytoplasm,mitochondrion,mitochondrion,centriole,cytosol,cytoskeleton,cytoskeleton,plasma membrane,plasma membrane,cAMP biosynthetic process,cAMP biosynthetic process,cAMP biosynthetic process,cAMP biosynthetic process,cAMP biosynthetic process,spermatogenesis,cyclic nucleotide biosynthetic process,membrane,membrane,lyase activity,phosphorus-oxygen lyase activity,manganese ion binding,axon,dendrite,growth cone,intracellular signal transduction,neuronal cell body,positive regulation of apoptotic process,apical part of cell,basal part of cell,metal ion binding,perinuclear region of cytoplasm,ATPase binding
comp32580_c0_seq49.p1	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	7.00E-28	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq49.p2	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	7.00E-28	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq49.p5	sp|Q9N2V9|PDE6_CAEEL_Probable_3',5'-cyclic_phosphodiesterase_pde-6_OS=Caenorhabditis_elegans_GN=pde-6_PE=2_SV=1	8.00E-12	GO:0004114,GO:0004114,GO:0004115,GO:0004871,GO:0007165,GO:0008081,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0016787,GO:0046872,GO:1900194	3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,signal transducer activity,signal transduction,phosphoric diester hydrolase activity,metabolic process,metabolic process,metabolic process,metabolic process,metabolic process,hydrolase activity,metal ion binding,negative regulation of oocyte maturation
comp32580_c0_seq49.p6	sp|Q9N2V9|PDE6_CAEEL_Probable_3',5'-cyclic_phosphodiesterase_pde-6_OS=Caenorhabditis_elegans_GN=pde-6_PE=2_SV=1	8.00E-12	GO:0004114,GO:0004114,GO:0004115,GO:0004871,GO:0007165,GO:0008081,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0016787,GO:0046872,GO:1900194	3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,signal transducer activity,signal transduction,phosphoric diester hydrolase activity,metabolic process,metabolic process,metabolic process,metabolic process,metabolic process,hydrolase activity,metal ion binding,negative regulation of oocyte maturation
comp32580_c0_seq52.p1	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	7.00E-28	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq52.p2				
comp32580_c0_seq52.p5	sp|Q9N2V9|PDE6_CAEEL_Probable_3',5'-cyclic_phosphodiesterase_pde-6_OS=Caenorhabditis_elegans_GN=pde-6_PE=2_SV=1	8.00E-12	GO:0004114,GO:0004114,GO:0004115,GO:0004871,GO:0007165,GO:0008081,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0016787,GO:0046872,GO:1900194	3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,signal transducer activity,signal transduction,phosphoric diester hydrolase activity,metabolic process,metabolic process,metabolic process,metabolic process,metabolic process,hydrolase activity,metal ion binding,negative regulation of oocyte maturation
comp32580_c0_seq6.p1	sp|Q9Z286|ADCYA_RAT_Adenylate_cyclase_type_10_OS=Rattus_norvegicus_GN=Adcy10_PE=1_SV=1	3.00E-42	GO:0000166,GO:0000287,GO:0004016,GO:0004016,GO:0004016,GO:0004016,GO:0004016,GO:0004016,GO:0005524,GO:0005737,GO:0005737,GO:0005739,GO:0005739,GO:0005814,GO:0005829,GO:0005856,GO:0005856,GO:0005886,GO:0005886,GO:0006171,GO:0006171,GO:0006171,GO:0006171,GO:0006171,GO:0007283,GO:0009190,GO:0016020,GO:0016020,GO:0016829,GO:0016849,GO:0030145,GO:0030424,GO:0030425,GO:0030426,GO:0035556,GO:0043025,GO:0043065,GO:0045177,GO:0045178,GO:0046872,GO:0048471,GO:0051117	nucleotide binding,magnesium ion binding,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,ATP binding,cytoplasm,cytoplasm,mitochondrion,mitochondrion,centriole,cytosol,cytoskeleton,cytoskeleton,plasma membrane,plasma membrane,cAMP biosynthetic process,cAMP biosynthetic process,cAMP biosynthetic process,cAMP biosynthetic process,cAMP biosynthetic process,spermatogenesis,cyclic nucleotide biosynthetic process,membrane,membrane,lyase activity,phosphorus-oxygen lyase activity,manganese ion binding,axon,dendrite,growth cone,intracellular signal transduction,neuronal cell body,positive regulation of apoptotic process,apical part of cell,basal part of cell,metal ion binding,perinuclear region of cytoplasm,ATPase binding
comp32580_c0_seq70.p1	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	5.00E-28	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq70.p2	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	7.00E-13	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq70.p5	sp|Q9N2V9|PDE6_CAEEL_Probable_3',5'-cyclic_phosphodiesterase_pde-6_OS=Caenorhabditis_elegans_GN=pde-6_PE=2_SV=1	8.00E-12	GO:0004114,GO:0004114,GO:0004115,GO:0004871,GO:0007165,GO:0008081,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0016787,GO:0046872,GO:1900194	3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,signal transducer activity,signal transduction,phosphoric diester hydrolase activity,metabolic process,metabolic process,metabolic process,metabolic process,metabolic process,hydrolase activity,metal ion binding,negative regulation of oocyte maturation
comp32580_c0_seq77.p1	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	5.00E-28	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq77.p2	sp|Q23917|PDE2_DICDI_3',5'-cyclic-nucleotide_phosphodiesterase_regA_OS=Dictyostelium_discoideum_GN=regA_PE=1_SV=1	7.00E-13	GO:0000160,GO:0000166,GO:0004114,GO:0004115,GO:0004115,GO:0005622,GO:0005737,GO:0005829,GO:0006198,GO:0006970,GO:0007165,GO:0007275,GO:0008081,GO:0016787,GO:0030435,GO:0030552,GO:0030587,GO:0030587,GO:0031276,GO:0031276,GO:0046058,GO:0046872,GO:0048837,GO:0051279,GO:0051281,GO:0047555	phosphorelay signal transduction system,nucleotide binding,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,intracellular,cytoplasm,cytosol,cAMP catabolic process,response to osmotic stress,signal transduction,multicellular organismal development,phosphoric diester hydrolase activity,hydrolase activity,sporulation resulting in formation of a cellular spore,cAMP binding,sorocarp development,sorocarp development,negative regulation of lateral pseudopodium assembly,negative regulation of lateral pseudopodium assembly,cAMP metabolic process,metal ion binding,sorus development,regulation of release of sequestered calcium ion into cytosol,positive regulation of release of sequestered calcium ion into cytosol,3',5'-cyclic-GMP phosphodiesterase activity
comp32580_c0_seq77.p5	sp|Q9N2V9|PDE6_CAEEL_Probable_3',5'-cyclic_phosphodiesterase_pde-6_OS=Caenorhabditis_elegans_GN=pde-6_PE=2_SV=1	8.00E-12	GO:0004114,GO:0004114,GO:0004115,GO:0004871,GO:0007165,GO:0008081,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0008152,GO:0016787,GO:0046872,GO:1900194	3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,signal transducer activity,signal transduction,phosphoric diester hydrolase activity,metabolic process,metabolic process,metabolic process,metabolic process,metabolic process,hydrolase activity,metal ion binding,negative regulation of oocyte maturation
comp32580_c0_seq83.p1				
comp32581_c0_seq1.p1				
comp32581_c0_seq10.p1	sp|A5PK39|TPP2_BOVIN_Tripeptidyl-peptidase_2_OS=Bos_taurus_GN=TPP2_PE=2_SV=1	0	GO:0004177,GO:0004252,GO:0004252,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006508,GO:0006508,GO:0006508,GO:0008233,GO:0008236,GO:0016787	aminopeptidase activity,serine-type endopeptidase activity,serine-type endopeptidase activity,nucleus,nucleus,cytoplasm,cytoplasm,proteolysis,proteolysis,proteolysis,peptidase activity,serine-type peptidase activity,hydrolase activity
comp32581_c0_seq10.p3				
comp32581_c0_seq11.p1	sp|Q9UT05|TPP2_SCHPO_Tripeptidyl-peptidase_2_homolog_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAP8A3.12c_PE=1_SV=1	9.00E-14	GO:0004177,GO:0004252,GO:0005737,GO:0005737,GO:0005829,GO:0006508,GO:0006508,GO:0008233,GO:0008240,GO:0016787	aminopeptidase activity,serine-type endopeptidase activity,cytoplasm,cytoplasm,cytosol,proteolysis,proteolysis,peptidase activity,tripeptidyl-peptidase activity,hydrolase activity
comp32581_c0_seq5.p1				
comp32581_c0_seq8.p1	sp|A5PK39|TPP2_BOVIN_Tripeptidyl-peptidase_2_OS=Bos_taurus_GN=TPP2_PE=2_SV=1	3.00E-54	GO:0004177,GO:0004252,GO:0004252,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006508,GO:0006508,GO:0006508,GO:0008233,GO:0008236,GO:0016787	aminopeptidase activity,serine-type endopeptidase activity,serine-type endopeptidase activity,nucleus,nucleus,cytoplasm,cytoplasm,proteolysis,proteolysis,proteolysis,peptidase activity,serine-type peptidase activity,hydrolase activity
comp32582_c0_seq14.p1	sp|Q8N8A2|ANR44_HUMAN_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_B_OS=Homo_sapiens_GN=ANKRD44_PE=1_SV=3	2.00E-58	GO:0005515,GO:0005515,GO:0005515	protein binding,protein binding,protein binding
comp32582_c0_seq14.p2	sp|Q9ULJ7|ANR50_HUMAN_Ankyrin_repeat_domain-containing_protein_50_OS=Homo_sapiens_GN=ANKRD50_PE=1_SV=4	1.00E-15	GO:0005515	protein binding
comp32582_c0_seq4.p1				
comp32582_c0_seq4.p2				
comp32582_c0_seq7.p1				
comp32582_c0_seq7.p2				
comp32582_c0_seq8.p1				
comp32583_c0_seq16.p1				
comp32583_c0_seq16.p2				
comp32583_c0_seq17.p1				
comp32583_c0_seq2.p2				
comp32583_c0_seq20.p1				
comp32583_c0_seq22.p1				
comp32583_c0_seq25.p1				
comp32583_c0_seq26.p1				
comp32583_c0_seq30.p1				
comp32583_c0_seq31.p1				
comp32583_c0_seq36.p1				
comp32583_c0_seq36.p2				
comp32585_c0_seq11.p1				

comp32585_c0_seq18.p1	sp|P46864|ATK2_ARATH_Kinesin-2_OS=Arabidopsis_thaliana_GN=ATK2_PE=2_SV=1	7.00E-41	GO:0000023,GO:0000070,GO:0000166,GO:0000226,GO:0000394,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005871,GO:0005871,GO:0005874,GO:0006200,GO:0007018,GO:0007018,GO:0008017,GO:0008017,GO:0008569,GO:0009086,GO:0010075,GO:0010228,GO:0016117,GO:0016887,GO:0019252,GO:0043085,GO:0051225	maltose metabolic process,mitotic sister chromatid segregation,nucleotide binding,microtubule cytoskeleton organization,RNA splicing, via endonucleolytic cleavage and ligation,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,kinesin complex,kinesin complex,microtubule,ATP catabolic process,microtubule-based movement,microtubule-based movement,microtubule binding,microtubule binding,minus-end-directed microtubule motor activity,methionine biosynthetic process,regulation of meristem growth,vegetative to reproductive phase transition of meristem,carotenoid biosynthetic process,ATPase activity,starch biosynthetic process,positive regulation of catalytic activity,spindle assembly
comp32585_c0_seq2.p1	sp|Q07970|ATK1_ARATH_Kinesin-1_OS=Arabidopsis_thaliana_GN=ATK1_PE=2_SV=1	5.00E-40	GO:0000070,GO:0000166,GO:0000226,GO:0000911,GO:0003777,GO:0005524,GO:0005524,GO:0005634,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005871,GO:0005872,GO:0005874,GO:0006200,GO:0006275,GO:0006306,GO:0006342,GO:0006346,GO:0007018,GO:0007018,GO:0007049,GO:0007067,GO:0008017,GO:0008569,GO:0008569,GO:0009524,GO:0009909,GO:0009971,GO:0010389,GO:0016570,GO:0016887,GO:0031047,GO:0031048,GO:0048449,GO:0051301,GO:0051321,GO:0051567	mitotic sister chromatid segregation,nucleotide binding,microtubule cytoskeleton organization,cytokinesis by cell plate formation,microtubule motor activity,ATP binding,ATP binding,nucleus,cytoplasm,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,kinesin complex,minus-end kinesin complex,microtubule,ATP catabolic process,regulation of DNA replication,DNA methylation,chromatin silencing,methylation-dependent chromatin silencing,microtubule-based movement,microtubule-based movement,cell cycle,mitotic nuclear division,microtubule binding,minus-end-directed microtubule motor activity,minus-end-directed microtubule motor activity,phragmoplast,regulation of flower development,anastral spindle assembly involved in male meiosis,regulation of G2/M transition of mitotic cell cycle,histone modification,ATPase activity,gene silencing by RNA,chromatin silencing by small RNA,floral organ formation,cell division,meiotic cell cycle,histone H3-K9 methylation
comp32585_c0_seq20.p1	sp|P28739|KLPA_EMENI_Kinesin-like_protein_klpA_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=klpA_PE=2_SV=3	1.00E-22	GO:0000070,GO:0000166,GO:0000235,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005871,GO:0005874,GO:0005876,GO:0005881,GO:0006200,GO:0007018,GO:0007018,GO:0007019,GO:0008017,GO:0008152,GO:0008152,GO:0008152,GO:0008569,GO:0008574,GO:0016887,GO:0090307	mitotic sister chromatid segregation,nucleotide binding,astral microtubule,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,kinesin complex,microtubule,spindle microtubule,cytoplasmic microtubule,ATP catabolic process,microtubule-based movement,microtubule-based movement,microtubule depolymerization,microtubule binding,metabolic process,metabolic process,metabolic process,minus-end-directed microtubule motor activity,plus-end-directed microtubule motor activity,ATPase activity,spindle assembly involved in mitosis
comp32585_c0_seq22.p1	sp|P46875|ATK3_ARATH_Kinesin-3_OS=Arabidopsis_thaliana_GN=ATK3_PE=2_SV=1	3.00E-40	GO:0000070,GO:0000166,GO:0000226,GO:0000911,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005871,GO:0005874,GO:0006200,GO:0007018,GO:0007018,GO:0007049,GO:0007067,GO:0008017,GO:0008017,GO:0008152,GO:0008152,GO:0008569,GO:0016887,GO:0051225,GO:0051301	mitotic sister chromatid segregation,nucleotide binding,microtubule cytoskeleton organization,cytokinesis by cell plate formation,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,kinesin complex,microtubule,ATP catabolic process,microtubule-based movement,microtubule-based movement,cell cycle,mitotic nuclear division,microtubule binding,microtubule binding,metabolic process,metabolic process,minus-end-directed microtubule motor activity,ATPase activity,spindle assembly,cell division
comp32585_c0_seq3.p2				
comp32585_c0_seq3.p3	sp|Q5XI63|KIFC1_RAT_Kinesin-like_protein_KIFC1_OS=Rattus_norvegicus_GN=Kifc1_PE=2_SV=1	1.00E-15	GO:0000070,GO:0000166,GO:0003777,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005737,GO:0005768,GO:0005769,GO:0005815,GO:0005819,GO:0005856,GO:0005871,GO:0005871,GO:0005874,GO:0006200,GO:0007018,GO:0007018,GO:0007049,GO:0007067,GO:0007080,GO:0008017,GO:0008152,GO:0008152,GO:0008569,GO:0016020,GO:0016887,GO:0051225,GO:0051301,GO:0090307	mitotic sister chromatid segregation,nucleotide binding,microtubule motor activity,ATP binding,ATP binding,nucleus,nucleus,cytoplasm,endosome,early endosome,microtubule organizing center,spindle,cytoskeleton,kinesin complex,kinesin complex,microtubule,ATP catabolic process,microtubule-based movement,microtubule-based movement,cell cycle,mitotic nuclear division,mitotic metaphase plate congression,microtubule binding,metabolic process,metabolic process,minus-end-directed microtubule motor activity,membrane,ATPase activity,spindle assembly,cell division,spindle assembly involved in mitosis
comp32585_c0_seq7.p1				
comp32585_c0_seq8.p1	sp|Q07970|ATK1_ARATH_Kinesin-1_OS=Arabidopsis_thaliana_GN=ATK1_PE=2_SV=1	2.00E-46	GO:0000070,GO:0000166,GO:0000226,GO:0000911,GO:0003777,GO:0005524,GO:0005524,GO:0005634,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005871,GO:0005872,GO:0005874,GO:0006200,GO:0006275,GO:0006306,GO:0006342,GO:0006346,GO:0007018,GO:0007018,GO:0007049,GO:0007067,GO:0008017,GO:0008569,GO:0008569,GO:0009524,GO:0009909,GO:0009971,GO:0010389,GO:0016570,GO:0016887,GO:0031047,GO:0031048,GO:0048449,GO:0051301,GO:0051321,GO:0051567	mitotic sister chromatid segregation,nucleotide binding,microtubule cytoskeleton organization,cytokinesis by cell plate formation,microtubule motor activity,ATP binding,ATP binding,nucleus,cytoplasm,cytoplasm,cytoskeleton,cytoskeleton,kinesin complex,kinesin complex,minus-end kinesin complex,microtubule,ATP catabolic process,regulation of DNA replication,DNA methylation,chromatin silencing,methylation-dependent chromatin silencing,microtubule-based movement,microtubule-based movement,cell cycle,mitotic nuclear division,microtubule binding,minus-end-directed microtubule motor activity,minus-end-directed microtubule motor activity,phragmoplast,regulation of flower development,anastral spindle assembly involved in male meiosis,regulation of G2/M transition of mitotic cell cycle,histone modification,ATPase activity,gene silencing by RNA,chromatin silencing by small RNA,floral organ formation,cell division,meiotic cell cycle,histone H3-K9 methylation
comp32586_c0_seq11.p1				
comp32586_c0_seq2.p1	sp|Q9SKK0|EBF1_ARATH_EIN3-binding_F-box_protein_1_OS=Arabidopsis_thaliana_GN=EBF1_PE=1_SV=1	1.00E-11	GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0006511,GO:0006511,GO:0009723,GO:0009873,GO:0010105,GO:0016567,GO:0042752	protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,nucleus,ubiquitin-dependent protein catabolic process,ubiquitin-dependent protein catabolic process,response to ethylene,ethylene-activated signaling pathway,negative regulation of ethylene-activated signaling pathway,protein ubiquitination,regulation of circadian rhythm
comp32586_c0_seq4.p1				
comp32586_c0_seq5.p1	sp|Q99NH0|ANR17_MOUSE_Ankyrin_repeat_domain-containing_protein_17_OS=Mus_musculus_GN=Ankrd17_PE=1_SV=2	1.00E-17	GO:0000785,GO:0001955,GO:0003682,GO:0003723,GO:0003723,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0006275,GO:0007492,GO:0016020,GO:0042742,GO:0043123,GO:0044822,GO:0045787,GO:0051151,GO:1900087,GO:1900245,GO:1900246	chromatin,blood vessel maturation,chromatin binding,RNA binding,RNA binding,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,cytoplasm,regulation of DNA replication,endoderm development,membrane,defense response to bacterium,positive regulation of I-kappaB kinase/NF-kappaB signaling,poly(A) RNA binding,positive regulation of cell cycle,negative regulation of smooth muscle cell differentiation,positive regulation of G1/S transition of mitotic cell cycle,positive regulation of MDA-5 signaling pathway,positive regulation of RIG-I signaling pathway
comp32587_c0_seq1.p1				
comp32587_c1_seq11.p1				
comp32587_c1_seq12.p1	sp|Q84M24|AB1A_ARATH_ABC_transporter_A_family_member_1_OS=Arabidopsis_thaliana_GN=ABCA1_PE=2_SV=2	0	GO:0000166,GO:0005524,GO:0005524,GO:0005774,GO:0006200,GO:0006486,GO:0006487,GO:0006810,GO:0016020,GO:0016020,GO:0016021,GO:0016887	nucleotide binding,ATP binding,ATP binding,vacuolar membrane,ATP catabolic process,protein glycosylation,protein N-linked glycosylation,transport,membrane,membrane,integral component of membrane,ATPase activity
comp32587_c1_seq2.p1	sp|Q84M24|AB1A_ARATH_ABC_transporter_A_family_member_1_OS=Arabidopsis_thaliana_GN=ABCA1_PE=2_SV=2	2.00E-95	GO:0000166,GO:0005524,GO:0005524,GO:0005774,GO:0006200,GO:0006486,GO:0006487,GO:0006810,GO:0016020,GO:0016020,GO:0016021,GO:0016887	nucleotide binding,ATP binding,ATP binding,vacuolar membrane,ATP catabolic process,protein glycosylation,protein N-linked glycosylation,transport,membrane,membrane,integral component of membrane,ATPase activity
comp32587_c1_seq3.p1	sp|Q84M24|AB1A_ARATH_ABC_transporter_A_family_member_1_OS=Arabidopsis_thaliana_GN=ABCA1_PE=2_SV=2	0	GO:0000166,GO:0005524,GO:0005524,GO:0005774,GO:0006200,GO:0006486,GO:0006487,GO:0006810,GO:0016020,GO:0016020,GO:0016021,GO:0016887	nucleotide binding,ATP binding,ATP binding,vacuolar membrane,ATP catabolic process,protein glycosylation,protein N-linked glycosylation,transport,membrane,membrane,integral component of membrane,ATPase activity
comp32587_c1_seq6.p1	sp|Q84M24|AB1A_ARATH_ABC_transporter_A_family_member_1_OS=Arabidopsis_thaliana_GN=ABCA1_PE=2_SV=2	6.00E-137	GO:0000166,GO:0005524,GO:0005524,GO:0005774,GO:0006200,GO:0006486,GO:0006487,GO:0006810,GO:0016020,GO:0016020,GO:0016021,GO:0016887	nucleotide binding,ATP binding,ATP binding,vacuolar membrane,ATP catabolic process,protein glycosylation,protein N-linked glycosylation,transport,membrane,membrane,integral component of membrane,ATPase activity
comp32587_c1_seq7.p1	sp|Q84M24|AB1A_ARATH_ABC_transporter_A_family_member_1_OS=Arabidopsis_thaliana_GN=ABCA1_PE=2_SV=2	4.00E-29	GO:0000166,GO:0005524,GO:0005524,GO:0005774,GO:0006200,GO:0006486,GO:0006487,GO:0006810,GO:0016020,GO:0016020,GO:0016021,GO:0016887	nucleotide binding,ATP binding,ATP binding,vacuolar membrane,ATP catabolic process,protein glycosylation,protein N-linked glycosylation,transport,membrane,membrane,integral component of membrane,ATPase activity
comp32587_c1_seq8.p1	sp|Q84M24|AB1A_ARATH_ABC_transporter_A_family_member_1_OS=Arabidopsis_thaliana_GN=ABCA1_PE=2_SV=2	0	GO:0000166,GO:0005524,GO:0005524,GO:0005774,GO:0006200,GO:0006486,GO:0006487,GO:0006810,GO:0016020,GO:0016020,GO:0016021,GO:0016887	nucleotide binding,ATP binding,ATP binding,vacuolar membrane,ATP catabolic process,protein glycosylation,protein N-linked glycosylation,transport,membrane,membrane,integral component of membrane,ATPase activity
comp32588_c0_seq12.p1				
comp32588_c0_seq16.p1				
comp32588_c0_seq26.p1				
comp32588_c0_seq27.p1				
comp32588_c0_seq57.p1				
comp32589_c0_seq12.p1	sp|Q2T9N0|FSCB_BOVIN_Fibrous_sheath_CABYR-binding_protein_OS=Bos_taurus_GN=FSCB_PE=2_SV=1	3.00E-13	GO:0005929,GO:0031514,GO:0042995	cilium,motile cilium,cell projection
comp32589_c0_seq12.p3				
comp32589_c0_seq14.p1				
comp32589_c0_seq15.p1				
comp32589_c0_seq4.p1				
comp32589_c0_seq6.p1	sp|Q2T9N0|FSCB_BOVIN_Fibrous_sheath_CABYR-binding_protein_OS=Bos_taurus_GN=FSCB_PE=2_SV=1	6.00E-11	GO:0005929,GO:0031514,GO:0042995	cilium,motile cilium,cell projection
comp32590_c0_seq15.p1				
comp32590_c0_seq15.p5				
comp32590_c0_seq16.p2				
comp32590_c0_seq4.p1				
comp32590_c0_seq4.p2				

comp32655_c2_seq14.p1				
comp32655_c2_seq2.p1				
comp32655_c2_seq2.p2				
comp32655_c2_seq32.p1				
comp32655_c2_seq5.p2				
comp32655_c2_seq9.p1				
comp32656_c0_seq11.p1				
comp32656_c0_seq6.p1				
comp32657_c1_seq1.p1				
comp32658_c0_seq1.p1				
comp32658_c0_seq13.p1				
comp32658_c0_seq14.p1				
comp32658_c0_seq14.p2				
comp32658_c0_seq19.p2				
comp32658_c0_seq4.p2				
comp32658_c0_seq5.p1	sp|Q7XQ12|AMT11_ORYSJ_Ammonium_transporter_1_member_1_OS=Oryza_sativa_subsp._japonica_GN=AMT1-1_PE=2_SV=1	2.00E-80	[illegible]	[illegible]
comp32658_c0_seq6.p1				
comp32658_c0_seq6.p2				
comp32658_c0_seq7.p2				
comp32659_c0_seq10.p1				
comp32659_c0_seq16.p1				
comp32659_c0_seq26.p1				
comp32659_c0_seq27.p1				
comp32659_c0_seq27.p2				
comp32659_c0_seq30.p1				
comp32659_c0_seq30.p5				
comp32659_c0_seq46.p1				
comp32659_c0_seq48.p1				
comp32659_c0_seq49.p1				
comp32659_c0_seq49.p3				
comp32659_c0_seq51.p1				
comp32659_c0_seq7.p2				
comp32660_c0_seq6.p1				
comp32661_c0_seq1.p1				
comp32661_c0_seq2.p1				
comp32661_c0_seq8.p1				
comp32662_c0_seq12.p1				
comp32662_c0_seq4.p2				
comp32663_c0_seq1.p1				
comp32664_c1_seq1.p1	sp|Q7Z494|NPHP3_HUMAN_Nephrocystin-3_OS=Homo_sapiens_GN=NPHP3_PE=1_SV=1	2.00E-43	[illegible]	[illegible]
comp32664_c1_seq2.p1	sp|Q7Z494|NPHP3_HUMAN_Nephrocystin-3_OS=Homo_sapiens_GN=NPHP3_PE=1_SV=1	8.00E-44	[illegible]	[illegible]
comp32664_c2_seq11.p1				
comp32664_c2_seq13.p2				
comp32664_c2_seq14.p1				
comp32664_c2_seq19.p1				
comp32664_c2_seq8.p1				
comp32664_c2_seq9.p1				
comp32664_c2_seq9.p2				
comp32665_c0_seq2.p1				
comp32665_c0_seq6.p1				
comp32665_c0_seq8.p1				
comp32666_c0_seq11.p2				
comp32666_c0_seq15.p1	sp|P53860|PDR16_YEAST_Phosphatidylinositol_transfer_protein_PDR16_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PDR16_PE=1_SV=1	2.00E-14	[illegible]	[illegible]
comp32666_c0_seq15.p4				
comp32666_c0_seq8.p1	sp|P53860|PDR16_YEAST_Phosphatidylinositol_transfer_protein_PDR16_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PDR16_PE=1_SV=1	4.00E-14	[illegible]	[illegible]
comp32667_c0_seq11.p1	sp|Q54T06|Y8206_DICDI_Probable_zinc_transporter_protein_DDB_G0282067_OS=Dictyostelium_discoideum_GN=DDB_G0282067_PE=2_SV=1	2.00E-14	[illegible]	[illegible]
comp32667_c0_seq14.p1	sp|O80842|CFTSY_ARATH_Cell_division_protein_FtsY_homolog,_chloroplastic_OS=Arabidopsis_thaliana_GN=CPFTSY_PE=1_SV=2	1.00E-52	[illegible]	[illegible]
comp32667_c0_seq2.p1				
comp32667_c0_seq2.p2				
comp32667_c0_seq20.p1				
comp32667_c0_seq21.p1				
comp32667_c0_seq3.p1				
comp32667_c0_seq4.p1	sp|Q54T06|Y8206_DICDI_Probable_zinc_transporter_protein_DDB_G0282067_OS=Dictyostelium_discoideum_GN=DDB_G0282067_PE=2_SV=1	1.00E-37	[illegible]	[illegible]
comp32667_c0_seq6.p1				
comp32667_c0_seq7.p1				
comp32668_c0_seq1.p1				
comp32668_c1_seq1.p1				
comp32668_c1_seq1.p3				
comp32668_c1_seq3.p1				
comp32668_c1_seq3.p10				
comp32669_c0_seq3.p1	sp|Q9FYC2|PAO_ARATH_Pheophorbide_a_oxygenase,_chloroplastic_OS=Arabidopsis_thaliana_GN=PAO_PE=1_SV=1	3.00E-63	[illegible]	[illegible]
comp32670_c0_seq4.p1				
comp32671_c0_seq1.p1				
comp32671_c0_seq14.p1	sp|Q5ZL33|STRAP_CHICK_Serine-threonine_kinase_receptor-associated_protein_OS=Gallus_gallus_GN=STRAP_PE=2_SV=2	3.00E-82	[illegible]	[illegible]
comp32671_c0_seq14.p2	sp|Q66H23|MFRN1_RAT_Mitoferrin-1_OS=Rattus_norvegicus_GN=Slc25a37_PE=2_SV=1	1.00E-17	[illegible]	[illegible]
comp32671_c0_seq14.p7				
comp32671_c0_seq7.p1				
comp32672_c1_seq2.p2				
comp32672_c3_seq1.p1				
comp32672_c3_seq6.p1				
comp32673_c0_seq11.p1	sp|Q588U8|CFDP2_TRAJA_Craniofacial_development_protein_2_OS=Tragulus_javanicus_GN=CFDP2_PE=2_SV=1	6.00E-16	[illegible]	[illegible]
comp32673_c0_seq2.p1				
comp32673_c0_seq2.p4				
comp32673_c0_seq8.p1				
comp32674_c0_seq1.p1				
comp32674_c0_seq12.p1				
comp32674_c0_seq2.p1				
comp32674_c1_seq1.p1				
comp32674_c2_seq10.p1				
comp32674_c2_seq2.p1				
comp32674_c2_seq7.p1				
comp32675_c0_seq2.p1	sp|Q8ERS7|PRPE_OCEIH_Bis(5'-nucleosyl)-tetraphosphatase_prpE_[asymmetrical]_OS=Oceanobacillus_iheyensis_(strain_DSM_14371_/_JCM_11309_/_KCTC_3954_/_HTE831)_GN=prpE_PE=3_SV=1	2.00E-21	[illegible]	[illegible]
comp32675_c1_seq1.p1				
comp32675_c2_seq11.p1	sp|Q9UTN3|CID14_SCHPO_Poly(A)_RNA_polymerase_cid14_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=cid14_PE=1_SV=2	2.00E-29	[illegible]	[illegible]
comp32675_c2_seq16.p1	sp|Q8IWF6|F116A_HUMAN_Protein_FAM116A_OS=Homo_sapiens_GN=FAM116A_PE=2_SV=1	7.00E-24	[illegible]	[illegible]
comp32675_c2_seq17.p1				
comp32675_c2_seq18.p1	sp|Q9UTN3|CID14_SCHPO_Poly(A)_RNA_polymerase_cid14_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=cid14_PE=1_SV=2	1.00E-29	[illegible]	[illegible]
comp32675_c2_seq4.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	2.00E-11		
comp32675_c2_seq4.p2	sp|Q5UR85|YR636_MIMIV_Putative_FNIP_repeat-containing_protein_R636_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_R636_PE=4_SV=1	1.00E-11		
comp32675_c5_seq1.p1				
comp32675_c6_seq1.p1				
comp32676_c0_seq13.p1				
comp32676_c0_seq6.p2				
comp32676_c0_seq8.p4				
comp32677_c0_seq1.p1				
comp32677_c0_seq1.p2				
comp32677_c0_seq3.p1	sp|P55201|BRPF1_HUMAN_Peregrin_OS=Homo_sapiens_GN=BRPF1_PE=1_SV=2	4.00E-31	[illegible]	[illegible]
comp32677_c0_seq7.p1				
comp32679_c0_seq16.p1				
comp32679_c0_seq3.p1				
comp32679_c0_seq5.p1				
comp32679_c0_seq7.p1				
comp32679_c0_seq8.p1				
comp32681_c0_seq7.p1				
comp32682_c0_seq12.p1				
comp32682_c0_seq15.p1				
comp32682_c0_seq17.p1				
comp32682_c0_seq19.p1				
comp32682_c0_seq2.p1	sp|Q54TE7|GPN2_DICDI_GPN-loop_GTPase_2_homolog_OS=Dictyostelium_discoideum_GN=gpn2_PE=2_SV=1	2.00E-71	[illegible]	[illegible]
comp32682_c0_seq21.p1				
comp32682_c0_seq24.p1				
comp32682_c0_seq26.p2				
comp32682_c0_seq26.p4				
comp32682_c0_seq30.p1				
comp32682_c0_seq33.p1				
comp32682_c0_seq39.p1				
comp32682_c0_seq39.p2				
comp32682_c0_seq42.p1				
comp32682_c0_seq6.p1				
comp32682_c0_seq8.p1				
comp32682_c1_seq1.p2				
comp32682_c1_seq2.p1				
comp32682_c2_seq1.p1	sp|Q54TU8|TMCO1_DICDI_Transmembrane_and_coiled-coil_domain-containing_protein_1_homolog_OS=Dictyostelium_discoideum_GN=tmco1_PE=2_SV=1	1.00E-24	[illegible]	[illegible]
comp32683_c0_seq2.p1				
comp32683_c0_seq3.p1				
comp32683_c0_seq5.p1				
comp32683_c1_seq1.p1	sp|Q9QXL1|KI21B_MOUSE_Kinesin-like_protein_KIF21B_OS=Mus_musculus_GN=Kif21b_PE=1_SV=2	5.00E-63	[illegible]	[illegible]
comp32683_c3_seq10.p1				
comp32683_c3_seq13.p1	sp|Q90640|KIF4_CHICK_Chromosome-associated_kinesin_KIF4_OS=Gallus_gallus_GN=KIF4_PE=2_SV=1	4.00E-18	[illegible]	[illegible]
comp32683_c3_seq17.p1	sp|Q8Q0U0|Y045_METMA_Putative_ankyrin_repeat_protein_MM_0045_OS=Methanosarcina_mazei_(strain_ATCC_BAA-159_/_DSM_3647_/_Goe1_/_Go1_/_JCM_11833_/_OCM_88)_GN=MM_0045_PE=4_SV=1	1.00E-28		
comp32683_c3_seq2.p2				
comp32683_c3_seq5.p1				
comp32683_c3_seq8.p1				
comp32684_c0_seq13.p1				
comp32684_c0_seq14.p1				
comp32684_c0_seq16.p1	sp|P50224|ST1A3_HUMAN_Sulfotransferase_1A3/1A4_OS=Homo_sapiens_GN=SULT1A3_PE=1_SV=1	9.00E-39		
comp32684_c0_seq3.p1				
comp32684_c0_seq3.p2				
comp32684_c0_seq5.p1				
comp32684_c0_seq7.p1				
comp32684_c0_seq9.p2				
comp32684_c0_seq9.p3				
comp32685_c0_seq18.p1				
comp32685_c0_seq19.p1				
comp32686_c0_seq5.p1				
comp32686_c0_seq7.p2				
comp32686_c0_seq8.p2				
comp32686_c0_seq9.p2				
comp32686_c1_seq1.p1	sp|A4FUY7|MOC2B_BOVIN_Molybdopterin_synthase_catalytic_subunit_OS=Bos_taurus_GN=MOCS2_PE=2_SV=2	3.00E-28	[illegible]	[illegible]
comp32686_c2_seq1.p1	sp|Q3YEC7|RBEL1_HUMAN_Rab-like_protein_1_OS=Homo_sapiens_GN=PARF_PE=1_SV=2	2.00E-23	[illegible]	[illegible]
comp32686_c2_seq1.p2	sp|Q8RY89|PI5K8_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_8_OS=Arabidopsis_thaliana_GN=PIP5K8_PE=2_SV=1	5.00E-24	[illegible]	[illegible]
comp32686_c2_seq1.p3	sp|Q8VXV4|DNJ16_ARATH_Chaperone_protein_dnaJ_16_OS=Arabidopsis_thaliana_GN=ATJ16_PE=2_SV=1	3.00E-54	[illegible]	[illegible]
comp32686_c2_seq10.p1	sp|Q8RY89|PI5K8_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_8_OS=Arabidopsis_thaliana_GN=PIP5K8_PE=2_SV=1	5.00E-24	[illegible]	[illegible]
comp32686_c2_seq10.p2	sp|Q3YEC7|RBEL1_HUMAN_Rab-like_protein_1_OS=Homo_sapiens_GN=PARF_PE=1_SV=2	4.00E-24	[illegible]	[illegible]
comp32686_c2_seq10.p3				
comp32686_c2_seq10.p4	sp|Q8VXV4|DNJ16_ARATH_Chaperone_protein_dnaJ_16_OS=Arabidopsis_thaliana_GN=ATJ16_PE=2_SV=1	3.00E-54	[illegible]	[illegible]
comp32686_c2_seq3.p1	sp|Q03730|YMB8_YEAST_Uncharacterized_vacuolar_membrane_protein_YML018C_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YML018C_PE=1_SV=1	1.00E-15	[illegible]	[illegible]
comp32686_c2_seq5.p1	sp|Q04083|THI74_YEAST_Thiamine-repressible_mitochondrial_transport_protein_THI74_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=THI74_PE=1_SV=1	5.00E-12	[illegible]	[illegible]
comp32686_c4_seq1.p1	sp|P70569|MYO5B_RAT_Unconventional_myosin-Vb_OS=Rattus_norvegicus_GN=Myo5b_PE=1_SV=1	2.00E-55	[illegible]	[illegible]
comp32687_c0_seq2.p1	sp|B1MGY6|Y572_MYCA9_Uncharacterized_tRNA/rRNA_methyltransferase_MAB_0572_OS=Mycobacterium_abscessus_(strain_ATCC_19977_/_DSM_44196)_GN=MAB_0572_PE=3_SV=1	2.00E-11	[illegible]	[illegible]
comp32688_c0_seq1.p1				
comp32688_c0_seq3.p1				
comp32688_c0_seq5.p1				
comp32688_c0_seq7.p1				
comp32689_c0_seq1.p1	sp|Q54BM8|U652_DICDI_UPF0652_protein_OS=Dictyostelium_discoideum_GN=DDB_G0293552_PE=3_SV=1	7.00E-36	[illegible]	[illegible]
comp32689_c0_seq10.p1	sp|Q54BM8|U652_DICDI_UPF0652_protein_OS=Dictyostelium_discoideum_GN=DDB_G0293552_PE=3_SV=1	6.00E-40	[illegible]	[illegible]
comp32689_c0_seq11.p1	sp|Q54BM8|U652_DICDI_UPF0652_protein_OS=Dictyostelium_discoideum_GN=DDB_G0293552_PE=3_SV=1	5.00E-36	[illegible]	[illegible]
comp32689_c0_seq12.p1				
comp32689_c0_seq18.p1	sp|Q54BM8|U652_DICDI_UPF0652_protein_OS=Dictyostelium_discoideum_GN=DDB_G0293552_PE=3_SV=1	8.00E-13	[illegible]	[illegible]
comp32689_c0_seq2.p1				
comp32689_c0_seq3.p1				
comp32689_c0_seq8.p1				
comp32690_c0_seq1.p1	sp|Q9CXY9|GPI8_MOUSE_GPI-anchor_transamidase_OS=Mus_musculus_GN=Pigk_PE=2_SV=2	1.00E-83	[illegible]	[illegible]
comp32690_c0_seq4.p1	sp|P49018|GPI8_YEAST_GPI-anchor_transamidase_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=GPI8_PE=1_SV=1	1.00E-81	[illegible]	[illegible]
comp32691_c0_seq10.p1	sp|A4IIK1|MFHA1_XENTR_Malignant_fibrous_histiocytoma-amplified_sequence_1_homolog_OS=Xenopus_tropicalis_GN=mfhas1_PE=2_SV=1	2.00E-14	[illegible]	[illegible]
comp32691_c0_seq12.p1				
comp32691_c0_seq12.p3				
comp32691_c0_seq2.p1				
comp32691_c0_seq8.p2				
comp32691_c0_seq9.p1	sp|A4IIK1|MFHA1_XENTR_Malignant_fibrous_histiocytoma-amplified_sequence_1_homolog_OS=Xenopus_tropicalis_GN=mfhas1_PE=2_SV=1	2.00E-14	[illegible]	[illegible]
comp32691_c1_seq2.p1				
comp32692_c0_seq1.p1				
comp32692_c0_seq2.p1				
comp32692_c0_seq5.p1				
comp32693_c0_seq1.p1				
comp32693_c0_seq22.p1				
comp32693_c0_seq6.p1				
comp32693_c0_seq7.p1				
comp32694_c1_seq11.p1				
comp32694_c1_seq13.p1	sp|Q54LB8|VP13A_DICDI_Putative_vacuolar_protein_sorting-associated_protein_13A_OS=Dictyostelium_discoideum_GN=vps13A_PE=2_SV=1	2.00E-16	[illegible]	[illegible]
comp32694_c1_seq2.p1				
comp32694_c1_seq7.p1				
comp32694_c1_seq8.p1				
comp32694_c1_seq8.p2	sp|Q8PBW9|MOAC_XANCP_Molybdenum_cofactor_biosynthesis_protein_C_OS=Xanthomonas_campestris_pv._campestris_GN=moaC_PE=3_SV=1	1.00E-39	[illegible]	[illegible]
comp32695_c0_seq1.p1				
comp32695_c2_seq1.p1				
comp32695_c2_seq2.p1				
comp32695_c2_seq5.p1				
comp32695_c3_seq1.p1				
comp32695_c3_seq1.p2				
comp32695_c3_seq2.p1				
comp32696_c0_seq1.p2				
comp32696_c2_seq1.p1	sp|Q9W2N0|CAPZA_DROME_F-actin-capping_protein_subunit_alpha_OS=Drosophila_melanogaster_GN=cpa_PE=2_SV=1	1.00E-33	[illegible]	[illegible]
comp32696_c3_seq5.p1				
comp32696_c3_seq6.p1	sp|O44006|KPYK_EIMTE_Pyruvate_kinase_OS=Eimeria_tenella_GN=PYK_PE=2_SV=1	2.00E-176	[illegible]	[illegible]
comp32696_c3_seq7.p1				
comp32696_c4_seq1.p1				
comp32696_c4_seq2.p1				
comp32697_c0_seq5.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	6.00E-29	[illegible]	[illegible]
comp32698_c0_seq14.p1	sp|Q42510|EMB30_ARATH_Pattern_formation_protein_EMB30_OS=Arabidopsis_thaliana_GN=EMB30_PE=1_SV=1	7.00E-30	[illegible]	[illegible]
comp32698_c0_seq16.p2				
comp32698_c0_seq18.p2				
comp32698_c0_seq19.p1				
comp32698_c0_seq20.p1				
comp32698_c0_seq26.p3				
comp32698_c0_seq27.p1				
comp32698_c0_seq28.p1				
comp32698_c0_seq3.p1	sp|Q42510|EMB30_ARATH_Pattern_formation_protein_EMB30_OS=Arabidopsis_thaliana_GN=EMB30_PE=1_SV=1	4.00E-30	[illegible]	[illegible]
comp32698_c0_seq9.p1				
comp32699_c0_seq1.p1				
comp32699_c0_seq12.p1				
comp32699_c0_seq13.p1				
comp32699_c0_seq18.p1				
comp32699_c0_seq19.p1				
comp32699_c0_seq20.p1				
comp32699_c0_seq21.p2				
comp32699_c0_seq24.p1	sp|Q64RE8|HIS8_BACFR_Histidinol-phosphate_aminotransferase_OS=Bacteroides_fragilis_(strain_YCH46)_GN=hisC_PE=3_SV=1	1.00E-90	[illegible]	[illegible]
comp32699_c0_seq25.p1				
comp32699_c0_seq31.p1				
comp32700_c0_seq10.p3				
comp32700_c0_seq14.p1				
comp32700_c0_seq22.p2				
comp32700_c0_seq24.p3				
comp32700_c0_seq28.p3				
comp32701_c0_seq2.p1	sp|Q724N6|SYM_LISMF_Methionine--tRNA_ligase_OS=Listeria_monocytogenes_serotype_4b_(strain_F2365)_GN=metG_PE=3_SV=1	4.00E-129	[illegible]	[illegible]
comp32702_c0_seq11.p2				
comp32702_c0_seq14.p1				
comp32702_c0_seq17.p1				
comp32702_c0_seq7.p1				
comp32702_c0_seq8.p2				
comp32702_c2_seq1.p1	sp|O05235|YUGF_BACSU_Uncharacterized_hydrolase_yugF_OS=Bacillus_subtilis_GN=yugF_PE=3_SV=1	2.00E-11	[illegible]	[illegible]
comp32703_c0_seq11.p1				
comp32703_c0_seq11.p3				
comp32703_c0_seq14.p1				
comp32703_c0_seq14.p2	sp|Q6YRM6|Y8219_ORYSJ_UPF0392_protein_Os08g0121900_OS=Oryza_sativa_subsp._japonica_GN=Os08g0121900_PE=2_SV=1	2.00E-11	[illegible]	[illegible]
comp32703_c0_seq20.p1				
comp32703_c0_seq20.p3				
comp32703_c0_seq23.p1				
comp32703_c0_seq23.p3				
comp32703_c0_seq24.p1	sp|Q6YRM6|Y8219_ORYSJ_UPF0392_protein_Os08g0121900_OS=Oryza_sativa_subsp._japonica_GN=Os08g0121900_PE=2_SV=1	8.00E-13	[illegible]	[illegible]
comp32703_c0_seq24.p2				
comp32703_c0_seq7.p1				
comp32703_c0_seq8.p1				
comp32703_c1_seq1.p1	sp|O43741|AAKB2_HUMAN_5'-AMP-activated_protein_kinase_subunit_beta-2_OS=Homo_sapiens_GN=PRKAB2_PE=1_SV=1	3.00E-37	[illegible]	[illegible]
comp32704_c0_seq11.p1				
comp32704_c0_seq18.p1				
comp32704_c0_seq19.p1				
comp32704_c0_seq19.p2				
comp32704_c0_seq21.p1				
comp32704_c0_seq23.p1	sp|A4VCH4|CP062_DANRE_UPF0505_protein_C16orf62_homolog_OS=Danio_rerio_GN=zgc:163107_PE=2_SV=1	7.00E-37	[illegible]	[illegible]
comp32704_c0_seq25.p1				
comp32704_c0_seq28.p1				
comp32704_c0_seq3.p1				
comp32704_c0_seq30.p1				
comp32704_c0_seq31.p1	sp|A4VCH4|CP062_DANRE_UPF0505_protein_C16orf62_homolog_OS=Danio_rerio_GN=zgc:163107_PE=2_SV=1	3.00E-41	[illegible]	[illegible]
comp32704_c0_seq33.p1	sp|Q27256|WHITE_ANOGA_Protein_white_OS=Anopheles_gambiae_GN=w_PE=2_SV=1	1.00E-73	[illegible]	[illegible]
comp32704_c0_seq7.p1				
comp32704_c0_seq7.p2				
comp32705_c0_seq1.p3				
comp32705_c0_seq3.p1				
comp32705_c0_seq5.p1				
comp32705_c0_seq6.p3				
comp32705_c2_seq1.p1				
comp32705_c2_seq4.p1				
comp32705_c2_seq5.p1				
comp32708_c0_seq3.p1				
comp32708_c0_seq5.p1				
comp32709_c0_seq1.p1				
comp32710_c0_seq10.p1	sp|P07514|NB5R3_BOVIN_NADH-cytochrome_b5_reductase_3_OS=Bos_taurus_GN=CYB5R3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp32710_c0_seq10.p2				
comp32710_c0_seq10.p5				
comp32710_c0_seq17.p1	sp|P07514|NB5R3_BOVIN_NADH-cytochrome_b5_reductase_3_OS=Bos_taurus_GN=CYB5R3_PE=1_SV=3	2.00E-41	[illegible]	[illegible]
comp32710_c0_seq17.p2				
comp32710_c0_seq23.p1	sp|P20070|NB5R3_RAT_NADH-cytochrome_b5_reductase_3_OS=Rattus_norvegicus_GN=Cyb5r3_PE=1_SV=2	3.00E-90	[illegible]	[illegible]
comp32710_c0_seq24.p2				
comp32710_c0_seq27.p1	sp|P07514|NB5R3_BOVIN_NADH-cytochrome_b5_reductase_3_OS=Bos_taurus_GN=CYB5R3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp32710_c0_seq27.p2				
comp32710_c0_seq28.p1	sp|P07514|NB5R3_BOVIN_NADH-cytochrome_b5_reductase_3_OS=Bos_taurus_GN=CYB5R3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp32710_c0_seq31.p1	sp|P07514|NB5R3_BOVIN_NADH-cytochrome_b5_reductase_3_OS=Bos_taurus_GN=CYB5R3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp32710_c0_seq31.p2				
comp32710_c0_seq31.p4				
comp32710_c0_seq36.p1	sp|P07514|NB5R3_BOVIN_NADH-cytochrome_b5_reductase_3_OS=Bos_taurus_GN=CYB5R3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp32710_c0_seq36.p2				
comp32710_c0_seq37.p1	sp|P07514|NB5R3_BOVIN_NADH-cytochrome_b5_reductase_3_OS=Bos_taurus_GN=CYB5R3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp32710_c0_seq37.p2				
comp32710_c0_seq39.p3				
comp32710_c0_seq45.p1				
comp32710_c0_seq45.p2				
comp32710_c0_seq47.p1				
comp32710_c0_seq47.p2				
comp32710_c0_seq5.p1	sp|P07514|NB5R3_BOVIN_NADH-cytochrome_b5_reductase_3_OS=Bos_taurus_GN=CYB5R3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp32710_c0_seq5.p4				
comp32710_c0_seq51.p1	sp|P07514|NB5R3_BOVIN_NADH-cytochrome_b5_reductase_3_OS=Bos_taurus_GN=CYB5R3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp32710_c0_seq51.p2				
comp32710_c0_seq6.p1	sp|P07514|NB5R3_BOVIN_NADH-cytochrome_b5_reductase_3_OS=Bos_taurus_GN=CYB5R3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp32710_c0_seq6.p3				
comp32710_c0_seq7.p1	sp|P07514|NB5R3_BOVIN_NADH-cytochrome_b5_reductase_3_OS=Bos_taurus_GN=CYB5R3_PE=1_SV=3	4.00E-41	[illegible]	[illegible]
comp32710_c0_seq7.p2				
comp32711_c0_seq1.p1	sp|Q54P59|TMM66_DICDI_Transmembrane_protein_66_OS=Dictyostelium_discoideum_GN=tmem66_PE=3_SV=1	4.00E-29	[illegible]	[illegible]
comp32711_c0_seq1.p2				
comp32711_c0_seq2.p1				
comp32711_c0_seq2.p3	sp|Q54P59|TMM66_DICDI_Transmembrane_protein_66_OS=Dictyostelium_discoideum_GN=tmem66_PE=3_SV=1	4.00E-30	[illegible]	[illegible]
comp32711_c1_seq1.p1				
comp32711_c1_seq14.p1				
comp32711_c1_seq14.p2				
comp32711_c1_seq28.p1	sp|P58710|GGLO_MOUSE_L-gulonolactone_oxidase_OS=Mus_musculus_GN=Gulo_PE=1_SV=3	2.00E-17	[illegible]	[illegible]
comp32713_c0_seq19.p1				
comp32713_c0_seq8.p1				
comp32714_c0_seq2.p1	sp|Q4SRI6|MKRN1_TETNG_Probable_E3_ubiquitin-protein_ligase_makorin-1_OS=Tetraodon_nigroviridis_GN=mkrn1_PE=3_SV=1	4.00E-27	[illegible]	[illegible]
comp32714_c0_seq6.p1	sp|Q9ERV1|MKRN2_MOUSE_Probable_E3_ubiquitin-protein_ligase_makorin-2_OS=Mus_musculus_GN=Mkrn2_PE=2_SV=2	1.00E-26	[illegible]	[illegible]
comp32715_c1_seq3.p1				
comp32715_c2_seq1.p1				
comp32715_c3_seq1.p1				
comp32715_c3_seq12.p1				
comp32715_c3_seq16.p1				
comp32715_c3_seq19.p1				
comp32715_c3_seq4.p1				
comp32715_c3_seq5.p1				
comp32715_c3_seq6.p1				
comp32716_c0_seq11.p1				
comp32716_c0_seq25.p1				
comp32716_c0_seq28.p1				
comp32716_c0_seq5.p1				
comp32717_c0_seq1.p1				
comp32717_c0_seq13.p2				
comp32717_c0_seq17.p1				
comp32717_c0_seq3.p1				
comp32717_c0_seq6.p2				
comp32718_c0_seq2.p1				
comp32718_c0_seq3.p1				
comp32718_c0_seq3.p2	sp|Q8BFQ4|WDR82_MOUSE_WD_repeat-containing_protein_82_OS=Mus_musculus_GN=Wdr82_PE=1_SV=1	9.00E-71	[illegible]	[illegible]
comp32719_c0_seq11.p1	sp|Q9FWX8|AB12B_ARATH_ABC_transporter_B_family_member_12_OS=Arabidopsis_thaliana_GN=ABCB12_PE=2_SV=2	7.00E-119	[illegible]	[illegible]
comp32719_c0_seq11.p5				
comp32719_c0_seq13.p1				
comp32719_c0_seq13.p5				
comp32719_c0_seq22.p1	sp|Q9FWX8|AB12B_ARATH_ABC_transporter_B_family_member_12_OS=Arabidopsis_thaliana_GN=ABCB12_PE=2_SV=2	7.00E-119	[illegible]	[illegible]
comp32719_c0_seq28.p2				
comp32719_c0_seq30.p1				
comp32719_c0_seq32.p1				
comp32719_c0_seq6.p1				
comp32719_c0_seq7.p1				
comp32719_c0_seq8.p1				
comp32719_c2_seq1.p1	sp|Q8T9W4|ABCB3_DICDI_ABC_transporter_B_family_member_3_OS=Dictyostelium_discoideum_GN=abcB3_PE=3_SV=1	1.00E-118	[illegible]	[illegible]
comp32720_c0_seq10.p1				
comp32720_c0_seq13.p1				
comp32720_c0_seq13.p3				
comp32720_c0_seq3.p1				
comp32720_c0_seq4.p1				
comp32720_c0_seq4.p2				
comp32720_c0_seq8.p1				
comp32721_c2_seq1.p1				
comp32721_c4_seq19.p1				
comp32721_c4_seq21.p2				

comp32721_c4_seq7.p1		
comp32721_c4_seq7.p2	sp|Q07DZ5|CTTB2_ORNAN_Cortactin-binding_protein_2_OS=Ornithorhynchus_anatinus_GN=CTTNBP2_PE=3_SV=1	2.00E-16
comp32721_c4_seq7.p5	sp|O54873|AIMP1_CRIGR_Aminoacyl_tRNA_synthase_complex-interacting_multifunctional_protein_1_OS=Cricetulus_griseus_GN=AIMP1_PE=2_SV=1	1.00E-16
comp32721_c4_seq7.p6		
comp32721_c4_seq8.p1	sp|A3PNM3|UBIG_RHOS1_3-demethylubiquinone-9_3-methyltransferase_OS=Rhodobacter_sphaeroides_(strain_ATCC_17029_/_ATH_2.4.9)_GN=ubiG_PE=3_SV=1	3.00E-68
comp32721_c4_seq9.p1		
comp32722_c0_seq1.p1		
comp32722_c0_seq1.p2		
comp32722_c0_seq3.p1		
comp32722_c0_seq3.p2		
comp32723_c0_seq3.p1		
comp32723_c0_seq4.p1		
comp32724_c0_seq1.p1		
comp32724_c0_seq3.p1		
comp32725_c0_seq1.p1	sp|Q09225|NRF6_CAEEL_Nose_resistant_to_fluoxetine_protein_6_OS=Caenorhabditis_elegans_GN=nrf-6_PE=1_SV=3	4.00E-39
comp32727_c1_seq1.p2		
comp32727_c1_seq10.p2		
comp32727_c1_seq4.p1		
comp32727_c1_seq5.p1		
comp32727_c1_seq6.p1		
comp32727_c1_seq9.p1		
comp32728_c0_seq13.p2		
comp32728_c0_seq13.p7		
comp32728_c0_seq15.p1		
comp32728_c0_seq18.p1	sp|Q0VA06|LETM1_XENTR_LETM1_and_EF-hand_domain-containing_protein_1,_mitochondrial_OS=Xenopus_tropicalis_GN=letm1_PE=2_SV=1	1.00E-71
comp32728_c0_seq18.p2		
comp32728_c0_seq18.p3	sp|Q13395|TARB1_HUMAN_Probable_methyltransferase_TARBP1_OS=Homo_sapiens_GN=TARBP1_PE=1_SV=1	3.00E-46
comp32728_c0_seq21.p1		
comp32728_c0_seq23.p2		
comp32728_c0_seq23.p7		
comp32728_c0_seq26.p2		
comp32728_c0_seq29.p1	sp|Q13395|TARB1_HUMAN_Probable_methyltransferase_TARBP1_OS=Homo_sapiens_GN=TARBP1_PE=1_SV=1	2.00E-43
comp32728_c0_seq29.p2	sp|Q0VA06|LETM1_XENTR_LETM1_and_EF-hand_domain-containing_protein_1,_mitochondrial_OS=Xenopus_tropicalis_GN=letm1_PE=2_SV=1	1.00E-71
comp32728_c0_seq31.p1		
comp32728_c0_seq33.p1	sp|Q13395|TARB1_HUMAN_Probable_methyltransferase_TARBP1_OS=Homo_sapiens_GN=TARBP1_PE=1_SV=1	1.00E-43
comp32728_c0_seq33.p3		
comp32728_c0_seq37.p1		
comp32728_c0_seq41.p1		
comp32728_c0_seq5.p1		
comp32728_c0_seq52.p1		
comp32728_c0_seq55.p1		
comp32729_c0_seq4.p1	sp|Q5ZKS8|UBIA1_CHICK_UbiA_prenyltransferase_domain-containing_protein_1_OS=Gallus_gallus_GN=UBIAD1_PE=2_SV=1	2.00E-32
comp32729_c0_seq4.p2	sp|P0ABU0|MENB_ECOLI_1,4-Dihydroxy-2-naphthoyl-CoA_synthase_OS=Escherichia_coli_(strain_K12)_GN=menB_PE=1_SV=1	2.00E-122
comp32729_c0_seq6.p1	sp|Q5ZKS8|UBIA1_CHICK_UbiA_prenyltransferase_domain-containing_protein_1_OS=Gallus_gallus_GN=UBIAD1_PE=2_SV=1	2.00E-32
comp32729_c0_seq6.p5	sp|P0ABU0|MENB_ECOLI_1,4-Dihydroxy-2-naphthoyl-CoA_synthase_OS=Escherichia_coli_(strain_K12)_GN=menB_PE=1_SV=1	3.00E-42
comp32730_c0_seq1.p1	sp|Q6MEK1|RNC_PARUW_Ribonuclease_3_OS=Protochlamydia_amoebophila_(strain_UWE25)_GN=rnc_PE=3_SV=1	2.00E-21
comp32730_c0_seq3.p1	sp|Q6MEK1|RNC_PARUW_Ribonuclease_3_OS=Protochlamydia_amoebophila_(strain_UWE25)_GN=rnc_PE=3_SV=1	6.00E-15
comp32730_c0_seq4.p1	sp|Q6MEK1|RNC_PARUW_Ribonuclease_3_OS=Protochlamydia_amoebophila_(strain_UWE25)_GN=rnc_PE=3_SV=1	2.00E-21
comp32730_c1_seq5.p1	sp|P50107|LGUL_YEAST_Lactoylglutathione_lyase_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=GLO1_PE=1_SV=1	5.00E-63
comp32730_c1_seq8.p1		
comp32730_c1_seq8.p2		
comp32731_c0_seq1.p1	sp|O96102|CALM_PHYPO_Calmodulin_OS=Physarum_polycephalum_PE=2_SV=3	3.00E-49
comp32732_c0_seq3.p1		
comp32732_c0_seq5.p1		
comp32733_c0_seq1.p1		
comp32733_c0_seq3.p1		
comp32734_c0_seq11.p2		
comp32734_c0_seq13.p2		
comp32734_c0_seq15.p1		
comp32734_c0_seq17.p1		
comp32734_c0_seq19.p1		
comp32734_c0_seq21.p1		
comp32734_c0_seq21.p2		
comp32734_c0_seq21.p4		
comp32734_c0_seq28.p1		
comp32734_c0_seq28.p2		
comp32734_c0_seq28.p4		
comp32734_c0_seq4.p1		
comp32734_c0_seq4.p3		
comp32734_c0_seq4.p5		
comp32734_c0_seq5.p1		
comp32735_c0_seq1.p2		
comp32735_c0_seq2.p2		
comp32735_c0_seq8.p3		
comp32736_c0_seq12.p1		
comp32736_c0_seq12.p2		
comp32736_c0_seq15.p1	sp|Q8IWV8|UBR2_HUMAN_E3_ubiquitin-protein_ligase_UBR2_OS=Homo_sapiens_GN=UBR2_PE=1_SV=1	1.00E-16
comp32736_c0_seq17.p1		
comp32736_c0_seq20.p1		
comp32736_c0_seq21.p1	sp|O70481|UBR1_MOUSE_E3_ubiquitin-protein_ligase_UBR1_OS=Mus_musculus_GN=Ubr1_PE=1_SV=2	8.00E-18
comp32736_c0_seq25.p1		
comp32736_c0_seq28.p1	sp|O70481|UBR1_MOUSE_E3_ubiquitin-protein_ligase_UBR1_OS=Mus_musculus_GN=Ubr1_PE=1_SV=2	8.00E-18
comp32736_c0_seq31.p1		
comp32736_c0_seq35.p1	sp|P53395|ODB2_MOUSE_Lipoamide_acyltransferase_component_of_branched-chain_alpha-keto_acid_dehydrogenase_complex,_mitochondrial_OS=Mus_musculus_GN=Dbt_PE=2_SV=2	1.00E-77
comp32736_c0_seq35.p2		
comp32736_c0_seq39.p1		
comp32736_c0_seq4.p1		
comp32736_c0_seq44.p1		
comp32736_c0_seq8.p1		
comp32737_c0_seq1.p1		
comp32737_c1_seq11.p1	sp|Q5M819|SERB_RAT_Phosphoserine_phosphatase_OS=Rattus_norvegicus_GN=Psph_PE=2_SV=1	7.00E-78
comp32737_c1_seq13.p1		
comp32737_c1_seq3.p1	sp|Q8PC00|ASPN_XANCP_Peptidyl-Asp_metalloendopeptidase_OS=Xanthomonas_campestris_pv._campestris_GN=XCC0955_PE=3_SV=1	9.00E-16
comp32737_c1_seq4.p1		
comp32737_c2_seq1.p1		
comp32738_c0_seq13.p1	sp|Q9NU22|MDN1_HUMAN_Midasin_OS=Homo_sapiens_GN=MDN1_PE=1_SV=2	3.00E-16
comp32738_c0_seq13.p2	sp|Q869L3|MDN1_DICDI_Midasin_OS=Dictyostelium_discoideum_GN=mdn1_PE=3_SV=2	2.00E-82
comp32738_c0_seq13.p4	sp|Q12019|MDN1_YEAST_Midasin_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=MDN1_PE=1_SV=1	9.00E-27
comp32738_c0_seq15.p1	sp|Q869L3|MDN1_DICDI_Midasin_OS=Dictyostelium_discoideum_GN=mdn1_PE=3_SV=2	4.00E-81
comp32738_c0_seq15.p3	sp|Q12019|MDN1_YEAST_Midasin_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=MDN1_PE=1_SV=1	9.00E-27
comp32738_c0_seq3.p1	sp|Q869L3|MDN1_DICDI_Midasin_OS=Dictyostelium_discoideum_GN=mdn1_PE=3_SV=2	3.00E-137
comp32738_c0_seq6.p1	sp|Q869L3|MDN1_DICDI_Midasin_OS=Dictyostelium_discoideum_GN=mdn1_PE=3_SV=2	4.00E-90
comp32738_c0_seq9.p1	sp|Q869L3|MDN1_DICDI_Midasin_OS=Dictyostelium_discoideum_GN=mdn1_PE=3_SV=2	0
comp32739_c0_seq2.p1		
comp32739_c0_seq4.p1		
comp32740_c0_seq1.p1		
comp32740_c0_seq14.p1		
comp32740_c0_seq4.p1		
comp32740_c0_seq6.p1		
comp32740_c0_seq9.p1		
comp32742_c0_seq2.p1		
comp32742_c0_seq3.p1		
comp32742_c0_seq4.p1		
comp32742_c0_seq6.p1		
comp32743_c0_seq12.p1	sp|Q6TUI4|DICER_BOVIN_Endoribonuclease_Dicer_OS=Bos_taurus_GN=DICER1_PE=2_SV=3	3.00E-15
comp32743_c0_seq16.p1	sp|Q3EBC8|DCL2_ARATH_Endoribonuclease_Dicer_homolog_2_OS=Arabidopsis_thaliana_GN=At3g03300_PE=1_SV=2	8.00E-27
comp32743_c0_seq19.p1	sp|Q6TUI4|DICER_BOVIN_Endoribonuclease_Dicer_OS=Bos_taurus_GN=DICER1_PE=2_SV=3	2.00E-15
comp32743_c0_seq2.p1	sp|Q3EBC8|DCL2_ARATH_Endoribonuclease_Dicer_homolog_2_OS=Arabidopsis_thaliana_GN=At3g03300_PE=1_SV=2	8.00E-27
comp32743_c0_seq5.p1	sp|Q3EBC8|DCL2_ARATH_Endoribonuclease_Dicer_homolog_2_OS=Arabidopsis_thaliana_GN=At3g03300_PE=1_SV=2	2.00E-27
comp32743_c0_seq9.p1	sp|Q6TUI4|DICER_BOVIN_Endoribonuclease_Dicer_OS=Bos_taurus_GN=DICER1_PE=2_SV=3	3.00E-15
comp32745_c0_seq2.p1	sp|Q02357|ANK1_MOUSE_Ankyrin-1_OS=Mus_musculus_GN=Ank1_PE=1_SV=2	8.00E-23
comp32745_c0_seq2.p2		
comp32746_c0_seq2.p1		
comp32746_c0_seq3.p1		
comp32746_c0_seq7.p1		
comp32747_c0_seq1.p1		
comp32747_c0_seq12.p1		
comp32747_c0_seq15.p1		
comp32747_c0_seq16.p1		
comp32747_c0_seq19.p1		
comp32747_c0_seq19.p2		
comp32747_c0_seq2.p1		
comp32747_c0_seq20.p1		
comp32747_c0_seq4.p1	sp|Q875X3|MYO2A_NAUCC_Myosin-2A_OS=Naumovozyma_castellii_(strain_ATCC_76901_/_CBS_4309_/_NBRC_1992_/_NRRL_Y-12630)_GN=MYO2A_PE=3_SV=2	2.00E-88
comp32747_c0_seq7.p1		
comp32748_c0_seq4.p1		
comp32748_c0_seq5.p1		
comp32748_c0_seq6.p1		
comp32748_c0_seq9.p1		
comp32748_c1_seq1.p1		
comp32748_c1_seq2.p1		
comp32749_c0_seq4.p4		
comp32749_c0_seq4.p5		
comp32749_c0_seq5.p4		
comp32750_c0_seq1.p3		
comp32750_c0_seq12.p2		
comp32750_c0_seq14.p2		
comp32750_c0_seq16.p1		
comp32750_c0_seq17.p1	sp|Q99436|PSB7_HUMAN_Proteasome_subunit_beta_type-7_OS=Homo_sapiens_GN=PSMB7_PE=1_SV=1	2.00E-48
comp32750_c0_seq23.p1	sp|Q99436|PSB7_HUMAN_Proteasome_subunit_beta_type-7_OS=Homo_sapiens_GN=PSMB7_PE=1_SV=1	1.00E-48
comp32750_c0_seq24.p1		
comp32750_c0_seq25.p1		
comp32750_c0_seq31.p1		
comp32750_c0_seq35.p1		
comp32750_c0_seq36.p4		
comp32750_c0_seq4.p1		
comp32750_c0_seq41.p4		
comp32750_c0_seq42.p1		
comp32750_c0_seq43.p2		
comp32751_c0_seq2.p1		
comp32751_c0_seq5.p1	sp|Q97AJ6|TRF3_THEVO_Tricorn_protease-interacting_factor_F3_OS=Thermoplasma_volcanium_(strain_ATCC_51530_/_DSM_4299_/_JCM_9571_/_NBRC_15438_/_GSS1)_GN=trf3_PE=3_SV=1	2.00E-52
comp32752_c0_seq14.p1	sp|Q9Y7X4|YGRG_SCHPO_Uncharacterized_membrane_protein_C365.16_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC365.16_PE=2_SV=1	4.00E-34
comp32752_c0_seq2.p1		
comp32752_c0_seq3.p1	sp|Q9Y7X4|YGRG_SCHPO_Uncharacterized_membrane_protein_C365.16_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC365.16_PE=2_SV=1	8.00E-33
comp32752_c0_seq9.p1	sp|Q9Y7X4|YGRG_SCHPO_Uncharacterized_membrane_protein_C365.16_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC365.16_PE=2_SV=1	5.00E-33
comp32753_c1_seq2.p1		
comp32753_c1_seq4.p1		
comp32754_c1_seq10.p1	sp|Q9ZU49|LPP1_ARATH_Lipid_phosphate_phosphatase_1_OS=Arabidopsis_thaliana_GN=LPP1_PE=2_SV=2	7.00E-13
comp32754_c1_seq16.p1		
comp32754_c1_seq16.p4	sp|Q5XIN3|MIPT3_RAT_TRAF3-interacting_protein_1_OS=Rattus_norvegicus_GN=Traf3ip1_PE=2_SV=1	4.00E-18
comp32754_c1_seq9.p1	sp|Q5XIN3|MIPT3_RAT_TRAF3-interacting_protein_1_OS=Rattus_norvegicus_GN=Traf3ip1_PE=2_SV=1	7.00E-25
comp32755_c0_seq3.p1		
comp32756_c0_seq5.p1		
comp32757_c0_seq2.p1		
comp32757_c0_seq4.p1		
comp32757_c0_seq4.p2		
comp32757_c0_seq5.p1		
comp32758_c0_seq1.p1		
comp32758_c0_seq2.p1	sp|P17439|GLCM_MOUSE_Glucosylceramidase_OS=Mus_musculus_GN=Gba_PE=1_SV=1	5.00E-52
comp32758_c0_seq5.p1	sp|P17439|GLCM_MOUSE_Glucosylceramidase_OS=Mus_musculus_GN=Gba_PE=1_SV=1	1.00E-61
comp32759_c0_seq2.p1		
comp32759_c0_seq6.p1		
comp32760_c0_seq1.p1	sp|Q8RNT4|LOX_PSEAI_Oleic_acid_lipoxygenase_OS=Pseudomonas_aeruginosa_GN=lox_PE=1_SV=2	2.00E-16
comp32760_c0_seq2.p1	sp|P48999|LOX5_MOUSE_Arachidonate_5-lipoxygenase_OS=Mus_musculus_GN=Alox5_PE=1_SV=3	7.00E-22
comp32760_c0_seq6.p1	sp|Q8RNT4|LOX_PSEAI_Oleic_acid_lipoxygenase_OS=Pseudomonas_aeruginosa_GN=lox_PE=1_SV=2	4.00E-19
comp32760_c1_seq2.p1		
comp32761_c0_seq15.p1		
comp32761_c0_seq16.p2		
comp32761_c0_seq17.p1		
comp32761_c0_seq21.p1		
comp32761_c0_seq9.p2		
comp32762_c0_seq2.p1		
comp32762_c0_seq4.p1		
comp32763_c0_seq1.p1		
comp32763_c0_seq3.p1		
comp32763_c0_seq4.p1		
comp32764_c2_seq1.p1		
comp32764_c3_seq1.p1		
comp32764_c3_seq2.p1		
comp32764_c5_seq10.p1	sp|Q8CIN6|CELF3_MOUSE_CUGBP_Elav-like_family_member_3_OS=Mus_musculus_GN=Celf3_PE=2_SV=1	2.00E-54
comp32764_c5_seq11.p1	sp|Q9SWE5|HAL3A_ARATH_Phosphopantothenoylcysteine_decarboxylase_OS=Arabidopsis_thaliana_GN=HAL3A_PE=1_SV=1	2.00E-48
comp32764_c5_seq12.p1		
comp32764_c5_seq13.p1	sp|A1KB29|EFTU_AZOSB_Elongation_factor_Tu_OS=Azoarcus_sp._(strain_BH72)_GN=tuf1_PE=3_SV=1	0
comp32764_c5_seq15.p1		
comp32764_c5_seq15.p2	sp|O08437|FKBA_AERHY_FKBP-type_peptidyl-prolyl_cis-trans_isomerase_fkpA_OS=Aeromonas_hydrophila_GN=fkpA_PE=3_SV=1	3.00E-25
comp32764_c5_seq17.p1		
comp32764_c5_seq18.p1	sp|Q9LK94|MDAR2_ARATH_Probable_monodehydroascorbate_reductase,_cytoplasmic_isoform_2_OS=Arabidopsis_thaliana_GN=At3g27820_PE=2_SV=1	3.00E-37
comp32764_c5_seq2.p1	sp|Q9LK94|MDAR2_ARATH_Probable_monodehydroascorbate_reductase,_cytoplasmic_isoform_2_OS=Arabidopsis_thaliana_GN=At3g27820_PE=2_SV=1	7.00E-40
comp32764_c5_seq20.p1	sp|Q4PEQ5|MCA1_USTMA_Metacaspase-1_OS=Ustilago_maydis_(strain_521_/_FGSC_9021)_GN=MCA1_PE=3_SV=1	1.00E-49
comp32764_c5_seq24.p1		
comp32764_c5_seq27.p1	sp|Q8CIN6|CELF3_MOUSE_CUGBP_Elav-like_family_member_3_OS=Mus_musculus_GN=Celf3_PE=2_SV=1	2.00E-54
comp32764_c5_seq28.p1	sp|Q4PEQ5|MCA1_USTMA_Metacaspase-1_OS=Ustilago_maydis_(strain_521_/_FGSC_9021)_GN=MCA1_PE=3_SV=1	7.00E-45
comp32764_c5_seq29.p1	sp|Q9SWE5|HAL3A_ARATH_Phosphopantothenoylcysteine_decarboxylase_OS=Arabidopsis_thaliana_GN=HAL3A_PE=1_SV=1	6.00E-62
comp32764_c5_seq32.p1	sp|Q9LK94|MDAR2_ARATH_Probable_monodehydroascorbate_reductase,_cytoplasmic_isoform_2_OS=Arabidopsis_thaliana_GN=At3g27820_PE=2_SV=1	3.00E-37
comp32764_c5_seq33.p1	sp|Q9SWE5|HAL3A_ARATH_Phosphopantothenoylcysteine_decarboxylase_OS=Arabidopsis_thaliana_GN=HAL3A_PE=1_SV=1	2.00E-48
comp32764_c5_seq34.p1		
comp32764_c5_seq4.p1	sp|O08437|FKBA_AERHY_FKBP-type_peptidyl-prolyl_cis-trans_isomerase_fkpA_OS=Aeromonas_hydrophila_GN=fkpA_PE=3_SV=1	2.00E-43
comp32764_c5_seq6.p2	sp|Q9CR60|GOT1B_MOUSE_Vesicle_transport_protein_GOT1B_OS=Mus_musculus_GN=Golt1b_PE=2_SV=1	3.00E-26
comp32764_c5_seq8.p1	sp|Q8H4S6|P2C64_ORYSJ_Probable_protein_phosphatase_2C_64_OS=Oryza_sativa_subsp._japonica_GN=Os07g0566200_PE=2_SV=2	2.00E-39
comp32764_c5_seq9.p2		
comp32765_c0_seq1.p1	sp|Q9JLG8|CAN15_MOUSE_Calpain-15_OS=Mus_musculus_GN=Solh_PE=1_SV=1	2.00E-48
comp32765_c0_seq5.p1	sp|Q9JLG8|CAN15_MOUSE_Calpain-15_OS=Mus_musculus_GN=Solh_PE=1_SV=1	2.00E-48
comp32765_c0_seq7.p1	sp|Q9JLG8|CAN15_MOUSE_Calpain-15_OS=Mus_musculus_GN=Solh_PE=1_SV=1	2.00E-48
comp32766_c0_seq3.p2		
comp32766_c0_seq5.p3		
comp32767_c0_seq11.p4		
comp32767_c0_seq6.p1	sp|Q9ULJ7|ANR50_HUMAN_Ankyrin_repeat_domain-containing_protein_50_OS=Homo_sapiens_GN=ANKRD50_PE=1_SV=4	2.00E-75
comp32768_c0_seq13.p1	sp|P43188|KADC_MAIZE_Adenylate_kinase,_chloroplastic_OS=Zea_mays_GN=ADK1_PE=1_SV=1	2.00E-62
comp32768_c0_seq13.p2	sp|Q9SNX2|PGMC_BROIN_Phosphoglucomutase,_cytoplasmic_OS=Bromus_inermis_GN=PGM1_PE=2_SV=1	7.00E-16
comp32768_c0_seq14.p3		
comp32768_c0_seq15.p1	sp|P43188|KADC_MAIZE_Adenylate_kinase,_chloroplastic_OS=Zea_mays_GN=ADK1_PE=1_SV=1	2.00E-62
comp32768_c0_seq15.p2	sp|Q9SNX2|PGMC_BROIN_Phosphoglucomutase,_cytoplasmic_OS=Bromus_inermis_GN=PGM1_PE=2_SV=1	9.00E-147
comp32768_c0_seq16.p1	sp|Q9SNX2|PGMC_BROIN_Phosphoglucomutase,_cytoplasmic_OS=Bromus_inermis_GN=PGM1_PE=2_SV=1	0
comp32768_c0_seq2.p1	sp|P43188|KADC_MAIZE_Adenylate_kinase,_chloroplastic_OS=Zea_mays_GN=ADK1_PE=1_SV=1	2.00E-64
comp32768_c0_seq6.p1	sp|Q9SNX2|PGMC_BROIN_Phosphoglucomutase,_cytoplasmic_OS=Bromus_inermis_GN=PGM1_PE=2_SV=1	2.00E-79
comp32769_c0_seq1.p1		
comp32770_c0_seq4.p1		
comp32770_c0_seq5.p1		
comp32771_c0_seq1.p2		
comp32771_c0_seq3.p1		
comp32771_c0_seq5.p1		
comp32771_c0_seq5.p2		
comp32772_c0_seq19.p1		
comp32772_c0_seq21.p1		
comp32772_c0_seq22.p1		
comp32772_c0_seq4.p1		
comp32772_c0_seq6.p1		
comp32773_c0_seq1.p1		
comp32773_c0_seq10.p1		
comp32773_c0_seq11.p1		
comp32773_c0_seq12.p1		
comp32773_c0_seq2.p1		
comp32773_c0_seq3.p1		
comp32773_c0_seq4.p1		
comp32773_c0_seq5.p1		
comp32773_c0_seq8.p1		
comp32774_c0_seq6.p2	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	2.00E-12
comp32774_c0_seq6.p4		
comp32774_c0_seq6.p5		
comp32774_c0_seq8.p2		
comp32777_c2_seq11.p1		
comp32777_c2_seq12.p1		
comp32777_c2_seq14.p1		
comp32777_c2_seq14.p2		
comp32777_c2_seq15.p1		
comp32777_c2_seq16.p1		
comp32777_c2_seq18.p1	sp|D3Z5L6|CF192_MOUSE_MFS-type_transporter_C6orf192_homolog_OS=Mus_musculus_PE=2_SV=2	4.00E-17
comp32777_c2_seq19.p3		
comp32777_c2_seq2.p1		
comp32777_c2_seq2.p2		
comp32777_c2_seq23.p1	sp|D3Z5L6|CF192_MOUSE_MFS-type_transporter_C6orf192_homolog_OS=Mus_musculus_PE=2_SV=2	2.00E-17
comp32777_c2_seq31.p1		
comp32777_c2_seq33.p1		
comp32777_c2_seq4.p1		
comp32777_c2_seq4.p2		
comp32777_c2_seq6.p1		
comp32777_c2_seq9.p1		
comp32777_c2_seq9.p2	sp|D3Z5L6|CF192_MOUSE_MFS-type_transporter_C6orf192_homolog_OS=Mus_musculus_PE=2_SV=2	9.00E-16
comp32778_c0_seq1.p2		
comp32778_c0_seq3.p2		
comp32779_c0_seq10.p1		
comp32779_c0_seq15.p1	sp|Q8VE65|TAF12_MOUSE_Transcription_initiation_factor_TFIID_subunit_12_OS=Mus_musculus_GN=Taf12_PE=1_SV=1	8.00E-12
comp32779_c0_seq2.p1	sp|B2J7M9|GSA_NOSP7_Glutamate-1-semialdehyde_2,1-aminomutase_OS=Nostoc_punctiforme_(strain_ATCC_29133_/_PCC_73102)_GN=hemL_PE=3_SV=1	0
comp32779_c0_seq2.p2		
comp32779_c0_seq3.p1	sp|Q58091|Y678_METJA_Uncharacterized_protein_MJ0678_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ0678_PE=4_SV=1	1.00E-11
comp32779_c0_seq8.p1		
comp32780_c1_seq10.p1		
comp32780_c1_seq3.p1		
comp32780_c1_seq3.p3		
comp32780_c1_seq6.p1		
comp32780_c1_seq9.p1		
comp32781_c0_seq2.p1	sp|Q0D4B2|CIPKL_ORYSJ_CBL-interacting_protein_kinase_21_OS=Oryza_sativa_subsp._japonica_GN=CIPK21_PE=2_SV=2	3.00E-33
comp32781_c0_seq3.p1	sp|Q9LDI3|CIPKO_ARATH_CBL-interacting_serine/threonine-protein_kinase_24_OS=Arabidopsis_thaliana_GN=CIPK24_PE=1_SV=1	1.00E-34
comp32782_c0_seq2.p1		
comp32782_c0_seq4.p1		
comp32782_c0_seq4.p2		
comp32783_c6_seq6.p1		
comp32784_c0_seq10.p2		
comp32784_c0_seq4.p3		
comp32784_c0_seq6.p1		
comp32784_c0_seq8.p1		
comp32784_c0_seq9.p1		
comp32785_c1_seq2.p1	sp|P47961|RS4_CRIGR_40S_ribosomal_protein_S4_OS=Cricetulus_griseus_GN=RPS4_PE=2_SV=2	2.00E-118
comp32786_c0_seq11.p1		
comp32786_c0_seq12.p1		
comp32786_c0_seq13.p1		
comp32786_c0_seq3.p1		
comp32786_c0_seq4.p1		
comp32786_c0_seq5.p1		
comp32786_c0_seq8.p1		
comp32787_c0_seq11.p1		
comp32787_c0_seq14.p2		
comp32787_c0_seq14.p3		
comp32787_c0_seq14.p4		
comp32787_c0_seq15.p1		
comp32787_c0_seq17.p2		
comp32787_c0_seq3.p1		
comp32787_c0_seq4.p2		
comp32787_c0_seq4.p3		
comp32787_c0_seq4.p4		
comp32787_c0_seq6.p1		
comp32789_c0_seq10.p1		
comp32789_c0_seq5.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-11
comp32790_c0_seq11.p1		
comp32790_c0_seq12.p2		
comp32790_c0_seq2.p2		
comp32790_c0_seq2.p3		
comp32790_c0_seq7.p2		
comp32790_c0_seq7.p3		
comp32790_c0_seq8.p1		
comp32790_c0_seq9.p1		
comp32791_c0_seq10.p1	sp|Q6PCJ1|DCTN1_XENLA_Dynactin_subunit_1_OS=Xenopus_laevis_GN=dctn1_PE=2_SV=1	2.00E-18
comp32791_c0_seq10.p2	sp|Q91WN1|DNJC9_MOUSE_DnaJ_homolog_subfamily_C_member_9_OS=Mus_musculus_GN=Dnajc9_PE=2_SV=2	2.00E-27
comp32791_c0_seq10.p4	sp|Q5RIV4|ADAT2_DANRE_tRNA-specific_adenosine_deaminase_2_OS=Danio_rerio_GN=adat2_PE=2_SV=2	3.00E-41
comp32791_c0_seq22.p1		
comp32791_c0_seq22.p2	sp|P13496|DCTN1_DROME_Dynactin_subunit_1_OS=Drosophila_melanogaster_GN=Gl_PE=1_SV=2	1.00E-15
comp32791_c0_seq22.p3	sp|Q91WN1|DNJC9_MOUSE_DnaJ_homolog_subfamily_C_member_9_OS=Mus_musculus_GN=Dnajc9_PE=2_SV=2	2.00E-34
comp32791_c0_seq22.p5	sp|Q5RIV4|ADAT2_DANRE_tRNA-specific_adenosine_deaminase_2_OS=Danio_rerio_GN=adat2_PE=2_SV=2	1.00E-43
comp32791_c0_seq36.p1	sp|Q6PCJ1|DCTN1_XENLA_Dynactin_subunit_1_OS=Xenopus_laevis_GN=dctn1_PE=2_SV=1	2.00E-18
comp32791_c0_seq36.p2	sp|Q91WN1|DNJC9_MOUSE_DnaJ_homolog_subfamily_C_member_9_OS=Mus_musculus_GN=Dnajc9_PE=2_SV=2	2.00E-27
comp32791_c0_seq36.p4	sp|Q5RIV4|ADAT2_DANRE_tRNA-specific_adenosine_deaminase_2_OS=Danio_rerio_GN=adat2_PE=2_SV=2	1.00E-43
comp32791_c0_seq38.p1		
comp32791_c0_seq38.p2	sp|P13496|DCTN1_DROME_Dynactin_subunit_1_OS=Drosophila_melanogaster_GN=Gl_PE=1_SV=2	1.00E-15
comp32791_c0_seq38.p3	sp|Q91WN1|DNJC9_MOUSE_DnaJ_homolog_subfamily_C_member_9_OS=Mus_musculus_GN=Dnajc9_PE=2_SV=2	2.00E-27
comp32791_c0_seq43.p1	sp|Q6PCJ1|DCTN1_XENLA_Dynactin_subunit_1_OS=Xenopus_laevis_GN=dctn1_PE=2_SV=1	2.00E-18
comp32791_c0_seq43.p2	sp|Q91WN1|DNJC9_MOUSE_DnaJ_homolog_subfamily_C_member_9_OS=Mus_musculus_GN=Dnajc9_PE=2_SV=2	2.00E-34
comp32791_c0_seq43.p4	sp|Q5RIV4|ADAT2_DANRE_tRNA-specific_adenosine_deaminase_2_OS=Danio_rerio_GN=adat2_PE=2_SV=2	1.00E-43
comp32791_c0_seq62.p1	sp|Q6PCJ1|DCTN1_XENLA_Dynactin_subunit_1_OS=Xenopus_laevis_GN=dctn1_PE=2_SV=1	2.00E-18
comp32791_c0_seq62.p2	sp|Q91WN1|DNJC9_MOUSE_DnaJ_homolog_subfamily_C_member_9_OS=Mus_musculus_GN=Dnajc9_PE=2_SV=2	2.00E-34
comp32791_c0_seq62.p4	sp|Q5RIV4|ADAT2_DANRE_tRNA-specific_adenosine_deaminase_2_OS=Danio_rerio_GN=adat2_PE=2_SV=2	3.00E-41
comp32792_c1_seq1.p1		
comp32792_c2_seq7.p1		

comp32792_c2_seq9.p1	sp|A0T0K6|EFTU_PHATC_Elongation_factor_Tu,_chloroplastic_OS=Phaeodactylum_tricornutum_(strain_CCAP_1055/1)_GN=tufA_PE=3_SV=1	0	GO:0000166,GO:0003746,GO:0003746,GO:0003[illegible] 0009507,GO:0009507,GO:0009507,GO:0009536	[illegible]
comp32792_c4_seq1.p1				
comp32792_c4_seq12.p1				
comp32792_c4_seq13.p1				
comp32792_c4_seq15.p1				
comp32792_c4_seq2.p1				
comp32792_c4_seq6.p1				
comp32792_c4_seq8.p1				
comp32793_c0_seq1.p1				
comp32793_c1_seq3.p1				
comp32793_c1_seq6.p1				
comp32794_c0_seq1.p1				
comp32794_c0_seq15.p2				
comp32794_c0_seq2.p1				
comp32794_c0_seq3.p2				
comp32794_c0_seq4.p1				
comp32794_c0_seq4.p2				
comp32794_c0_seq4.p3	sp|Q7Z6Z7|HUWE1_HUMAN_E3_ubiquitin-protein_ligase_HUWE1_OS=Homo_sapiens_GN=HUWE1_PE=1_SV=3	3.00E-12	[illegible]	[illegible]
comp32794_c0_seq7.p1				
comp32794_c1_seq2.p1	sp|Q8GY23|UPL1_ARATH_E3_ubiquitin-protein_ligase_UPL1_OS=Arabidopsis_thaliana_GN=UPL1_PE=1_SV=3	3.00E-139	GO:0004842,GO:0016567,GO:0016874	[illegible]
comp32795_c1_seq2.p1				
comp32795_c1_seq4.p1				
comp32795_c1_seq8.p1				
comp32795_c2_seq3.p1				
comp32795_c2_seq4.p1				
comp32795_c2_seq5.p1				
comp32797_c0_seq7.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	8.00E-19	[illegible]	[illegible]
comp32797_c0_seq8.p1				
comp32797_c1_seq19.p1				
comp32797_c1_seq6.p1	sp|O23240|D2HDH_ARATH_D-2-hydroxyglutarate_dehydrogenase,_mitochondrial_OS=Arabidopsis_thaliana_GN=D2HGDH_PE=1_SV=3	5.00E-153	[illegible]	[illegible]
comp32798_c0_seq10.p1	sp|Q9SSE7|AROD2_ARATH_Arogenate_dehydratase/prephenate_dehydratase_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=ADT2_PE=1_SV=1	8.00E-68	[illegible]	[illegible]
comp32798_c0_seq11.p1	sp|Q9SR97|YIPL1_ARATH_Protein_yippee-like_At3g08990_OS=Arabidopsis_thaliana_GN=At3g08990_PE=2_SV=2	4.00E-32		
comp32798_c0_seq13.p1	sp|Q9SR97|YIPL1_ARATH_Protein_yippee-like_At3g08990_OS=Arabidopsis_thaliana_GN=At3g08990_PE=2_SV=2	4.00E-32		
comp32798_c0_seq5.p1	sp|Q66GI4|PP179_ARATH_Pentatricopeptide_repeat-containing_protein_At2g32230,_mitochondrial_OS=Arabidopsis_thaliana_GN=At2g32230_PE=2_SV=1	2.00E-15	[illegible]	[illegible]
comp32798_c0_seq6.p1				
comp32798_c0_seq8.p2	sp|Q7Y214|GTE7_ARATH_Transcription_factor_GTE7_OS=Arabidopsis_thaliana_GN=GTE7_PE=2_SV=1	1.00E-16	[illegible]	[illegible]
comp32800_c1_seq4.p1	sp|Q9UT49|CID13_SCHPO_Poly(A)_RNA_polymerase_cid13_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=cid13_PE=1_SV=1	1.00E-32	[illegible]	[illegible]
comp32800_c1_seq6.p1	sp|Q9UT49|CID13_SCHPO_Poly(A)_RNA_polymerase_cid13_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=cid13_PE=1_SV=1	9.00E-33	[illegible]	[illegible]
comp32800_c1_seq7.p1				
comp32801_c0_seq3.p1	sp|P57760|STK16_RAT_Serine/threonine-protein_kinase_16_OS=Rattus_norvegicus_GN=Stk16_PE=2_SV=2	4.00E-50	[illegible]	[illegible]
comp32801_c0_seq3.p2				
comp32801_c0_seq6.p1				
comp32801_c0_seq8.p1				
comp32801_c1_seq1.p2				
comp32801_c1_seq1.p4	sp|Q2QQS5|CCT14_ORYSJ_Cyclin-T1-4_OS=Oryza_sativa_subsp._japonica_GN=CYCT1-1_PE=2_SV=1	1.00E-17	[illegible]	[illegible]
comp32801_c1_seq11.p1				
comp32801_c1_seq12.p1	sp|Q2QQS5|CCT14_ORYSJ_Cyclin-T1-4_OS=Oryza_sativa_subsp._japonica_GN=CYCT1-1_PE=2_SV=1	3.00E-32	[illegible]	[illegible]
comp32801_c1_seq12.p4				
comp32801_c1_seq6.p1	sp|Q2QQS5|CCT14_ORYSJ_Cyclin-T1-4_OS=Oryza_sativa_subsp._japonica_GN=CYCT1-1_PE=2_SV=1	2.00E-37	[illegible]	[illegible]
comp32801_c1_seq9.p1				
comp32802_c0_seq2.p2				
comp32802_c0_seq5.p1				
comp32803_c0_seq17.p1				
comp32803_c0_seq23.p2				
comp32804_c0_seq4.p1				
comp32804_c0_seq5.p1				
comp32805_c0_seq2.p1	sp|Q5ZKI0|KCC2D_CHICK_Calcium/calmodulin-dependent_protein_kinase_type_II_delta_chain_OS=Gallus_gallus_GN=CAMK2D_PE=2_SV=1	2.00E-65	[illegible]	[illegible]
comp32805_c1_seq1.p1	sp|A8X6H4|CMK1_CAEBR_Calcium/calmodulin-dependent_protein_kinase_type_1_OS=Caenorhabditis_briggsae_GN=cmk-1_PE=3_SV=3	2.00E-44	[illegible]	[illegible]
comp32806_c0_seq2.p1				
comp32806_c0_seq3.p1				
comp32807_c1_seq13.p1				
comp32808_c1_seq1.p3				
comp32808_c1_seq3.p1				
comp32810_c0_seq11.p1				
comp32810_c0_seq12.p1				
comp32810_c0_seq16.p1				
comp32810_c0_seq2.p1				
comp32810_c0_seq3.p1				
comp32810_c0_seq6.p1				
comp32810_c0_seq7.p1	sp|Q54WA3|PEX7_DICDI_Peroxisomal_targeting_signal_2_receptor_OS=Dictyostelium_discoideum_GN=pex7_PE=3_SV=1	2.00E-76	[illegible]	[illegible]
comp32810_c0_seq9.p1				
comp32811_c0_seq10.p1	sp|Q60817|NACA_MOUSE_Nascent_polypeptide-associated_complex_subunit_alpha_OS=Mus_musculus_GN=Naca_PE=1_SV=1	1.00E-15	[illegible]	[illegible]
comp32811_c0_seq12.p1				
comp32811_c0_seq13.p1	sp|Q6ICZ8|NACA3_ARATH_Nascent_polypeptide-associated_complex_subunit_alpha-like_protein_3_OS=Arabidopsis_thaliana_GN=At5g13850_PE=1_SV=1	1.00E-11	[illegible]	[illegible]
comp32811_c0_seq15.p1				
comp32811_c0_seq16.p1	sp|P70670|NACAM_MOUSE_Nascent_polypeptide-associated_complex_subunit_alpha,_muscle-specific_form_OS=Mus_musculus_GN=Naca_PE=1_SV=2	2.00E-25	[illegible]	[illegible]
comp32811_c0_seq5.p1				
comp32811_c0_seq7.p1				
comp32812_c0_seq3.p1	sp|P59895|NEK6_RAT_Serine/threonine-protein_kinase_Nek6_OS=Rattus_norvegicus_GN=Nek6_PE=1_SV=1	3.00E-58	[illegible]	[illegible]
comp32812_c0_seq3.p2				
comp32812_c1_seq1.p1	sp|P53871|DUG3_YEAST_Probable_glutamine_amidotransferase_DUG3_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=DUG3_PE=1_SV=1	5.00E-37	[illegible]	[illegible]
comp32812_c1_seq3.p1				
comp32812_c1_seq5.p1				
comp32812_c1_seq7.p1	sp|P53871|DUG3_YEAST_Probable_glutamine_amidotransferase_DUG3_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=DUG3_PE=1_SV=1	3.00E-33	[illegible]	[illegible]
comp32812_c2_seq2.p1				
comp32812_c2_seq5.p1				
comp32812_c2_seq6.p1				
comp32813_c0_seq2.p1				
comp32813_c0_seq4.p1				
comp32814_c0_seq10.p1				
comp32814_c0_seq11.p1				
comp32814_c0_seq16.p1				
comp32814_c0_seq18.p1				
comp32814_c0_seq20.p1				
comp32814_c0_seq22.p1				
comp32814_c0_seq23.p1				
comp32814_c0_seq26.p1				
comp32814_c0_seq3.p1				
comp32814_c0_seq4.p1				
comp32814_c0_seq5.p1				
comp32814_c0_seq6.p1				
comp32815_c0_seq1.p1	sp|Q9SJ44|UEV1C_ARATH_Ubiquitin-conjugating_enzyme_E2_variant_1C_OS=Arabidopsis_thaliana_GN=UEV1C_PE=1_SV=1	2.00E-42	[illegible]	[illegible]
comp32815_c1_seq2.p1				
comp32815_c1_seq3.p1				
comp32816_c1_seq3.p1				
comp32816_c1_seq7.p1				
comp32816_c1_seq7.p14	sp|A4QND5|NIP7_XENTR_60S_ribosome_subunit_biogenesis_protein_NIP7_homolog_OS=Xenopus_tropicalis_GN=nip7_PE=2_SV=1	9.00E-60	[illegible]	[illegible]
comp32816_c1_seq7.p2	sp|Q7Z7G8|VP13B_HUMAN_Vacuolar_protein_sorting-associated_protein_13B_OS=Homo_sapiens_GN=VPS13B_PE=1_SV=2	3.00E-16	[illegible]	[illegible]
comp32817_c0_seq12.p2	sp|P42765|THIM_HUMAN_3-ketoacyl-CoA_thiolase,_mitochondrial_OS=Homo_sapiens_GN=ACAA2_PE=1_SV=2	1.00E-159	[illegible]	[illegible]
comp32818_c0_seq16.p1				
comp32818_c0_seq2.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	8.00E-11	[illegible]	[illegible]
comp32818_c0_seq3.p2				
comp32818_c0_seq7.p1				
comp32818_c0_seq8.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	8.00E-11	[illegible]	[illegible]
comp32819_c0_seq2.p1				
comp32819_c0_seq2.p2				
comp32820_c1_seq1.p1				
comp32820_c1_seq2.p2				
comp32820_c1_seq3.p2				
comp32820_c1_seq4.p1				
comp32821_c0_seq2.p1				
comp32821_c0_seq3.p1				
comp32821_c2_seq10.p1				
comp32821_c2_seq17.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	1.00E-17	[illegible]	[illegible]
comp32821_c2_seq18.p1				
comp32821_c2_seq19.p1				
comp32821_c2_seq23.p1				
comp32821_c2_seq5.p1				
comp32821_c2_seq5.p2				
comp32822_c0_seq2.p1				
comp32823_c0_seq13.p2				
comp32823_c0_seq19.p1				
comp32823_c0_seq2.p1				
comp32823_c0_seq6.p2				
comp32826_c0_seq10.p1				
comp32826_c0_seq11.p1				
comp32826_c0_seq14.p1				
comp32826_c0_seq5.p1	sp|Q10496|YDG9_SCHPO_TBC_domain-containing_protein_C26F1.09_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC26F1.09_PE=2_SV=1	4.00E-12	[illegible]	[illegible]
comp32826_c0_seq6.p1	sp|Q10496|YDG9_SCHPO_TBC_domain-containing_protein_C26F1.09_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC26F1.09_PE=2_SV=1	5.00E-13	[illegible]	[illegible]
comp32827_c0_seq11.p1				
comp32827_c0_seq12.p3				
comp32827_c0_seq18.p1				
comp32827_c0_seq19.p3				
comp32827_c0_seq22.p1				
comp32827_c0_seq31.p1				
comp32827_c0_seq31.p2				
comp32827_c0_seq34.p1	sp|Q99K82|SMOX_MOUSE_Spermine_oxidase_OS=Mus_musculus_GN=Smox_PE=1_SV=1	2.00E-19	[illegible]	[illegible]
comp32827_c0_seq38.p2				
comp32827_c2_seq1.p1				
comp32828_c0_seq3.p1	sp|Q6AZB8|HARB1_DANRE_Putative_nuclease_HARBI1_OS=Danio_rerio_GN=harbi1_PE=2_SV=1	1.00E-12	[illegible]	[illegible]
comp32829_c0_seq3.p1				
comp32829_c0_seq7.p1				
comp32829_c1_seq1.p1				
comp32829_c1_seq1.p3				
comp32829_c1_seq2.p1				
comp32829_c1_seq3.p1				
comp32829_c1_seq4.p1				
comp32829_c1_seq5.p1				
comp32829_c1_seq6.p1				
comp32829_c1_seq6.p2				
comp32830_c0_seq7.p1				
comp32830_c0_seq8.p2				
comp32830_c0_seq9.p1				
comp32831_c0_seq1.p1	sp|Q80VP5|CL065_MOUSE_Probable_peptide_chain_release_factor_C12orf65_homolog,_mitochondrial_OS=Mus_musculus_PE=2_SV=1	6.00E-15	[illegible]	[illegible]
comp32831_c0_seq2.p1	sp|Q9Y811|YONI_SCHPO_Uncharacterized_peptide_chain_release_factor-like_protein_C1105.18c,_mitochondrial_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC1105.18c_PE=3_SV=2	8.00E-21	[illegible]	[illegible]
comp32831_c2_seq3.p1	sp|Q28EL0|CCYL1_XENTR_Cyclin-Y-like_protein_1_OS=Xenopus_tropicalis_GN=ccnyl1_PE=2_SV=1	2.00E-28	[illegible]	[illegible]
comp32833_c0_seq1.p1				
comp32833_c0_seq3.p1				
comp32833_c0_seq4.p1				
comp32833_c0_seq5.p1				
comp32834_c0_seq11.p1				
comp32834_c0_seq12.p1				
comp32834_c0_seq17.p1				
comp32834_c0_seq5.p1				
comp32834_c0_seq8.p1				
comp32835_c0_seq4.p1	sp|O13737|YDR2_SCHPO_Uncharacterized_endoplasmic_reticulum_membrane_protein_C16E8.02_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC16E8.02_PE=2_SV=2	2.00E-11	[illegible]	[illegible]
comp32835_c0_seq6.p1				
comp32835_c0_seq8.p1				
comp32836_c1_seq1.p1				
comp32837_c1_seq12.p1	sp|Q9SZJ5|GLYM_ARATH_Serine_hydroxymethyltransferase,_mitochondrial_OS=Arabidopsis_thaliana_GN=SHM1_PE=1_SV=1	2.00E-68	[illegible]	[illegible]
comp32837_c1_seq16.p1				
comp32837_c1_seq19.p1	sp|P07511|GLYC_RABIT_Serine_hydroxymethyltransferase,_cytosolic_OS=Oryctolagus_cuniculus_GN=SHMT1_PE=1_SV=2	2.00E-74	[illegible]	[illegible]
comp32837_c1_seq20.p1	sp|Q9SZJ5|GLYM_ARATH_Serine_hydroxymethyltransferase,_mitochondrial_OS=Arabidopsis_thaliana_GN=SHM1_PE=1_SV=1	2.00E-68	[illegible]	[illegible]
comp32837_c1_seq22.p1	sp|Q9SZJ5|GLYM_ARATH_Serine_hydroxymethyltransferase,_mitochondrial_OS=Arabidopsis_thaliana_GN=SHM1_PE=1_SV=1	2.00E-68	[illegible]	[illegible]
comp32837_c1_seq5.p1				
comp32839_c0_seq2.p1				
comp32839_c1_seq10.p1				
comp32839_c1_seq11.p2				
comp32839_c1_seq11.p3				
comp32839_c1_seq12.p1				
comp32839_c1_seq18.p2				
comp32839_c1_seq2.p1				
comp32839_c1_seq4.p1				
comp32839_c1_seq6.p1	sp|Q9JMF7|DOPP1_MOUSE_Dolichyldiphosphatase_1_OS=Mus_musculus_GN=Dolpp1_PE=2_SV=1	4.00E-22	[illegible]	[illegible]
comp32839_c1_seq7.p1	sp|Q9BV68|RN126_HUMAN_RING_finger_protein_126_OS=Homo_sapiens_GN=RNF126_PE=1_SV=1	7.00E-12	[illegible]	[illegible]
comp32839_c1_seq9.p1	sp|Q9BV68|RN126_HUMAN_RING_finger_protein_126_OS=Homo_sapiens_GN=RNF126_PE=1_SV=1	1.00E-11	[illegible]	[illegible]
comp32840_c2_seq12.p1	sp|Q26614|FGFR_STRPU_Fibroblast_growth_factor_receptor_OS=Strongylocentrotus_purpuratus_GN=FGFR_PE=2_SV=1	6.00E-15	[illegible]	[illegible]
comp32840_c2_seq12.p10				
comp32840_c2_seq12.p2	sp|Q08759|MYB_XENLA_Transcriptional_activator_Myb_OS=Xenopus_laevis_GN=myb_PE=2_SV=1	2.00E-25	[illegible]	[illegible]
comp32840_c2_seq21.p1	sp|Q54YZ9|DHKJ_DICDI_Hybrid_signal_transduction_histidine_kinase_J_OS=Dictyostelium_discoideum_GN=dhkJ_PE=3_SV=2	2.00E-23	[illegible]	[illegible]
comp32840_c2_seq27.p1	sp|P01103|MYB_CHICK_Transcriptional_activator_Myb_OS=Gallus_gallus_GN=MYB_PE=2_SV=1	3.00E-28	[illegible]	[illegible]
comp32840_c2_seq29.p1				
comp32840_c2_seq29.p2	sp|Q9LY14|MSRA3_ARATH_Peptide_methionine_sulfoxide_reductase_A3_OS=Arabidopsis_thaliana_GN=MSRA3_PE=1_SV=1	1.00E-52	[illegible]	[illegible]
comp32840_c2_seq37.p1	sp|Q9R0L1|HSF4_MOUSE_Heat_shock_factor_protein_4_OS=Mus_musculus_GN=Hsf4_PE=1_SV=2	1.00E-12	[illegible]	[illegible]
comp32840_c2_seq38.p1	sp|Q54YZ9|DHKJ_DICDI_Hybrid_signal_transduction_histidine_kinase_J_OS=Dictyostelium_discoideum_GN=dhkJ_PE=3_SV=2	2.00E-23	[illegible]	[illegible]
comp32840_c2_seq38.p2				
comp32840_c2_seq39.p1	sp|Q26614|FGFR_STRPU_Fibroblast_growth_factor_receptor_OS=Strongylocentrotus_purpuratus_GN=FGFR_PE=2_SV=1	6.00E-15	[illegible]	[illegible]
comp32840_c2_seq39.p2	sp|Q54YZ9|DHKJ_DICDI_Hybrid_signal_transduction_histidine_kinase_J_OS=Dictyostelium_discoideum_GN=dhkJ_PE=3_SV=2	2.00E-23	[illegible]	[illegible]
comp32840_c2_seq4.p1	sp|Q08759|MYB_XENLA_Transcriptional_activator_Myb_OS=Xenopus_laevis_GN=myb_PE=2_SV=1	2.00E-25	[illegible]	[illegible]
comp32840_c2_seq4.p10				
comp32840_c2_seq4.p2				
comp32840_c2_seq46.p1	sp|P16924|P4HA1_CHICK_Prolyl_4-hydroxylase_subunit_alpha-1_OS=Gallus_gallus_GN=P4HA1_PE=1_SV=1	2.00E-15	[illegible]	[illegible]
comp32840_c2_seq8.p1	sp|Q08759|MYB_XENLA_Transcriptional_activator_Myb_OS=Xenopus_laevis_GN=myb_PE=2_SV=1	2.00E-25	[illegible]	[illegible]
comp32840_c2_seq8.p6				
comp32840_c2_seq9.p2				
comp32840_c2_seq9.p6				
comp32840_c3_seq2.p1				
comp32840_c3_seq3.p1				
comp32840_c3_seq6.p1				
comp32840_c7_seq1.p1	sp|O43290|SNUT1_HUMAN_U4/U6.U5_tri-snRNP-associated_protein_1_OS=Homo_sapiens_GN=SART1_PE=1_SV=1	1.00E-18	[illegible]	[illegible]
comp32841_c2_seq1.p1				
comp32842_c0_seq4.p2				
comp32842_c0_seq5.p1				
comp32843_c0_seq1.p1				
comp32843_c0_seq2.p2	sp|P62317|SMD2_MOUSE_Small_nuclear_ribonucleoprotein_Sm_D2_OS=Mus_musculus_GN=Snrpd2_PE=2_SV=1	4.00E-38	[illegible]	[illegible]
comp32844_c0_seq13.p1				
comp32844_c0_seq18.p1				
comp32844_c0_seq19.p1				
comp32844_c0_seq9.p1				
comp32845_c0_seq1.p1				
comp32845_c0_seq5.p1				
comp32846_c0_seq13.p2				
comp32846_c0_seq20.p1	sp|Q9JII6|AK1A1_MOUSE_Alcohol_dehydrogenase_[NADP(+)]_OS=Mus_musculus_GN=Akr1a1_PE=1_SV=3	1.00E-76	[illegible]	[illegible]
comp32846_c0_seq26.p2				
comp32846_c0_seq28.p1	sp|Q55027|SRPC_SYNE7_Probable_chromate_transport_protein_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=srpC_PE=2_SV=1	3.00E-34	[illegible]	[illegible]
comp32846_c0_seq32.p1				
comp32846_c0_seq6.p3				
comp32847_c0_seq10.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	5.00E-33		
comp32847_c0_seq11.p1				
comp32847_c0_seq3.p1				
comp32847_c0_seq8.p1				
comp32848_c1_seq2.p1				
comp32848_c1_seq3.p1				
comp32849_c0_seq10.p1	sp|Q5JHX4|Y2061_PYRKO_Putative_phosphate_permease_TK2061_OS=Pyrococcus_kodakaraensis_(strain_ATCC_BAA-918_/_JCM_12380_/_KOD1)_GN=TK2061_PE=3_SV=1	9.00E-49	[illegible]	[illegible]
comp32849_c0_seq8.p1	sp|Q9UYV6|Y1401_PYRAB_Putative_phosphate_permease_PYRAB14010_OS=Pyrococcus_abyssi_(strain_GE5_/_Orsay)_GN=PYRAB14010_PE=3_SV=1	6.00E-28	[illegible]	[illegible]
comp32849_c0_seq9.p1	sp|P65713|Y2302_MYCBO_Putative_phosphate_permease_Mb2302_OS=Mycobacterium_bovis_GN=Mb2302_PE=3_SV=1	2.00E-11	[illegible]	[illegible]
comp3285_c0_seq1.p1	sp|Q46916|GUDP_ECOLI_Probable_glucarate_transporter_OS=Escherichia_coli_(strain_K12)_GN=gudP_PE=1_SV=1	2.00E-76	[illegible]	[illegible]
comp3285_c1_seq1.p2	sp|Q46916|GUDP_ECOLI_Probable_glucarate_transporter_OS=Escherichia_coli_(strain_K12)_GN=gudP_PE=1_SV=1	4.00E-70	[illegible]	[illegible]
comp32850_c0_seq11.p1	sp|Q7SYN4|5NT3_DANRE_Cytosolic_5'-nucleotidase_3_OS=Danio_rerio_GN=nt5c3_PE=2_SV=2	2.00E-68	[illegible]	[illegible]
comp32850_c0_seq12.p1				
comp32850_c0_seq12.p2				
comp32850_c0_seq12.p3				
comp32850_c0_seq15.p1				
comp32850_c0_seq18.p1				
comp32850_c0_seq18.p2				
comp32850_c0_seq21.p1				
comp32850_c0_seq21.p2				
comp32850_c0_seq7.p1	sp|P20753|PPIA_SALTY_Peptidyl-prolyl_cis-trans_isomerase_A_OS=Salmonella_typhimurium_GN=ppiA_PE=3_SV=2	6.00E-17	[illegible]	[illegible]
comp32850_c1_seq3.p1				
comp32850_c1_seq4.p1	sp|P42925|PXMP2_MOUSE_Peroxisomal_membrane_protein_2_OS=Mus_musculus_GN=Pxmp2_PE=2_SV=2	3.00E-15	[illegible]	[illegible]
comp32851_c0_seq1.p1	sp|Q8NBN7|RDH13_HUMAN_Retinol_dehydrogenase_13_OS=Homo_sapiens_GN=RDH13_PE=1_SV=2	1.00E-57	[illegible]	[illegible]
comp32851_c1_seq10.p1	sp|O34456|EXUT_BACSU_Hexuronate_transporter_OS=Bacillus_subtilis_GN=exuT_PE=2_SV=1	2.00E-17	[illegible]	[illegible]
comp32851_c1_seq19.p1	sp|Q803R5|MTR1_DANRE_Cap-specific_mRNA_(nucleoside-2'-O-)-methyltransferase_1_OS=Danio_rerio_GN=ftsjd2_PE=2_SV=1	6.00E-12	[illegible]	[illegible]
comp32851_c1_seq21.p1	sp|Q8C0I1|ADAS_MOUSE_Alkyldihydroxyacetonephosphate_synthase,_peroxisomal_OS=Mus_musculus_GN=Agps_PE=1_SV=1	1.00E-106	[illegible]	[illegible]
comp32851_c1_seq21.p5	sp|O22643|ACBP_FRIAG_Acyl-CoA-binding_protein_OS=Fritillaria_agrestis_GN=ACABP_PE=3_SV=1	9.00E-12	[illegible]	[illegible]
comp32851_c1_seq22.p1				
comp32851_c1_seq23.p1				
comp32851_c1_seq5.p1	sp|P0AC59|GLRX2_ECOLI_Glutaredoxin-2_OS=Escherichia_coli_(strain_K12)_GN=grxB_PE=1_SV=1	1.00E-39	[illegible]	[illegible]
comp32852_c0_seq1.p1				
comp32852_c0_seq5.p1				
comp32854_c0_seq8.p1				
comp32854_c0_seq9.p1				
comp32856_c1_seq1.p1				
comp32857_c0_seq11.p2				
comp32857_c0_seq11.p4				
comp32857_c0_seq5.p1	sp|Q54Z40|MYBH_DICDI_Myb-like_protein_H_OS=Dictyostelium_discoideum_GN=mybH_PE=3_SV=1	9.00E-19	[illegible]	[illegible]
comp32857_c0_seq5.p5				
comp32857_c0_seq6.p1	sp|Q54Z40|MYBH_DICDI_Myb-like_protein_H_OS=Dictyostelium_discoideum_GN=mybH_PE=3_SV=1	1.00E-18	[illegible]	[illegible]
comp32857_c0_seq8.p1				
comp32857_c0_seq9.p1	sp|Q54Z40|MYBH_DICDI_Myb-like_protein_H_OS=Dictyostelium_discoideum_GN=mybH_PE=3_SV=1	8.00E-19	[illegible]	[illegible]
comp32858_c1_seq1.p1	sp|P16332|MUTA_MOUSE_Methylmalonyl-CoA_mutase,_mitochondrial_OS=Mus_musculus_GN=Mut_PE=2_SV=2	0	[illegible]	[illegible]
comp32858_c1_seq1.p2	sp|Q88WJ1|RL19_LACPL_50S_ribosomal_protein_L19_OS=Lactobacillus_plantarum_(strain_ATCC_BAA-793_/_NCIMB_8826_/_WCFS1)_GN=rplS_PE=3_SV=1	6.00E-12	[illegible]	[illegible]
comp32858_c2_seq12.p1	sp|Q93V78|TMT1_BRAOL_Thiocyanate_methyltransferase_1_OS=Brassica_oleracea_GN=TMT1_PE=1_SV=1	3.00E-39	[illegible]	[illegible]
comp32858_c2_seq15.p1	sp|Q9ASQ7|SLAH2_ARATH_S-type_anion_channel_SLAH2_OS=Arabidopsis_thaliana_GN=SLAH2_PE=2_SV=1	5.00E-32	[illegible]	[illegible]
comp32858_c2_seq16.p1	sp|Q9ASQ7|SLAH2_ARATH_S-type_anion_channel_SLAH2_OS=Arabidopsis_thaliana_GN=SLAH2_PE=2_SV=1	4.00E-31	[illegible]	[illegible]
comp32858_c2_seq18.p1				
comp32858_c2_seq19.p1	sp|Q93V78|TMT1_BRAOL_Thiocyanate_methyltransferase_1_OS=Brassica_oleracea_GN=TMT1_PE=1_SV=1	9.00E-45	[illegible]	[illegible]
comp32858_c2_seq3.p1	sp|Q9ASQ7|SLAH2_ARATH_S-type_anion_channel_SLAH2_OS=Arabidopsis_thaliana_GN=SLAH2_PE=2_SV=1	3.00E-32	[illegible]	[illegible]
comp32858_c2_seq5.p1	sp|Q6PEH9|S39AA_DANRE_Zinc_transporter_ZIP10_OS=Danio_rerio_GN=slc39a10_PE=2_SV=1	3.00E-21	[illegible]	[illegible]
comp32858_c2_seq7.p2				
comp32858_c2_seq8.p1	sp|Q6PEH9|S39AA_DANRE_Zinc_transporter_ZIP10_OS=Danio_rerio_GN=slc39a10_PE=2_SV=1	7.00E-23	[illegible]	[illegible]
comp32859_c0_seq1.p1				
comp32859_c0_seq4.p1	sp|P02840|SGS3_DROME_Salivary_glue_protein_Sgs-3_OS=Drosophila_melanogaster_GN=Sgs3_PE=2_SV=1	5.00E-11	[illegible]	[illegible]
comp32859_c0_seq5.p1				
comp32860_c0_seq10.p2				
comp32860_c0_seq3.p1				
comp32860_c0_seq7.p1				
comp32860_c0_seq7.p2				
comp32860_c0_seq8.p1				
comp32860_c0_seq9.p1				
comp32861_c0_seq10.p1				
comp32861_c0_seq13.p1				
comp32861_c0_seq14.p1				
comp32861_c0_seq15.p1				
comp32861_c0_seq16.p2				
comp32861_c0_seq17.p1				
comp32861_c0_seq6.p1				
comp32861_c0_seq8.p1				
comp32861_c0_seq9.p1				
comp32862_c0_seq12.p1				
comp32862_c0_seq2.p1	sp|B2RC85|R10B2_HUMAN_Radial_spoke_head_10_homolog_B2_OS=Homo_sapiens_GN=RSPH10B2_PE=2_SV=2	5.00E-64		
comp32862_c0_seq2.p3				
comp32862_c0_seq2.p7				
comp32862_c0_seq7.p1	sp|B2RC85|R10B2_HUMAN_Radial_spoke_head_10_homolog_B2_OS=Homo_sapiens_GN=RSPH10B2_PE=2_SV=2	5.00E-64		
comp32862_c0_seq7.p2				
comp32863_c0_seq21.p1	sp|Q55774|Y182_SYNY3_Uncharacterized_ABC_transporter_ATP-binding_protein_sll0182_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll0182_PE=3_SV=1	3.00E-51	[illegible]	[illegible]
comp32864_c0_seq1.p1				
comp32864_c0_seq4.p1				
comp32865_c0_seq10.p1				
comp32865_c0_seq12.p1				
comp32865_c0_seq6.p2				
comp32865_c0_seq9.p1				
comp32867_c0_seq4.p1				
comp32867_c0_seq7.p1				
comp32867_c0_seq8.p1				
comp32868_c0_seq1.p1	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	1.00E-18	[illegible]	[illegible]
comp32869_c0_seq1.p1				
comp32869_c0_seq4.p1				
comp32870_c0_seq1.p1				
comp32870_c0_seq17.p1	sp|Q4WGB7|MSH3_ASPFU_DNA_mismatch_repair_protein_msh3_OS=Neosartorya_fumigata_(strain_ATCC_MYA-4609_/_Af293_/_CBS_101355_/_FGSC_A1100)_GN=msh3_PE=3_SV=1	1.00E-115	[illegible]	[illegible]
comp32870_c0_seq18.p1				
comp32870_c0_seq20.p1				
comp32870_c0_seq3.p1				
comp32870_c0_seq4.p1				
comp32870_c0_seq5.p1				
comp32870_c0_seq6.p1				
comp32870_c0_seq7.p1				
comp32870_c0_seq9.p1	sp|Q4WGB7|MSH3_ASPFU_DNA_mismatch_repair_protein_msh3_OS=Neosartorya_fumigata_(strain_ATCC_MYA-4609_/_Af293_/_CBS_101355_/_FGSC_A1100)_GN=msh3_PE=3_SV=1	8.00E-116	[illegible]	[illegible]
comp32871_c1_seq3.p1				
comp32871_c1_seq7.p2				
comp32872_c0_seq1.p1				
comp32872_c0_seq8.p1				
comp32873_c0_seq2.p1	sp|O77203|PIAA_DICDI_Protein_pianissimo_A_OS=Dictyostelium_discoideum_GN=piaA_PE=1_SV=1	6.00E-68	[illegible]	[illegible]
comp32873_c0_seq5.p1	sp|O77203|PIAA_DICDI_Protein_pianissimo_A_OS=Dictyostelium_discoideum_GN=piaA_PE=1_SV=1	1.00E-35	[illegible]	[illegible]
comp32873_c0_seq5.p2	sp|O77203|PIAA_DICDI_Protein_pianissimo_A_OS=Dictyostelium_discoideum_GN=piaA_PE=1_SV=1	5.00E-20	[illegible]	[illegible]
comp32873_c1_seq17.p3				
comp32873_c1_seq21.p1				
comp32873_c1_seq23.p1				
comp32873_c1_seq24.p1				
comp32873_c1_seq29.p1				
comp32873_c1_seq31.p1	sp|O07631|TYPA_BACSU_GTP-binding_protein_TypA/BipA_homolog_OS=Bacillus_subtilis_GN=typA_PE=3_SV=1	0	[illegible]	[illegible]
comp32873_c1_seq31.p2	sp|Q4FZV2|SFT2B_RAT_Vesicle_transport_protein_SFT2B_OS=Rattus_norvegicus_GN=Sft2d2_PE=2_SV=1	2.00E-21	[illegible]	[illegible]
comp32873_c1_seq7.p1	sp|Q9CR62|M2OM_MOUSE_Mitochondrial_2-oxoglutarate/malate_carrier_protein_OS=Mus_musculus_GN=Slc25a11_PE=1_SV=3	9.00E-65	[illegible]	[illegible]
comp32873_c1_seq9.p1				
comp32873_c2_seq1.p1	sp|Q1HPK6|EF2_BOMMO_Translation_elongation_factor_2_OS=Bombyx_mori_GN=tef2_PE=1_SV=1	0	[illegible]	[illegible]
comp32874_c0_seq1.p1				
comp32874_c0_seq3.p1				
comp32875_c1_seq16.p1				
comp32875_c1_seq16.p2				
comp32875_c1_seq2.p1				
comp32875_c1_seq21.p1				
comp32875_c1_seq21.p2				
comp32875_c1_seq3.p1				
comp32877_c0_seq1.p1				
comp32877_c0_seq10.p1	sp|Q9VH90|TRBID_DROME_Ubiquitin_thioesterase_trabid_OS=Drosophila_melanogaster_GN=trbd_PE=1_SV=1	2.00E-13	[illegible]	[illegible]
comp32877_c0_seq4.p1	sp|Q8HY87|RNZ2_MACFA_Zinc_phosphodiesterase_ELAC_protein_2_OS=Macaca_fascicularis_GN=ELAC2_PE=2_SV=1	3.00E-42	[illegible]	[illegible]

comp32877_c0_seq5.p1	sp|Q9NBD7|CLASP_DROME_CLIP-associating_protein_OS=Drosophila_melanogaster_GN=chb_PE=1_SV=1	3.00E-12
comp32877_c0_seq6.p1		
comp32877_c0_seq8.p1		
comp32878_c0_seq13.p1		
comp32878_c0_seq17.p1	sp|Q6DED9|CE028_XENLA_Transmembrane_protein_C5orf28_homolog_OS=Xenopus_laevis_PE=2_SV=1	1.00E-13
comp32878_c0_seq18.p1		
comp32878_c0_seq18.p6		
comp32878_c0_seq18.p8		
comp32878_c0_seq22.p1		
comp32878_c0_seq28.p1		
comp32878_c0_seq32.p1		
comp32878_c0_seq5.p1		
comp32878_c0_seq7.p1		
comp32878_c0_seq7.p6		
comp32878_c0_seq7.p8		
comp32879_c0_seq1.p1		
comp32879_c0_seq1.p2		
comp32879_c0_seq2.p1		
comp32880_c0_seq11.p1		
comp32880_c0_seq11.p3		
comp32880_c0_seq15.p1		
comp32880_c0_seq18.p5		
comp32880_c0_seq18.p6		
comp32880_c0_seq2.p1		
comp32880_c0_seq21.p1		
comp32880_c0_seq21.p3		
comp32880_c0_seq22.p1		
comp32880_c0_seq23.p1	sp|Q9K7A0|CSD_BACHD_Probable_cysteine_desulfurase_OS=Bacillus_halodurans_(strain_ATCC_BAA-125_/_DSM_18197_/_FERM_7344_/_JCM_9153_/_C-125)_GN=csd_PE=3_SV=2	2.00E-20
comp32880_c0_seq4.p4		
comp32880_c0_seq4.p5		
comp32880_c0_seq5.p2		
comp32880_c0_seq5.p3	sp|Q8NK13|SKP1_NEUCR_E3_ubiquitin_ligase_complex_SCF_subunit_scon-3_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=scon-3_PE=1_SV=1	2.00E-51
comp32880_c0_seq8.p1		
comp32880_c0_seq9.p2	sp|Q8NK13|SKP1_NEUCR_E3_ubiquitin_ligase_complex_SCF_subunit_scon-3_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=scon-3_PE=1_SV=1	2.00E-51
comp32881_c0_seq1.p1		
comp32881_c0_seq1.p3	sp|Q54CI5|DPH4_DICDI_DPH4_homolog_OS=Dictyostelium_discoideum_GN=dph4_PE=3_SV=1	2.00E-17
comp32881_c0_seq12.p1	sp|Q8CDP0|CBPC3_MOUSE_Cytosolic_carboxypeptidase_3_OS=Mus_musculus_GN=Agbl3_PE=1_SV=1	3.00E-97
comp32881_c0_seq12.p3		
comp32881_c0_seq13.p1		
comp32881_c0_seq19.p1		
comp32881_c0_seq19.p2		
comp32881_c0_seq19.p4	sp|Q54CI5|DPH4_DICDI_DPH4_homolog_OS=Dictyostelium_discoideum_GN=dph4_PE=3_SV=1	2.00E-17
comp32881_c0_seq2.p1		
comp32881_c0_seq22.p2	sp|Q54CI5|DPH4_DICDI_DPH4_homolog_OS=Dictyostelium_discoideum_GN=dph4_PE=3_SV=1	2.00E-17
comp32881_c0_seq22.p3		
comp32881_c0_seq25.p1	sp|Q5U5Z8|CBPC2_HUMAN_Cytosolic_carboxypeptidase_2_OS=Homo_sapiens_GN=AGBL2_PE=2_SV=2	1.00E-37
comp32881_c0_seq28.p1		
comp32881_c0_seq28.p3	sp|Q54CI5|DPH4_DICDI_DPH4_homolog_OS=Dictyostelium_discoideum_GN=dph4_PE=3_SV=1	2.00E-17
comp32881_c0_seq29.p1		
comp32881_c0_seq30.p1		
comp32881_c0_seq31.p1		
comp32881_c0_seq32.p1	sp|Q5U5Z8|CBPC2_HUMAN_Cytosolic_carboxypeptidase_2_OS=Homo_sapiens_GN=AGBL2_PE=2_SV=2	8.00E-126
comp32881_c0_seq34.p2		
comp32881_c0_seq7.p1		
comp32882_c1_seq12.p1	sp|Q2S0I2|RSMA_SALRD_Ribosomal_RNA_small_subunit_methyltransferase_A_OS=Salinibacter_ruber_(strain_DSM_13855_/_M31)_GN=rsmA_PE=3_SV=1	1.00E-61
comp32882_c1_seq4.p1		
comp32882_c1_seq5.p1		
comp32882_c1_seq6.p1	sp|Q7Z4G4|TRM11_HUMAN_tRNA_(guanine(10)-N2)-methyltransferase_homolog_OS=Homo_sapiens_GN=TRMT11_PE=1_SV=1	4.00E-68
comp32883_c0_seq13.p1		
comp32883_c0_seq15.p1		
comp32883_c0_seq23.p1		
comp32883_c0_seq26.p1		
comp32883_c0_seq31.p1		
comp32883_c0_seq38.p1		
comp32883_c0_seq43.p1		
comp32883_c0_seq44.p1		
comp32885_c0_seq1.p1		
comp32885_c1_seq1.p1		
comp32886_c0_seq1.p1	sp|O22928|PUSH_ARATH_Putative_tRNA_pseudouridine_synthase_OS=Arabidopsis_thaliana_GN=At2g30320_PE=2_SV=1	1.00E-36
comp32886_c0_seq10.p2		
comp32886_c0_seq3.p2		
comp32886_c0_seq4.p1		
comp32886_c0_seq5.p1		
comp32886_c0_seq7.p1		
comp32886_c0_seq9.p1		
comp32886_c1_seq12.p1	sp|Q6GPL3|AUKBB_XENLA_Aurora_kinase_B-B_OS=Xenopus_laevis_GN=aurkb-b_PE=2_SV=1	2.00E-110
comp32886_c1_seq16.p1		
comp32886_c1_seq18.p1		
comp32886_c1_seq4.p2		
comp32886_c1_seq7.p2		
comp32886_c1_seq9.p1	sp|Q96GD4|AURKB_HUMAN_Aurora_kinase_B_OS=Homo_sapiens_GN=AURKB_PE=1_SV=3	5.00E-125
comp32887_c0_seq19.p1		
comp32887_c1_seq1.p3		
comp32887_c2_seq2.p1	sp|Q7PZD5|K0664_ANOGA_Protein_KIAA0664_homolog_OS=Anopheles_gambiae_GN=AGAP011851_PE=3_SV=4	4.00E-13
comp32887_c2_seq2.p2		
comp32887_c2_seq2.p3	sp|P36525|RM24_YEAST_54S_ribosomal_protein_L24,_mitochondrial_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=MRPL24_PE=1_SV=2	7.00E-15
comp32887_c2_seq2.p8		
comp32887_c3_seq2.p1		
comp32887_c3_seq4.p1		
comp32888_c0_seq11.p1		
comp32888_c0_seq14.p1		
comp32888_c0_seq15.p2		
comp32888_c0_seq16.p1		
comp32888_c0_seq3.p2		
comp32888_c0_seq6.p1		
comp32888_c0_seq7.p1		
comp32888_c0_seq9.p1		
comp32889_c0_seq2.p1		
comp32889_c1_seq12.p2		
comp32889_c1_seq15.p1		
comp32889_c1_seq16.p1		
comp32889_c1_seq5.p1		
comp32889_c1_seq7.p1		
comp32890_c0_seq14.p1		
comp32890_c0_seq24.p1		
comp32891_c0_seq1.p1		
comp32893_c0_seq1.p1		
comp32893_c0_seq12.p1		
comp32893_c0_seq13.p1		
comp32893_c0_seq14.p1		
comp32893_c0_seq17.p1		
comp32893_c0_seq18.p1		
comp32893_c0_seq22.p1		
comp32893_c0_seq22.p2		
comp32893_c0_seq4.p1		
comp32893_c0_seq6.p1		
comp32893_c0_seq8.p1		
comp32894_c1_seq2.p1	sp|Q7LHG5|YI31B_YEAST_Transposon_Ty3-I_Gag-Pol_polyprotein_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TY3B-I_PE=3_SV=2	2.00E-20
comp32895_c0_seq4.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	3.00E-16
comp32896_c0_seq1.p1		
comp32896_c0_seq10.p1		
comp32896_c0_seq12.p2		
comp32896_c0_seq22.p1		
comp32897_c0_seq1.p1		
comp32897_c0_seq11.p1		
comp32897_c0_seq13.p1		
comp32897_c0_seq5.p1		
comp32897_c0_seq7.p1		
comp32897_c0_seq8.p1		
comp32897_c0_seq8.p2		
comp32898_c0_seq1.p1		
comp32898_c0_seq10.p1	sp|Q54VC0|Y9865_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0280461_OS=Dictyostelium_discoideum_GN=DDB_G0280461_PE=3_SV=1	2.00E-52
comp32898_c0_seq10.p2	sp|Q28717|PTPA_RABIT_Serine/threonine-protein_phosphatase_2A_activator_OS=Oryctolagus_cuniculus_GN=PPP2R4_PE=1_SV=1	2.00E-93
comp32898_c0_seq6.p1		
comp32898_c0_seq7.p1	sp|Q8CDM1|ATAD2_MOUSE_ATPase_family_AAA_domain-containing_protein_2_OS=Mus_musculus_GN=Atad2_PE=1_SV=1	3.00E-115
comp32898_c0_seq7.p2		
comp32898_c0_seq8.p1	sp|Q54VC0|Y9865_DICDI_Probable_serine/threonine-protein_kinase_DDB_G0280461_OS=Dictyostelium_discoideum_GN=DDB_G0280461_PE=3_SV=1	2.00E-52
comp32898_c0_seq8.p2	sp|Q28717|PTPA_RABIT_Serine/threonine-protein_phosphatase_2A_activator_OS=Oryctolagus_cuniculus_GN=PPP2R4_PE=1_SV=1	2.00E-90
comp32898_c0_seq9.p1		
comp32901_c0_seq1.p1		
comp32901_c0_seq9.p2		
comp32902_c0_seq10.p1		
comp32902_c0_seq12.p1		
comp32902_c0_seq13.p1		
comp32902_c0_seq15.p1		
comp32902_c0_seq17.p1		
comp32902_c0_seq18.p1	sp|P73245|Y1917_SYNY3_Oxygen-independent_coproporphyrinogen-III_oxidase-like_protein_sll1917_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll1917_PE=3_SV=1	2.00E-17
comp32902_c0_seq18.p2		
comp32902_c0_seq18.p4		
comp32902_c0_seq20.p1	sp|P73245|Y1917_SYNY3_Oxygen-independent_coproporphyrinogen-III_oxidase-like_protein_sll1917_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll1917_PE=3_SV=1	4.00E-29
comp32902_c0_seq20.p2		
comp32902_c0_seq20.p5		
comp32902_c0_seq3.p1	sp|P73245|Y1917_SYNY3_Oxygen-independent_coproporphyrinogen-III_oxidase-like_protein_sll1917_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=sll1917_PE=3_SV=1	5.00E-88
comp32902_c0_seq3.p2		
comp32902_c0_seq3.p5		
comp32902_c0_seq7.p1		
comp32902_c0_seq9.p1		
comp32903_c0_seq10.p1		
comp32903_c0_seq11.p1		
comp32903_c0_seq13.p1		
comp32903_c0_seq13.p2		
comp32903_c0_seq5.p1		
comp32903_c0_seq6.p1		
comp32903_c0_seq8.p2		
comp32904_c0_seq11.p2		
comp32904_c0_seq21.p1		
comp32904_c0_seq22.p1		
comp32904_c0_seq24.p1		
comp32904_c0_seq33.p1		
comp32904_c0_seq35.p1		
comp32904_c0_seq4.p1		
comp32904_c0_seq40.p1		
comp32905_c0_seq10.p1		
comp32905_c0_seq12.p1	sp|P84675|PFM_CHAGB_Putative_fungistatic_metabolite_OS=Chaetomium_globosum_(strain_ATCC_6205_/_CBS_148.51_/_DSM_1962_/_NBRC_6347_/_NRRL_1970)_GN=CHGG_05463_PE=1_SV=2	1.00E-13
comp32905_c0_seq14.p1	sp|Q5QQ53|XYLT_DROPS_Xylosyltransferase_oxt_OS=Drosophila_pseudoobscura_pseudoobscura_GN=oxt_PE=2_SV=1	6.00E-11
comp32905_c0_seq15.p1		
comp32905_c0_seq19.p1	sp|P84675|PFM_CHAGB_Putative_fungistatic_metabolite_OS=Chaetomium_globosum_(strain_ATCC_6205_/_CBS_148.51_/_DSM_1962_/_NBRC_6347_/_NRRL_1970)_GN=CHGG_05463_PE=1_SV=2	6.00E-16
comp32905_c0_seq22.p1		
comp32905_c0_seq3.p1	sp|P84675|PFM_CHAGB_Putative_fungistatic_metabolite_OS=Chaetomium_globosum_(strain_ATCC_6205_/_CBS_148.51_/_DSM_1962_/_NBRC_6347_/_NRRL_1970)_GN=CHGG_05463_PE=1_SV=2	9.00E-17
comp32905_c0_seq30.p1	sp|P70805|ALGG_AZOVI_Poly(beta-D-mannuronate)_C5_epimerase_OS=Azotobacter_vinelandii_GN=algG_PE=2_SV=1	8.00E-15
comp32905_c0_seq33.p1	sp|P70805|ALGG_AZOVI_Poly(beta-D-mannuronate)_C5_epimerase_OS=Azotobacter_vinelandii_GN=algG_PE=2_SV=1	8.00E-15
comp32905_c0_seq4.p1	sp|P84675|PFM_CHAGB_Putative_fungistatic_metabolite_OS=Chaetomium_globosum_(strain_ATCC_6205_/_CBS_148.51_/_DSM_1962_/_NBRC_6347_/_NRRL_1970)_GN=CHGG_05463_PE=1_SV=2	2.00E-14
comp32906_c0_seq10.p1	sp|Q6DFT3|PP4R3_XENTR_Serine/threonine-protein_phosphatase_4_regulatory_subunit_3_OS=Xenopus_tropicalis_GN=smek2_PE=2_SV=1	2.00E-18
comp32906_c0_seq13.p1	sp|P35567|CDK1A_XENLA_Cyclin-dependent_kinase_1-A_OS=Xenopus_laevis_GN=cdk1-a_PE=1_SV=1	1.00E-122
comp32906_c0_seq8.p1	sp|Q6DFT3|PP4R3_XENTR_Serine/threonine-protein_phosphatase_4_regulatory_subunit_3_OS=Xenopus_tropicalis_GN=smek2_PE=2_SV=1	3.00E-25
comp32907_c0_seq1.p2		
comp32907_c0_seq25.p1		
comp32907_c0_seq25.p2		
comp32907_c0_seq26.p2		
comp32907_c0_seq27.p1		
comp32907_c0_seq27.p3		
comp32907_c0_seq31.p1		
comp32907_c0_seq31.p4		
comp32907_c0_seq31.p7		
comp32907_c0_seq5.p1		
comp32907_c0_seq5.p4		
comp32907_c0_seq5.p5		
comp32908_c0_seq2.p1	sp|Q8UWA5|CAH2_TRIHK_Carbonic_anhydrase_2_OS=Tribolodon_hakonensis_GN=ca2_PE=2_SV=3	2.00E-22
comp32908_c0_seq4.p1		
comp32908_c0_seq5.p1	sp|P43166|CAH7_HUMAN_Carbonic_anhydrase_7_OS=Homo_sapiens_GN=CA7_PE=1_SV=1	2.00E-25
comp32909_c0_seq10.p1		
comp32909_c0_seq14.p1		
comp32909_c0_seq4.p1		
comp32910_c0_seq1.p1		
comp32910_c0_seq2.p1		
comp32910_c0_seq6.p2		
comp32911_c0_seq1.p1		
comp32911_c0_seq1.p2		
comp32911_c0_seq13.p1		
comp32911_c0_seq13.p2		
comp32911_c0_seq2.p1		
comp32911_c0_seq2.p2		
comp32911_c0_seq3.p1		
comp32911_c0_seq5.p1		
comp32911_c0_seq5.p2		
comp32911_c0_seq9.p1		
comp32912_c0_seq1.p1		
comp32912_c0_seq2.p1		
comp32912_c0_seq7.p1		
comp32912_c0_seq9.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	9.00E-19
comp32913_c0_seq6.p1		
comp32913_c0_seq9.p1		
comp32914_c1_seq1.p1	sp|A7SXZ6|OSGEP_NEMVE_Probable_tRNA_threonylcarbamoyladenosine_biosynthesis_protein_osgep_OS=Nematostella_vectensis_GN=osgep_PE=3_SV=1	7.00E-159
comp32914_c1_seq1.p2	sp|Q40296|FCPB_MACPY_Fucoxanthin-chlorophyll_a-c_binding_protein_B,_chloroplastic_OS=Macrocystis_pyrifera_GN=FCPB_PE=2_SV=1	1.00E-123
comp32914_c1_seq10.p1	sp|Q40296|FCPB_MACPY_Fucoxanthin-chlorophyll_a-c_binding_protein_B,_chloroplastic_OS=Macrocystis_pyrifera_GN=FCPB_PE=2_SV=1	7.00E-86
comp32914_c1_seq12.p1	sp|Q40296|FCPB_MACPY_Fucoxanthin-chlorophyll_a-c_binding_protein_B,_chloroplastic_OS=Macrocystis_pyrifera_GN=FCPB_PE=2_SV=1	1.00E-123
comp32914_c1_seq7.p1	sp|Q40296|FCPB_MACPY_Fucoxanthin-chlorophyll_a-c_binding_protein_B,_chloroplastic_OS=Macrocystis_pyrifera_GN=FCPB_PE=2_SV=1	1.00E-123
comp32914_c1_seq8.p1	sp|Q40296|FCPB_MACPY_Fucoxanthin-chlorophyll_a-c_binding_protein_B,_chloroplastic_OS=Macrocystis_pyrifera_GN=FCPB_PE=2_SV=1	1.00E-123
comp32915_c1_seq13.p1		
comp32915_c1_seq15.p1		
comp32915_c1_seq16.p1		
comp32916_c0_seq1.p1	sp|O08999|LTBP2_MOUSE_Latent-transforming_growth_factor_beta-binding_protein_2_OS=Mus_musculus_GN=Ltbp2_PE=1_SV=2	4.00E-12
comp32916_c0_seq10.p1	sp|P12359|PSBO_SPIOL_Oxygen-evolving_enhancer_protein_1,_chloroplastic_OS=Spinacia_oleracea_GN=PSBO_PE=1_SV=1	2.00E-58
comp32916_c0_seq4.p1	sp|P46483|PSBO_EUGGR_Oxygen-evolving_enhancer_protein_1,_chloroplastic_OS=Euglena_gracilis_GN=PSBO_PE=1_SV=2	3.00E-54
comp32916_c0_seq7.p1		
comp32917_c0_seq2.p1		
comp32917_c0_seq4.p1	sp|Q9SSR1|Y1259_ARATH_DCC_family_protein_At1g52590,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g52590_PE=1_SV=1	5.00E-30
comp32917_c0_seq7.p1	sp|Q9SSR1|Y1259_ARATH_DCC_family_protein_At1g52590,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g52590_PE=1_SV=1	4.00E-32
comp32917_c0_seq9.p1		
comp32918_c0_seq1.p1		
comp32918_c0_seq6.p1		
comp32918_c0_seq9.p1		
comp32919_c0_seq1.p1	sp|Q940M4|OCT7_ARATH_Organic_cation/carnitine_transporter_7_OS=Arabidopsis_thaliana_GN=OCT7_PE=2_SV=1	1.00E-56
comp32919_c0_seq2.p1	sp|Q6A4L0|S22AD_MOUSE_Solute_carrier_family_22_member_13_OS=Mus_musculus_GN=Slc22a13_PE=2_SV=3	8.00E-21
comp32920_c1_seq10.p1		
comp32920_c1_seq10.p2		
comp32920_c1_seq16.p1		
comp32920_c1_seq16.p2		
comp32920_c1_seq21.p2		
comp32920_c1_seq21.p4	sp|O74327|YH07_SCHPO_Putative_amino_acid_permease_C1685.07c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC1685.07c_PE=2_SV=1	9.00E-19
comp32920_c1_seq24.p1	sp|Q9K7A0|CSD_BACHD_Probable_cysteine_desulfurase_OS=Bacillus_halodurans_(strain_ATCC_BAA-125_/_DSM_18197_/_FERM_7344_/_JCM_9153_/_C-125)_GN=csd_PE=3_SV=2	5.00E-25
comp32920_c1_seq26.p2		
comp32920_c1_seq26.p3	sp|O74327|YH07_SCHPO_Putative_amino_acid_permease_C1685.07c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC1685.07c_PE=2_SV=1	2.00E-20
comp32920_c1_seq29.p3		
comp32920_c1_seq29.p4		
comp32920_c1_seq3.p2		
comp32920_c1_seq4.p2		
comp32920_c1_seq7.p2		
comp32920_c1_seq7.p4		
comp32920_c2_seq1.p1	sp|Q8VHS5|ASB16_MOUSE_Ankyrin_repeat_and_SOCS_box_protein_16_OS=Mus_musculus_GN=Asb16_PE=2_SV=1	2.00E-12
comp32920_c3_seq1.p1		
comp32921_c1_seq11.p2		
comp32921_c1_seq13.p1		
comp32921_c1_seq15.p1		
comp32921_c1_seq17.p1	sp|P37709|TRHY_RABIT_Trichohyalin_OS=Oryctolagus_cuniculus_GN=TCHH_PE=2_SV=1	1.00E-12
comp32921_c1_seq17.p2	sp|Q9Y2D2|S35A3_HUMAN_UDP-N-acetylglucosamine_transporter_OS=Homo_sapiens_GN=SLC35A3_PE=2_SV=1	3.00E-76
comp32921_c1_seq3.p1	sp|P37709|TRHY_RABIT_Trichohyalin_OS=Oryctolagus_cuniculus_GN=TCHH_PE=2_SV=1	3.00E-13
comp32921_c1_seq3.p2	sp|Q9Y2D2|S35A3_HUMAN_UDP-N-acetylglucosamine_transporter_OS=Homo_sapiens_GN=SLC35A3_PE=2_SV=1	3.00E-76
comp32921_c1_seq4.p1	sp|Q968A5|FUCT1_CAEEL_GDP-fucose_transporter_OS=Caenorhabditis_elegans_GN=C50F4.14_PE=1_SV=1	1.00E-66
comp32921_c1_seq8.p2	sp|Q9UJM8|HAOX1_HUMAN_Hydroxyacid_oxidase_1_OS=Homo_sapiens_GN=HAO1_PE=1_SV=1	3.00E-123
comp32921_c1_seq8.p3		
comp32922_c0_seq1.p1	sp|P79942|NOCT_XENLA_Nocturnin_OS=Xenopus_laevis_GN=ccrn4l_PE=2_SV=1	1.00E-15
comp32922_c1_seq2.p1		
comp32922_c2_seq2.p1		
comp32922_c3_seq4.p1		
comp32922_c3_seq6.p2		
comp32923_c0_seq1.p1		
comp32923_c0_seq1.p2		
comp32923_c0_seq13.p2		
comp32923_c0_seq14.p1		
comp32923_c0_seq18.p1		
comp32923_c0_seq2.p1		
comp32924_c0_seq1.p1		
comp32924_c0_seq4.p1		
comp32924_c0_seq5.p1		
comp32925_c0_seq2.p2		
comp32927_c0_seq1.p1		
comp32927_c0_seq11.p1		
comp32927_c0_seq17.p1	sp|Q7M732|RTL1_MOUSE_Retrotransposon-like_protein_1_OS=Mus_musculus_GN=Rtl1_PE=2_SV=1	9.00E-11
comp32927_c0_seq21.p1		
comp32927_c0_seq21.p2		
comp32927_c0_seq23.p2		
comp32927_c0_seq23.p3	sp|P09125|MSP8_EIMAC_Merozoite_surface_protein_CMZ-8_(Fragment)_OS=Eimeria_acervulina_PE=2_SV=1	6.00E-14
comp32927_c0_seq28.p1	sp|P09125|MSP8_EIMAC_Merozoite_surface_protein_CMZ-8_(Fragment)_OS=Eimeria_acervulina_PE=2_SV=1	5.00E-15
comp32927_c0_seq34.p4		
comp32927_c0_seq38.p2		
comp32927_c0_seq5.p1		
comp32927_c0_seq5.p2	sp|P09125|MSP8_EIMAC_Merozoite_surface_protein_CMZ-8_(Fragment)_OS=Eimeria_acervulina_PE=2_SV=1	5.00E-15
comp32927_c0_seq6.p2	sp|P09125|MSP8_EIMAC_Merozoite_surface_protein_CMZ-8_(Fragment)_OS=Eimeria_acervulina_PE=2_SV=1	6.00E-14
comp32928_c0_seq14.p1	sp|Q9M1Q9|AB21B_ARATH_ABC_transporter_B_family_member_21_OS=Arabidopsis_thaliana_GN=ABCB21_PE=1_SV=2	3.00E-173
comp32928_c0_seq14.p2	sp|Q54BT3|ABCB2_DICDI_ABC_transporter_B_family_member_2_OS=Dictyostelium_discoideum_GN=abcB2_PE=3_SV=1	7.00E-92
comp32928_c0_seq16.p1	sp|F4I7I0|ALAT1_ARATH_Alanine_aminotransferase_1,_mitochondrial_OS=Arabidopsis_thaliana_GN=ALAAT1_PE=1_SV=1	5.00E-159
comp32928_c0_seq6.p1	sp|P34106|ALA2_PANMI_Alanine_aminotransferase_2_OS=Panicum_miliaceum_PE=1_SV=1	2.00E-62
comp32928_c0_seq8.p1	sp|P21447|MDR1A_MOUSE_Multidrug_resistance_protein_1A_OS=Mus_musculus_GN=Abcb1a_PE=1_SV=3	0
comp32929_c0_seq1.p1		
comp32930_c0_seq1.p2	sp|P82898|H1A_OLILU_Histone_H1A_(Fragment)_OS=Olisthodiscus_luteus_PE=1_SV=1	5.00E-11
comp32930_c0_seq1.p3		
comp32930_c0_seq18.p1		
comp32930_c0_seq2.p1	sp|Q3ZBG9|PLS2_BOVIN_Phospholipid_scramblase_2_OS=Bos_taurus_GN=PLSCR2_PE=2_SV=1	2.00E-34
comp32930_c0_seq3.p1		
comp32930_c0_seq4.p1		
comp32930_c0_seq5.p1		
comp32930_c0_seq6.p2	sp|P82898|H1A_OLILU_Histone_H1A_(Fragment)_OS=Olisthodiscus_luteus_PE=1_SV=1	5.00E-11
comp32930_c0_seq6.p3		
comp32930_c0_seq7.p2		
comp32931_c1_seq14.p1		
comp32931_c1_seq37.p2		
comp32932_c0_seq1.p1		
comp32932_c0_seq2.p1		
comp32932_c0_seq2.p2		
comp32932_c0_seq4.p1	sp|Q6B9X6|VWKA_DICDI_Alpha-protein_kinase_vwkA_OS=Dictyostelium_discoideum_GN=vwkA_PE=1_SV=1	3.00E-23
comp32932_c0_seq5.p1		
comp32932_c0_seq6.p1	sp|Q6B9X6|VWKA_DICDI_Alpha-protein_kinase_vwkA_OS=Dictyostelium_discoideum_GN=vwkA_PE=1_SV=1	7.00E-23
comp32933_c0_seq1.p1	sp|P49731|MCM6_SCHPO_DNA_replication_licensing_factor_mcm6_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=mcm6_PE=1_SV=2	0
comp32933_c0_seq1.p2	sp|Q9D7M8|RPB4_MOUSE_DNA-directed_RNA_polymerase_II_subunit_RPB4_OS=Mus_musculus_GN=Polr2d_PE=2_SV=2	3.00E-11
comp32933_c0_seq10.p1	sp|Q9D7M8|RPB4_MOUSE_DNA-directed_RNA_polymerase_II_subunit_RPB4_OS=Mus_musculus_GN=Polr2d_PE=2_SV=2	3.00E-11
comp32933_c0_seq3.p1	sp|P49731|MCM6_SCHPO_DNA_replication_licensing_factor_mcm6_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=mcm6_PE=1_SV=2	0
comp32933_c0_seq3.p3	sp|Q9D7M8|RPB4_MOUSE_DNA-directed_RNA_polymerase_II_subunit_RPB4_OS=Mus_musculus_GN=Polr2d_PE=2_SV=2	3.00E-11
comp32933_c0_seq8.p1		
comp32933_c0_seq9.p1	sp|O05389|YRBE_BACSU_Uncharacterized_oxidoreductase_yrbE_OS=Bacillus_subtilis_GN=yrbE_PE=3_SV=2	3.00E-73
comp32933_c1_seq1.p1		
comp32933_c1_seq3.p1	sp|P46436|GST1_ASCSU_Glutathione_S-transferase_1_OS=Ascaris_suum_GN=GST1_PE=1_SV=3	1.00E-19
comp32934_c0_seq3.p1		
comp32935_c0_seq3.p1	sp|Q4UMX2|SYM_RICFE_Methionine--tRNA_ligase_OS=Rickettsia_felis_(strain_ATCC_VR-1525_/_URRWXCal2)_GN=metG_PE=3_SV=1	0
comp32935_c4_seq1.p1	sp|Q8L831|NUDT3_ARATH_Nudix_hydrolase_3_OS=Arabidopsis_thaliana_GN=NUDT3_PE=1_SV=1	5.00E-24
comp32935_c4_seq11.p1	sp|Q8L831|NUDT3_ARATH_Nudix_hydrolase_3_OS=Arabidopsis_thaliana_GN=NUDT3_PE=1_SV=1	1.00E-27
comp32935_c4_seq14.p1	sp|O75000|RL12_SCHPO_60S_ribosomal_protein_L12_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpl1201_PE=1_SV=1	9.00E-53
comp32935_c4_seq3.p1	sp|O75000|RL12_SCHPO_60S_ribosomal_protein_L12_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpl1201_PE=1_SV=1	9.00E-53
comp32935_c4_seq9.p1		
comp32936_c0_seq14.p1		
comp32936_c0_seq17.p1		
comp32936_c0_seq18.p1		
comp32936_c0_seq2.p1		
comp32936_c0_seq2.p2		
comp32936_c0_seq20.p1		
comp32936_c0_seq20.p4		
comp32936_c0_seq21.p1		
comp32936_c0_seq23.p1		
comp32936_c0_seq30.p1		
comp32936_c0_seq31.p1		
comp32936_c0_seq4.p1		
comp32936_c0_seq7.p4		
comp32936_c0_seq8.p2		
comp32937_c0_seq5.p1		
comp32938_c0_seq1.p1	sp|E1BNQ4|NNRD_BOVIN_ATP-dependent_(S)-NAD(P)H-hydrate_dehydratase_OS=Bos_taurus_GN=CARKD_PE=3_SV=1	7.00E-63
comp32938_c1_seq1.p1		
comp32938_c1_seq12.p1		
comp32938_c1_seq13.p1		
comp32938_c1_seq14.p1		
comp32938_c1_seq24.p1		
comp32938_c1_seq5.p1		
comp32938_c1_seq7.p1		

comp32939_c0_seq1.p1	sp|P57151|NUSG_BUCAI_Transcription_antitermination_protein_nusG_OS=Buchnera_aphidicola_subsp._Acyrthosiphon_pisum_(strain_APS)_GN=nusG_PE=3_SV=1	2.00E-14	[illegible]	[illegible]
comp32939_c0_seq10.p1				
comp32939_c0_seq11.p1	sp|Q9R9J1|MYCC_BACSU_Mycosubtilin_synthase_subunit_C_OS=Bacillus_subtilis_GN=mycC_PE=3_SV=1	2.00E-22	[illegible]	[illegible]
comp32939_c0_seq15.p1				
comp32939_c0_seq5.p1				
comp32939_c0_seq7.p1				
comp32939_c0_seq8.p2				
comp32940_c0_seq13.p1	sp|B8GPV3|AROB_THISH_3-dehydroquinate_synthase_OS=Thioalkalivibrio_sp._(strain_HL-EbGR7)_GN=aroB_PE=3_SV=1	5.00E-135	[illegible]	[illegible]
comp32940_c0_seq17.p1	sp|P38254|TTL_YEAST_Probable_tubulin--tyrosine_ligase_PBY1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PBY1_PE=1_SV=2	9.00E-19	[illegible]	[illegible]
comp32940_c1_seq2.p1				
comp32941_c0_seq1.p1				
comp32941_c0_seq12.p1				
comp32941_c0_seq13.p1				
comp32941_c0_seq14.p1				
comp32941_c0_seq15.p1				
comp32941_c0_seq16.p1				
comp32941_c0_seq19.p1				
comp32941_c0_seq21.p1				
comp32941_c0_seq3.p1				
comp32943_c0_seq7.p1	sp|Q54S77|VPS15_DICDI_Probable_serine/threonine-protein_kinase_vps15_OS=Dictyostelium_discoideum_GN=vps15_PE=3_SV=1	9.00E-20	[illegible]	[illegible]
comp32943_c0_seq9.p1	sp|Q5R9I3|PI3R4_PONAB_Phosphoinositide_3-kinase_regulatory_subunit_4_OS=Pongo_abelii_GN=PIK3R4_PE=2_SV=3	1.00E-22	[illegible]	[illegible]
comp32944_c0_seq1.p1				
comp32944_c0_seq11.p1				
comp32944_c0_seq12.p2				
comp32944_c0_seq12.p3				
comp32944_c0_seq15.p1				
comp32944_c0_seq2.p2				
comp32944_c0_seq2.p3				
comp32944_c0_seq7.p1				
comp32945_c2_seq1.p1	sp|P50567|H2A_CHLRE_Histone_H2A_OS=Chlamydomonas_reinhardtii_GN=H2A-II_PE=3_SV=1	3.00E-53	[illegible]	[illegible]
comp32945_c2_seq2.p1	sp|P50567|H2A_CHLRE_Histone_H2A_OS=Chlamydomonas_reinhardtii_GN=H2A-II_PE=3_SV=1	3.00E-53	[illegible]	[illegible]
comp32945_c4_seq1.p1	sp|Q03441|RMD1_YEAST_Sporulation_protein_RMD1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=RMD1_PE=1_SV=1	2.00E-38	[illegible]	[illegible]
comp32945_c5_seq10.p1				
comp32945_c5_seq3.p1				
comp32945_c5_seq5.p1	sp|Q8C8R3|ANK2_MOUSE_Ankyrin-2_OS=Mus_musculus_GN=Ank2_PE=1_SV=2	1.00E-33	[illegible]	[illegible]
comp32945_c5_seq9.p1				
comp32946_c0_seq1.p1	sp|Q8IZH2|XRN1_HUMAN_5'-3'_exoribonuclease_1_OS=Homo_sapiens_GN=XRN1_PE=1_SV=1	5.00E-102	[illegible]	[illegible]
comp32946_c0_seq2.p1	sp|P97789|XRN1_MOUSE_5'-3'_exoribonuclease_1_OS=Mus_musculus_GN=Xrn1_PE=1_SV=1	4.00E-151	[illegible]	[illegible]
comp32946_c0_seq3.p1	sp|Q8IZH2|XRN1_HUMAN_5'-3'_exoribonuclease_1_OS=Homo_sapiens_GN=XRN1_PE=1_SV=1	5.00E-102	[illegible]	[illegible]
comp32946_c0_seq4.p1	sp|P97789|XRN1_MOUSE_5'-3'_exoribonuclease_1_OS=Mus_musculus_GN=Xrn1_PE=1_SV=1	7.00E-118	[illegible]	[illegible]
comp32946_c2_seq1.p3				
comp32946_c2_seq10.p1				
comp32946_c2_seq11.p1				
comp32946_c2_seq12.p1	sp|P40383|XRN1_SCHPO_5'-3'_exoribonuclease_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=exo2_PE=1_SV=1	6.00E-32	[illegible]	[illegible]
comp32946_c2_seq2.p1				
comp32946_c2_seq3.p1				
comp32946_c2_seq8.p1				
comp32946_c2_seq9.p1				
comp32947_c0_seq3.p1				
comp32947_c0_seq5.p1				
comp32947_c0_seq7.p1				
comp32948_c0_seq1.p1				
comp32948_c1_seq1.p1				
comp32948_c1_seq4.p1				
comp32948_c1_seq5.p1				
comp32949_c4_seq14.p1				
comp32949_c4_seq24.p1				
comp32950_c0_seq15.p1				
comp32950_c0_seq17.p1				
comp32950_c0_seq18.p1				
comp32950_c0_seq19.p1				
comp32950_c0_seq2.p1				
comp32950_c0_seq22.p1				
comp32950_c0_seq22.p3				
comp32950_c0_seq27.p1				
comp32950_c0_seq28.p1				
comp32950_c0_seq33.p1	sp|Q4KLJ8|PDCL3_RAT_Phosducin-like_protein_3_OS=Rattus_norvegicus_GN=Pdcl3_PE=2_SV=1	9.00E-38	[illegible]	[illegible]
comp32950_c0_seq34.p1				
comp32950_c0_seq8.p1				
comp32951_c0_seq12.p1				
comp32951_c0_seq16.p1				
comp32951_c0_seq20.p1				
comp32951_c0_seq20.p2				
comp32951_c0_seq20.p3				
comp32951_c0_seq22.p1				
comp32951_c0_seq22.p2				
comp32951_c0_seq24.p1				
comp32951_c0_seq26.p1	sp|P59828|ALGG_PSEFL_Poly(beta-D-mannuronate)_C5_epimerase_OS=Pseudomonas_fluorescens_GN=algG_PE=1_SV=1	3.00E-23	[illegible]	[illegible]
comp32951_c0_seq27.p1				
comp32951_c0_seq27.p2				
comp32951_c0_seq34.p1				
comp32951_c0_seq35.p1				
comp32951_c0_seq4.p1	sp|P59828|ALGG_PSEFL_Poly(beta-D-mannuronate)_C5_epimerase_OS=Pseudomonas_fluorescens_GN=algG_PE=1_SV=1	3.00E-23	[illegible]	[illegible]
comp32951_c0_seq43.p1				
comp32951_c0_seq43.p2				
comp32952_c0_seq1.p1				
comp32952_c0_seq2.p1				
comp32952_c0_seq5.p1				
comp32953_c10_seq1.p2	sp|P30157|TBB6_ECTVR_Tubulin_beta-6_chain_OS=Ectocarpus_variabilis_GN=TUBB6_PE=2_SV=1	3.00E-164	[illegible]	[illegible]
comp32953_c4_seq10.p1				
comp32953_c4_seq11.p1				
comp32953_c4_seq12.p1	sp|P32495|NHP2_YEAST_H/ACA_ribonucleoprotein_complex_subunit_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=NHP2_PE=1_SV=2	1.00E-30	[illegible]	[illegible]
comp32953_c4_seq2.p1				
comp32953_c4_seq2.p2	sp|P32495|NHP2_YEAST_H/ACA_ribonucleoprotein_complex_subunit_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=NHP2_PE=1_SV=2	1.00E-30	[illegible]	[illegible]
comp32953_c4_seq21.p1				
comp32953_c4_seq29.p1	sp|P00507|AATM_RAT_Aspartate_aminotransferase,_mitochondrial_OS=Rattus_norvegicus_GN=Got2_PE=1_SV=2	6.00E-160	[illegible]	[illegible]
comp32953_c4_seq3.p1				
comp32953_c4_seq3.p3				
comp32953_c4_seq3.p5				
comp32953_c4_seq30.p1	sp|Q9SR77|HBPL1_ARATH_Heme-binding-like_protein_At3g10130,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g10130_PE=1_SV=1	1.00E-13	[illegible]	[illegible]
comp32953_c4_seq30.p2	sp|P32495|NHP2_YEAST_H/ACA_ribonucleoprotein_complex_subunit_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=NHP2_PE=1_SV=2	1.00E-30	[illegible]	[illegible]
comp32953_c4_seq35.p1	sp|Q9SR77|HBPL1_ARATH_Heme-binding-like_protein_At3g10130,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g10130_PE=1_SV=1	1.00E-13	[illegible]	[illegible]
comp32953_c4_seq35.p2				
comp32953_c4_seq37.p3				
comp32953_c4_seq50.p1				
comp32953_c4_seq50.p2				
comp32953_c4_seq54.p1	sp|P32495|NHP2_YEAST_H/ACA_ribonucleoprotein_complex_subunit_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=NHP2_PE=1_SV=2	2.00E-30	[illegible]	[illegible]
comp32953_c4_seq56.p1				
comp32953_c4_seq58.p2				
comp32953_c4_seq58.p3	sp|P32495|NHP2_YEAST_H/ACA_ribonucleoprotein_complex_subunit_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=NHP2_PE=1_SV=2	1.00E-30	[illegible]	[illegible]
comp32953_c4_seq58.p5				
comp32953_c4_seq60.p1	sp|P32495|NHP2_YEAST_H/ACA_ribonucleoprotein_complex_subunit_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=NHP2_PE=1_SV=2	1.00E-30	[illegible]	[illegible]
comp32953_c4_seq9.p1	sp|P00507|AATM_RAT_Aspartate_aminotransferase,_mitochondrial_OS=Rattus_norvegicus_GN=Got2_PE=1_SV=2	1.00E-106	[illegible]	[illegible]
comp32953_c4_seq9.p2	sp|P46643|AAT1_ARATH_Aspartate_aminotransferase,_mitochondrial_OS=Arabidopsis_thaliana_GN=ASP1_PE=1_SV=1	7.00E-46	[illegible]	[illegible]
comp32953_c7_seq2.p1	sp|Q80UP8|S20A2_MOUSE_Sodium-dependent_phosphate_transporter_2_OS=Mus_musculus_GN=Slc20a2_PE=1_SV=2	8.00E-18	[illegible]	[illegible]
comp32953_c7_seq3.p1	sp|Q8WUM9|S20A1_HUMAN_Sodium-dependent_phosphate_transporter_1_OS=Homo_sapiens_GN=SLC20A1_PE=1_SV=1	1.00E-35	[illegible]	[illegible]
comp32953_c9_seq1.p2				
comp32954_c1_seq1.p1				
comp32954_c1_seq2.p1				
comp32954_c2_seq13.p1	sp|Q84Y01|ITPK1_MAIZE_Inositol-tetrakisphosphate_1-kinase_1_OS=Zea_mays_GN=ITPK1_PE=2_SV=1	1.00E-31	[illegible]	[illegible]
comp32954_c2_seq2.p1				
comp32954_c2_seq3.p1				
comp32954_c2_seq3.p3				
comp32954_c2_seq3.p7				
comp32954_c2_seq5.p1				
comp32954_c3_seq1.p1	sp|Q9Y6D6|BIG1_HUMAN_Brefeldin_A-inhibited_guanine_nucleotide-exchange_protein_1_OS=Homo_sapiens_GN=ARFGEF1_PE=1_SV=2	1.00E-67	[illegible]	[illegible]
comp32954_c3_seq2.p1	sp|Q9Y6D6|BIG1_HUMAN_Brefeldin_A-inhibited_guanine_nucleotide-exchange_protein_1_OS=Homo_sapiens_GN=ARFGEF1_PE=1_SV=2	1.00E-68	[illegible]	[illegible]
comp32954_c3_seq7.p1				
comp32954_c5_seq2.p1				
comp32954_c5_seq2.p4				
comp32954_c5_seq5.p1				
comp32955_c0_seq4.p2				
comp32955_c0_seq5.p2				
comp32955_c0_seq6.p1				
comp32955_c0_seq9.p1	sp|Q17QR8|HARB1_BOVIN_Putative_nuclease_HARBI1_OS=Bos_taurus_GN=HARBI1_PE=2_SV=1	2.00E-15	[illegible]	[illegible]
comp32956_c0_seq5.p1				
comp32957_c0_seq14.p1				
comp32957_c0_seq18.p1				
comp32957_c0_seq5.p2				
comp32957_c0_seq7.p1				
comp32957_c1_seq1.p1				
comp32957_c2_seq6.p1				
comp32957_c2_seq7.p1				
comp32958_c0_seq2.p1				
comp32958_c0_seq4.p1	sp|Q5UR45|YL572_MIMIV_Putative_AAA_family_ATPase_L572_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L572_PE=3_SV=1	6.00E-11	[illegible]	[illegible]
comp32959_c0_seq12.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	3.00E-31	[illegible]	[illegible]
comp32959_c0_seq13.p1				
comp32960_c0_seq1.p1	sp|Q0CR35|EXGA_ASPTN_Probable_glucan_1,3-beta-glucosidase_A_OS=Aspergillus_terreus_(strain_NIH_2624_/_FGSC_A1156)_GN=exgA_PE=3_SV=1	2.00E-48	[illegible]	[illegible]
comp32961_c0_seq11.p1				
comp32961_c0_seq5.p1				
comp32961_c0_seq5.p2				
comp32961_c0_seq5.p5				
comp32961_c0_seq5.p7				
comp32961_c0_seq8.p1				
comp32961_c0_seq9.p1				
comp32961_c0_seq9.p2				
comp32961_c0_seq9.p6				
comp32962_c0_seq2.p1				
comp32962_c0_seq6.p1				
comp32962_c0_seq8.p1	sp|Q05944|HSP70_HYDVU_Heat_shock_70_kDa_protein_OS=Hydra_vulgaris_GN=HSP70.1_PE=3_SV=1	3.00E-22	GO:0000166,GO:0005524	[illegible]
comp32963_c1_seq18.p1	sp|Q9LFB8|PTR5_ARATH_Peptide_transporter_PTR5_OS=Arabidopsis_thaliana_GN=PTR5_PE=2_SV=1	8.00E-68	[illegible]	[illegible]
comp32963_c1_seq2.p1	sp|P71019|FABD_BACSU_Malonyl_CoA-acyl_carrier_protein_transacylase_OS=Bacillus_subtilis_GN=fabD_PE=3_SV=2	7.00E-61	[illegible]	[illegible]
comp32963_c1_seq20.p1				
comp32963_c1_seq21.p1				
comp32963_c1_seq22.p1				
comp32963_c1_seq29.p1				
comp32963_c1_seq32.p1				
comp32963_c1_seq32.p2				
comp32963_c1_seq33.p1				
comp32964_c1_seq13.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	2.00E-16		
comp32964_c1_seq3.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	7.00E-17		
comp32964_c1_seq5.p1				
comp32964_c1_seq6.p1				
comp32964_c1_seq8.p1				
comp32965_c0_seq15.p1	sp|Q6LA54|YF48_SCHPO_Uncharacterized_WD_repeat-containing_protein_C3H5.08c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC3H5.08c_PE=1_SV=2	1.00E-29	[illegible]	[illegible]
comp32965_c0_seq2.p1				
comp32965_c0_seq2.p3				
comp32965_c0_seq4.p1				
comp32966_c0_seq2.p1	sp|Q5ZJ60|HIBCH_CHICK_3-hydroxyisobutyryl-CoA_hydrolase,_mitochondrial_OS=Gallus_gallus_GN=HIBCH_PE=2_SV=1	7.00E-67	[illegible]	[illegible]
comp32966_c1_seq3.p1	sp|Q2TAF8|LONP2_XENLA_Lon_protease_homolog_2,_peroxisomal_OS=Xenopus_laevis_GN=lonp2_PE=2_SV=1	5.00E-106	[illegible]	[illegible]
comp32966_c1_seq4.p1	sp|P36774|LON2_MYXXA_Lon_protease_2_OS=Myxococcus_xanthus_GN=lon2_PE=1_SV=3	2.00E-55	[illegible]	[illegible]
comp32966_c1_seq4.p3				
comp32967_c0_seq1.p1				
comp32967_c1_seq16.p1				
comp32967_c1_seq21.p1				
comp32967_c1_seq23.p2				
comp32967_c1_seq3.p1				
comp32967_c1_seq6.p1				
comp32968_c0_seq1.p2				
comp32968_c0_seq1.p3				
comp32968_c0_seq11.p2				
comp32968_c0_seq12.p1				
comp32968_c0_seq15.p3				
comp32968_c0_seq15.p5				
comp32968_c0_seq16.p1				
comp32969_c0_seq1.p1				
comp32969_c0_seq2.p1				
comp32970_c0_seq3.p1	sp|Q54X15|HDA21_DICDI_Type-2_histone_deacetylase_1_OS=Dictyostelium_discoideum_GN=hdaD_PE=2_SV=1	1.00E-29	[illegible]	[illegible]
comp32970_c0_seq3.p3				
comp32970_c0_seq4.p1	sp|Q55E45|MCFE_DICDI_Mitochondrial_substrate_carrier_family_protein_E_OS=Dictyostelium_discoideum_GN=mcfE_PE=3_SV=1	2.00E-19	[illegible]	[illegible]
comp32970_c0_seq4.p2	sp|Q55E45|MCFE_DICDI_Mitochondrial_substrate_carrier_family_protein_E_OS=Dictyostelium_discoideum_GN=mcfE_PE=3_SV=1	4.00E-11	[illegible]	[illegible]
comp32970_c1_seq1.p1	sp|P41753|HSP70_ACHKL_Heat_shock_70_kDa_protein_OS=Achlya_klebsiana_GN=HSP70_PE=2_SV=1	0	GO:0000166,GO:0005524	[illegible]
comp32970_c1_seq2.p1	sp|Q9S9N1|HSP7E_ARATH_Heat_shock_70_kDa_protein_5_OS=Arabidopsis_thaliana_GN=HSP70-5_PE=2_SV=1	0	[illegible]	[illegible]
comp32970_c1_seq7.p1	sp|P41753|HSP70_ACHKL_Heat_shock_70_kDa_protein_OS=Achlya_klebsiana_GN=HSP70_PE=2_SV=1	0	GO:0000166,GO:0005524	[illegible]
comp32971_c0_seq1.p1				
comp32972_c0_seq16.p1				
comp32973_c0_seq1.p1				
comp32973_c0_seq2.p1				
comp32973_c0_seq3.p1				
comp32974_c0_seq1.p1				
comp32974_c0_seq10.p1	sp|O42953|YGM4_SCHPO_HMG_box-containing_protein_C19G7.04_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC19G7.04_PE=2_SV=2	2.00E-32	[illegible]	[illegible]
comp32974_c0_seq10.p2				
comp32974_c0_seq6.p1				
comp32975_c0_seq1.p1				
comp32975_c0_seq3.p1				
comp32975_c0_seq7.p1				
comp32976_c1_seq1.p1				
comp32976_c1_seq2.p1	sp|Q9RC92|UGL_BACGL_Unsaturated_glucuronyl_hydrolase_OS=Bacillus_sp._(strain_GL1)_GN=ugl_PE=1_SV=1	3.00E-41	[illegible]	[illegible]
comp32976_c1_seq6.p1				
comp32976_c1_seq6.p3				
comp32978_c0_seq12.p1	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	5.00E-11	[illegible]	[illegible]
comp32978_c0_seq13.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp32978_c0_seq4.p1				
comp32978_c0_seq8.p1				
comp32978_c0_seq9.p1				
comp32979_c0_seq11.p1				
comp32979_c0_seq14.p1	sp|Q6ZQB6|VIP2_MOUSE_Inositol_hexakisphosphate_and_diphosphoinositol-pentakisphosphate_kinase_2_OS=Mus_musculus_GN=Ppip5k2_PE=1_SV=3	3.00E-103	[illegible]	[illegible]
comp32979_c0_seq24.p1				
comp32979_c0_seq24.p2				
comp32981_c0_seq4.p1				
comp32981_c0_seq4.p2				
comp32982_c0_seq1.p1	sp|P47032|PRY1_YEAST_Protein_PRY1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PRY1_PE=1_SV=1	4.00E-17	[illegible]	[illegible]
comp32982_c0_seq10.p1				
comp32982_c0_seq11.p1				
comp32982_c0_seq2.p2				
comp32982_c0_seq20.p1				
comp32982_c0_seq5.p1				
comp32983_c1_seq16.p1	sp|Q8ZIK1|RLUA_YERPE_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Yersinia_pestis_GN=rluA_PE=3_SV=1	1.00E-31	[illegible]	[illegible]
comp32983_c1_seq16.p2				
comp32983_c1_seq21.p2				
comp32983_c1_seq24.p1	sp|Q8ZIK1|RLUA_YERPE_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Yersinia_pestis_GN=rluA_PE=3_SV=1	2.00E-43	[illegible]	[illegible]
comp32983_c1_seq27.p1	sp|P0AA38|RLUA_SHIFL_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Shigella_flexneri_GN=rluA_PE=3_SV=2	1.00E-52	[illegible]	[illegible]
comp32983_c1_seq27.p2				
comp32983_c1_seq29.p1				
comp32983_c1_seq29.p3				
comp32983_c1_seq29.p4	sp|Q8RXE7|AGD14_ARATH_Probable_ADP-ribosylation_factor_GTPase-activating_protein_AGD14_OS=Arabidopsis_thaliana_GN=AGD14_PE=1_SV=2	2.00E-13	[illegible]	[illegible]
comp32983_c1_seq43.p1				
comp32983_c1_seq44.p1				
comp32983_c1_seq46.p1				
comp32983_c1_seq46.p6	sp|Q8RXE7|AGD14_ARATH_Probable_ADP-ribosylation_factor_GTPase-activating_protein_AGD14_OS=Arabidopsis_thaliana_GN=AGD14_PE=1_SV=2	2.00E-13	[illegible]	[illegible]
comp32983_c1_seq56.p1	sp|P0AA38|RLUA_SHIFL_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Shigella_flexneri_GN=rluA_PE=3_SV=2	1.00E-52	[illegible]	[illegible]
comp32983_c1_seq56.p2				
comp32983_c1_seq59.p1				
comp32983_c1_seq59.p3	sp|Q8ZIK1|RLUA_YERPE_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Yersinia_pestis_GN=rluA_PE=3_SV=1	3.00E-23	[illegible]	[illegible]
comp32983_c1_seq63.p1	sp|Q8ZIK1|RLUA_YERPE_Ribosomal_large_subunit_pseudouridine_synthase_A_OS=Yersinia_pestis_GN=rluA_PE=3_SV=1	1.00E-31	[illegible]	[illegible]
comp32983_c1_seq63.p2				
comp32984_c0_seq12.p1				
comp32984_c0_seq2.p1				
comp32985_c0_seq4.p1				
comp32985_c0_seq5.p1				
comp32985_c0_seq6.p1				
comp32986_c0_seq2.p1				
comp32986_c1_seq14.p1				
comp32986_c1_seq6.p1	sp|Q38950|2AAB_ARATH_Serine/threonine-protein_phosphatase_2A_65_kDa_regulatory_subunit_A_beta_isoform_OS=Arabidopsis_thaliana_GN=PP2AA2_PE=1_SV=2	0	[illegible]	[illegible]
comp32987_c0_seq1.p1				
comp32987_c0_seq1.p2				
comp32987_c0_seq10.p1				
comp32987_c0_seq11.p1				
comp32987_c0_seq12.p1				
comp32987_c0_seq6.p1				
comp32987_c0_seq7.p1				
comp32987_c0_seq8.p1				
comp32987_c0_seq9.p1	sp|P49792|RBP2_HUMAN_E3_SUMO-protein_ligase_RanBP2_OS=Homo_sapiens_GN=RANBP2_PE=1_SV=2	7.00E-11	[illegible]	[illegible]
comp32988_c0_seq12.p1				
comp32988_c0_seq14.p1				
comp32988_c0_seq17.p1				
comp32988_c0_seq19.p1				
comp32988_c0_seq2.p1				
comp32988_c0_seq20.p2				
comp32988_c0_seq4.p1				
comp32988_c0_seq8.p1				
comp32988_c0_seq8.p6				
comp32988_c0_seq9.p2				
comp32989_c0_seq2.p1				
comp32989_c0_seq4.p1				
comp32989_c0_seq6.p4				
comp32989_c0_seq9.p1				
comp32989_c0_seq9.p5				
comp32990_c0_seq11.p1				
comp32990_c0_seq12.p1	sp|Q9C1W5|TIM16_SCHPO_Mitochondrial_import_inner_membrane_translocase_subunit_tim16_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=pam16_PE=2_SV=1	9.00E-20	[illegible]	[illegible]
comp32990_c0_seq22.p1				
comp32990_c0_seq32.p1	sp|Q5RB68|IF2B2_PONAB_Insulin-like_growth_factor_2_mRNA-binding_protein_2_OS=Pongo_abelii_GN=IGF2BP2_PE=2_SV=1	3.00E-16	[illegible]	[illegible]
comp32990_c0_seq32.p5				
comp32990_c0_seq34.p1				
comp32990_c0_seq4.p3				
comp32990_c0_seq5.p1	sp|Q5RB68|IF2B2_PONAB_Insulin-like_growth_factor_2_mRNA-binding_protein_2_OS=Pongo_abelii_GN=IGF2BP2_PE=2_SV=1	3.00E-16	[illegible]	[illegible]
comp32990_c0_seq5.p5				
comp32990_c0_seq6.p3				
comp32990_c0_seq7.p1				
comp32991_c0_seq1.p1	sp|Q9DB25|ALG5_MOUSE_Dolichyl-phosphate_beta-glucosyltransferase_OS=Mus_musculus_GN=Alg5_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp32991_c0_seq2.p1	sp|Q9DB25|ALG5_MOUSE_Dolichyl-phosphate_beta-glucosyltransferase_OS=Mus_musculus_GN=Alg5_PE=2_SV=1	5.00E-78	[illegible]	[illegible]
comp32991_c0_seq2.p2				
comp32991_c1_seq1.p1	sp|Q8TD26|CHD6_HUMAN_Chromodomain-helicase-DNA-binding_protein_6_OS=Homo_sapiens_GN=CHD6_PE=1_SV=4	1.00E-150	[illegible]	[illegible]
comp32991_c2_seq1.p1				
comp32991_c2_seq11.p2				
comp32991_c2_seq14.p1				
comp32991_c2_seq14.p2				
comp32991_c2_seq14.p4				
comp32991_c2_seq16.p1				
comp32991_c2_seq17.p1				
comp32991_c2_seq18.p1	sp|B1AY13|UBP24_MOUSE_Ubiquitin_carboxyl-terminal_hydrolase_24_OS=Mus_musculus_GN=Usp24_PE=1_SV=1	2.00E-44	[illegible]	[illegible]
comp32991_c2_seq18.p3				
comp32991_c2_seq18.p4				
comp32991_c2_seq18.p6				
comp32991_c2_seq8.p1				
comp32992_c0_seq4.p1				
comp32992_c0_seq4.p5	sp|O42926|VP13B_SCHPO_Vacuolar_protein_sorting-associated_protein_13b_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=vps13b_PE=2_SV=1	3.00E-13	[illegible]	[illegible]
comp32993_c0_seq1.p1	sp|Q5QQ53|XYLT_DROPS_Xylosyltransferase_oxt_OS=Drosophila_pseudoobscura_pseudoobscura_GN=oxt_PE=2_SV=1	1.00E-14	[illegible]	[illegible]
comp32993_c1_seq1.p1				
comp32993_c1_seq2.p1	sp|Q96JK4|HIPL1_HUMAN_HHIP-like_protein_1_OS=Homo_sapiens_GN=HHIPL1_PE=2_SV=2	3.00E-31	[illegible]	[illegible]
comp32993_c1_seq5.p1				
comp32994_c1_seq2.p1				
comp32995_c0_seq5.p1	sp|O69671|EGTB_MYCTU_Iron(II)-dependent_oxidoreductase_EgtB_OS=Mycobacterium_tuberculosis_GN=egtB_PE=3_SV=1	1.00E-20	[illegible]	[illegible]
comp32996_c0_seq17.p1				
comp32997_c1_seq12.p1				
comp32997_c1_seq13.p1				
comp32997_c1_seq18.p1				
comp32997_c1_seq20.p1				
comp32997_c1_seq25.p1				
comp32997_c1_seq28.p1				
comp32997_c1_seq29.p1				
comp32997_c1_seq30.p1				
comp32997_c1_seq4.p1				
comp32997_c1_seq7.p1				
comp32998_c0_seq8.p1	sp|Q921G7|ETFD_MOUSE_Electron_transfer_flavoprotein-ubiquinone_oxidoreductase,_mitochondrial_OS=Mus_musculus_GN=Etfdh_PE=1_SV=1	1.00E-176	[illegible]	[illegible]
comp32998_c0_seq8.p3				
comp32998_c0_seq8.p5				
comp32999_c0_seq7.p1				
comp33000_c0_seq1.p1	sp|A5PK63|RS17_BOVIN_40S_ribosomal_protein_S17_OS=Bos_taurus_GN=RPS17_PE=2_SV=1	2.00E-50	[illegible]	[illegible]
comp33000_c0_seq10.p1				
comp33000_c0_seq11.p1				
comp33000_c0_seq14.p1	sp|P0C582|M2OM_NEUCR_Putative_mitochondrial_2-oxoglutarate/malate_carrier_protein_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=NCU04792_PE=3_SV=1	7.00E-69	[illegible]	[illegible]
comp33000_c0_seq5.p1				
comp33000_c0_seq8.p1	sp|A5PK63|RS17_BOVIN_40S_ribosomal_protein_S17_OS=Bos_taurus_GN=RPS17_PE=2_SV=1	2.00E-50	[illegible]	[illegible]
comp33001_c0_seq13.p1	sp|Q96G74|OTUD5_HUMAN_OTU_domain-containing_protein_5_OS=Homo_sapiens_GN=OTUD5_PE=1_SV=1	2.00E-16	[illegible]	[illegible]
comp33001_c0_seq22.p1	sp|Q6GL44|OTUD5_XENTR_OTU_domain-containing_protein_5_OS=Xenopus_tropicalis_GN=otud5_PE=2_SV=1	2.00E-16	[illegible]	[illegible]
comp33001_c0_seq25.p1	sp|Q6GL44|OTUD5_XENTR_OTU_domain-containing_protein_5_OS=Xenopus_tropicalis_GN=otud5_PE=2_SV=1	2.00E-17	[illegible]	[illegible]
comp33001_c0_seq35.p1				
comp33001_c0_seq39.p1				
comp33001_c0_seq44.p1	sp|Q96G74|OTUD5_HUMAN_OTU_domain-containing_protein_5_OS=Homo_sapiens_GN=OTUD5_PE=1_SV=1	2.00E-17	[illegible]	[illegible]
comp33001_c0_seq6.p1	sp|Q96G74|OTUD5_HUMAN_OTU_domain-containing_protein_5_OS=Homo_sapiens_GN=OTUD5_PE=1_SV=1	2.00E-16	[illegible]	[illegible]
comp33001_c0_seq8.p1	sp|B2RRE7|OTUD4_MOUSE_OTU_domain-containing_protein_4_OS=Mus_musculus_GN=Otud4_PE=1_SV=1	9.00E-13	[illegible]	[illegible]
comp33002_c0_seq5.p1				
comp33004_c0_seq10.p1				
comp33004_c0_seq12.p1				
comp33004_c0_seq15.p1	sp|Q5B4E7|PPID_EMENI_Peptidyl-prolyl_cis-trans_isomerase_D_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=cpr6_PE=3_SV=1	5.00E-72	[illegible]	[illegible]
comp33004_c0_seq15.p2				

comp33004_c0_seq22.p1			
comp33004_c0_seq25.p1			
comp33004_c0_seq32.p1			
comp33004_c0_seq36.p1			
comp33004_c0_seq39.p1			
comp33004_c0_seq40.p1			
comp33004_c0_seq43.p1			
comp33005_c0_seq22.p1	sp|Q9KG32|Y283_BACHD_Uncharacterized_isomerase_BH0283_OS=Bacillus_halodurans_(strain_ATCC_BAA-125_/_DSM_18197_/_FERM_7344_/_JCM_9153_/_C-125)_GN=BH0283_PE=3_SV=1	1.00E-57	GO:0003824,GO:0009058,GO:0016853
comp33005_c0_seq4.p1			
comp33005_c0_seq5.p1			
comp33006_c1_seq10.p1			
comp33006_c1_seq12.p1	sp|Q8RWB8|UPL6_ARATH_E3_ubiquitin-protein_ligase_UPL6_OS=Arabidopsis_thaliana_GN=UPL6_PE=2_SV=1	4.00E-98	GO:0004842,GO:0004842,GO:0005634,GO:0005737,GO:0016567,GO:0016874,GO:0042787
comp33006_c1_seq16.p1			
comp33006_c1_seq2.p1			
comp33006_c1_seq2.p3	sp|Q9BY66|KDM5D_HUMAN_Lysine-specific_demethylase_5D_OS=Homo_sapiens_GN=KDM5D_PE=1_SV=2	4.00E-17	GO:0003677,GO:0005575,GO:0005622,GO:0005634,GO:0005634,GO:0005634,GO:0008270,GO:0016491,GO:0016568,GO:0016706,GO:0032453,GO:0034720,GO:0046872,GO:0051213,GO:0055114,GO:0055114
comp33006_c1_seq20.p1	sp|Q95SX7|RTBS_DROME_Probable_RNA-directed_DNA_polymerase_from_transposon_BS_OS=Drosophila_melanogaster_GN=RTase_PE=2_SV=1	1.00E-17	GO:0003964,GO:0003964,GO:0003964,GO:0005575,GO:0006278,GO:0006278,GO:0006278,GO:0006313,GO:0016740,GO:0016779
comp33006_c1_seq22.p1			
comp33006_c1_seq25.p1	sp|Q61T02|KDM5_CAEBR_Lysine-specific_demethylase_rbr-2_OS=Caenorhabditis_briggsae_GN=rbr-2_PE=3_SV=2	8.00E-15	GO:0003677,GO:0005622,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0008270,GO:0016491,GO:0016568,GO:0016706,GO:0046872,GO:0051213,GO:0055114,GO:0055114
comp33006_c1_seq3.p1	sp|Q9NSK0|KLC4_HUMAN_Kinesin_light_chain_4_OS=Homo_sapiens_GN=KLC4_PE=1_SV=3	1.00E-21	GO:0003777,GO:0005737,GO:0005856,GO:0005856,GO:0005871,GO:0005874,GO:0008152
comp33006_c1_seq4.p2			
comp33006_c1_seq6.p1			
comp33007_c0_seq22.p1			
comp33007_c0_seq26.p1			
comp33007_c0_seq4.p1			
comp33008_c0_seq1.p2	sp|Q84Q72|HS181_ORYSJ_18.1_kDa_class_I_heat_shock_protein_OS=Oryza_sativa_subsp._japonica_GN=HSP18.1_PE=2_SV=1	1.00E-22	GO:0005737,GO:0005737,GO:0009408,GO:0042542,GO:0045471,GO:0046685,GO:0046686,GO:0046688
comp33008_c0_seq2.p1	sp|Q84Q72|HS181_ORYSJ_18.1_kDa_class_I_heat_shock_protein_OS=Oryza_sativa_subsp._japonica_GN=HSP18.1_PE=2_SV=1	1.00E-22	GO:0005737,GO:0005737,GO:0009408,GO:0042542,GO:0045471,GO:0046685,GO:0046686,GO:0046688
comp33008_c0_seq6.p1	sp|Q84Q72|HS181_ORYSJ_18.1_kDa_class_I_heat_shock_protein_OS=Oryza_sativa_subsp._japonica_GN=HSP18.1_PE=2_SV=1	4.00E-23	GO:0005737,GO:0005737,GO:0009408,GO:0042542,GO:0045471,GO:0046685,GO:0046686,GO:0046688
comp33008_c0_seq8.p1	sp|Q84Q72|HS181_ORYSJ_18.1_kDa_class_I_heat_shock_protein_OS=Oryza_sativa_subsp._japonica_GN=HSP18.1_PE=2_SV=1	4.00E-23	GO:0005737,GO:0005737,GO:0009408,GO:0042542,GO:0045471,GO:0046685,GO:0046686,GO:0046688
comp33009_c0_seq3.p1			
comp33010_c0_seq1.p1			
comp33010_c1_seq1.p2			
comp33010_c1_seq2.p1	sp|Q7A5L8|TDCB_STAAN_L-threonine_dehydratase_catabolic_TdcB_OS=Staphylococcus_aureus_(strain_N315)_GN=tdcB_PE=1_SV=1	2.00E-49	GO:0000166,GO:0003824,GO:0004794,GO:0004794,GO:0006520,GO:0006567,GO:0008152,GO:0016829,GO:0030170,GO:0070689
comp33010_c2_seq1.p1	sp|B9EKI3|TMF1_MOUSE_TATA_element_modulatory_factor_OS=Mus_musculus_GN=Tmf1_PE=1_SV=2	1.00E-13	GO:0000139,GO:0001675,GO:0001819,GO:0003677,GO:0005515,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005783,GO:0005794,GO:0005794,GO:0005794,GO:0005794,GO:0006351,GO:0006355,GO:0007286,GO:0007286,GO:0007289,GO:0008584,GO:0008584,GO:0010629,GO:0016020,GO:0030317,GO:0032275,GO:0033327,GO:0042742,GO:0043066,GO:0061136,GO:0071407,GO:2000845
comp33010_c3_seq1.p1			
comp33010_c3_seq2.p1			
comp33010_c5_seq24.p1	sp|A1L1R0|SHQ1_DANRE_Protein_SHQ1_homolog_OS=Danio_rerio_GN=shq1_PE=1_SV=1	1.00E-35	GO:0005634,GO:0005654,GO:0005737,GO:0005829,GO:0022618
comp33010_c5_seq29.p1			
comp33010_c5_seq32.p1	sp|Q05B18|SHQ1_XENTR_Protein_SHQ1_homolog_OS=Xenopus_tropicalis_GN=shq1_PE=2_SV=1	2.00E-58	GO:0005634,GO:0005654,GO:0005737,GO:0005829,GO:0022618
comp33010_c6_seq1.p1			
comp33010_c7_seq1.p1			
comp33012_c0_seq1.p1	sp|Q6GL44|OTUD5_XENTR_OTU_domain-containing_protein_5_OS=Xenopus_tropicalis_GN=otud5_PE=2_SV=1	1.00E-23	GO:0004843,GO:0006508,GO:0008233,GO:0008234,GO:0016787,GO:0032496,GO:0070536,GO:0071108
comp33012_c1_seq2.p1	sp|Q5ZIV1|MTMR2_CHICK_Myotubularin-related_protein_2_OS=Gallus_gallus_GN=MTMR2_PE=2_SV=1	5.00E-37	GO:0004438,GO:0004438,GO:0004725,GO:0005737,GO:0005737,GO:0005768,GO:0005829,GO:0006629,GO:0016020,GO:0016311,GO:0016787,GO:0016791,GO:0031901,GO:0035335,GO:0046856,GO:0052629
comp33012_c2_seq1.p1	sp|Q9P1Y6|PHRF1_HUMAN_PHD_and_RING_finger_domain-containing_protein_1_OS=Homo_sapiens_GN=PHRF1_PE=1_SV=3	3.00E-13	GO:0006366,GO:0006397,GO:0008270,GO:0016020,GO:0019904,GO:0046872,GO:0070063,GO:0070063
comp33012_c2_seq11.p1			
comp33012_c2_seq11.p4			
comp33012_c2_seq14.p2			
comp33012_c2_seq15.p3			
comp33012_c2_seq21.p1			
comp33012_c2_seq4.p1	sp|Q61T02|KDM5_CAEBR_Lysine-specific_demethylase_rbr-2_OS=Caenorhabditis_briggsae_GN=rbr-2_PE=3_SV=2	5.00E-12	GO:0003677,GO:0005622,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006355,GO:0008270,GO:0016491,GO:0016568,GO:0016706,GO:0046872,GO:0051213,GO:0055114,GO:0055114
comp33012_c2_seq6.p1			
comp33012_c2_seq6.p4			
comp33013_c0_seq2.p1			
comp33013_c0_seq3.p1			
comp33015_c0_seq2.p1			
comp33016_c0_seq1.p1			
comp33017_c0_seq12.p1			
comp33017_c0_seq14.p1			
comp33017_c0_seq21.p1			
comp33017_c0_seq25.p1			
comp33017_c0_seq3.p1			
comp33017_c0_seq31.p1			
comp33017_c0_seq6.p1			
comp33018_c0_seq1.p1	sp|P45482|FTSZ_NOSS1_Cell_division_protein_FtsZ_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=ftsZ_PE=3_SV=2	4.00E-106	GO:0000166,GO:0000917,GO:0003924,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006184,GO:0007049,GO:0032153,GO:0043093,GO:0043234,GO:0051258,GO:0051258,GO:0051301
comp33018_c1_seq1.p1	sp|Q8R3N6|THOC1_MOUSE_THO_complex_subunit_1_OS=Mus_musculus_GN=Thoc1_PE=1_SV=1	7.00E-14	GO:0000018,GO:0000018,GO:0000346,GO:0000347,GO:0000445,GO:0003677,GO:0003723,GO:0005515,GO:0005634,GO:0005634,GO:0005654,GO:0005737,GO:0005737,GO:0005737,GO:0006351,GO:0006355,GO:0006397,GO:0006406,GO:0006406,GO:0006810,GO:0006915,GO:0006915,GO:0006915,GO:0007165,GO:0008380,GO:0016363,GO:0016607,GO:0031297,GO:0031297,GO:0032784,GO:0032786,GO:0032786,GO:0042981,GO:0045171,GO:0046784,GO:0048297,GO:0051028,GO:2000002,GO:2000002
comp33018_c2_seq3.p1			
comp33018_c2_seq3.p3			
comp33018_c3_seq1.p1			
comp33018_c3_seq6.p1			
comp33018_c3_seq7.p1			
comp33018_c4_seq1.p1			
comp33018_c4_seq5.p1			
comp33018_c4_seq7.p1			
comp33018_c5_seq10.p1			
comp33018_c5_seq4.p2			
comp33018_c5_seq5.p1			
comp33018_c5_seq5.p4			
comp33018_c5_seq6.p3			
comp33018_c5_seq7.p1			
comp33019_c1_seq14.p1			
comp33019_c1_seq15.p1			
comp33019_c1_seq18.p1	sp|Q182E7|DNAJ_CLOD6_Chaperone_protein_DnaJ_OS=Clostridium_difficile_(strain_630)_GN=dnaJ_PE=3_SV=1	3.00E-13	GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0006260,GO:0006457,GO:0008270,GO:0009408,GO:0031072,GO:0046872,GO:0051082,GO:0051082
comp33019_c1_seq20.p1	sp|Q2W2T6|SYY_MAGSA_Tyrosine--tRNA_ligase_OS=Magnetospirillum_magneticum_(strain_AMB-1_/_ATCC_700264)_GN=tyrS_PE=3_SV=1	1.00E-168	GO:0000166,GO:0000166,GO:0003723,GO:0003723,GO:0004812,GO:0004812,GO:0004831,GO:0004831,GO:0004831,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006418,GO:0006437,GO:0006437,GO:0016874
comp33019_c1_seq21.p1	sp|O84345|DNAJ_CHLTR_Chaperone_protein_DnaJ_OS=Chlamydia_trachomatis_(strain_D/UW-3/Cx)_GN=dnaJ_PE=3_SV=1	3.00E-11	GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0006260,GO:0006457,GO:0008270,GO:0009408,GO:0031072,GO:0046872,GO:0051082,GO:0051082
comp33019_c1_seq24.p1	sp|Q9Z9E9|DNAJ_CHLPN_Chaperone_protein_DnaJ_OS=Chlamydia_pneumoniae_GN=dnaJ_PE=3_SV=1	1.00E-14	GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0006260,GO:0006457,GO:0008270,GO:0009408,GO:0031072,GO:0046872,GO:0051082,GO:0051082
comp33019_c1_seq3.p1			
comp33019_c1_seq5.p1			
comp33019_c1_seq7.p1			
comp33019_c1_seq7.p2			
comp33020_c0_seq1.p1			
comp33020_c0_seq2.p1			
comp33020_c0_seq4.p1			
comp33020_c0_seq8.p1			
comp33020_c0_seq8.p2			
comp33021_c0_seq16.p1			
comp33021_c0_seq18.p1			
comp33021_c0_seq30.p1			
comp33021_c0_seq4.p1			
comp33022_c1_seq1.p1	sp|Q9SLA1|P2C22_ARATH_Probable_protein_phosphatase_2C_22_OS=Arabidopsis_thaliana_GN=At2g25620_PE=1_SV=1	6.00E-36	GO:0003824,GO:0004721,GO:0004721,GO:0004722,GO:0005634,GO:0005829,GO:0006470,GO:0016787,GO:0046872,GO:0050688
comp33022_c1_seq2.p1			
comp33022_c1_seq4.p1	sp|Q9SLA1|P2C22_ARATH_Probable_protein_phosphatase_2C_22_OS=Arabidopsis_thaliana_GN=At2g25620_PE=1_SV=1	4.00E-36	GO:0003824,GO:0004721,GO:0004721,GO:0004722,GO:0005634,GO:0005829,GO:0006470,GO:0016787,GO:0046872,GO:0050688
comp33022_c1_seq8.p1	sp|P50526|SSP1_SCHPO_Serine/threonine-protein_kinase_ssp1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ssp1_PE=1_SV=1	3.00E-16	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004683,GO:0005516,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0006468,GO:0006995,GO:0007165,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0030042,GO:0030428,GO:0030950,GO:0042149,GO:0051285,GO:0051519,GO:0051519,GO:0070317,GO:0071963
comp33023_c0_seq1.p1	sp|Q338B9|GCN5_ORYSJ_Histone_acetyltransferase_GCN5_OS=Oryza_sativa_subsp._japonica_GN=GCN5_PE=2_SV=1	1.00E-27	GO:0000123,GO:0003677,GO:0004402,GO:0004402,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006351,GO:0006355,GO:0006355,GO:0008080,GO:0008080,GO:0009410,GO:0009416,GO:0009640,GO:0009908,GO:0010015,GO:0010388,GO:0010484,GO:0016567,GO:0016568,GO:0016568,GO:0016571,GO:0016573,GO:0016579,GO:0016740,GO:0016740,GO:0016746,GO:0016746,GO:0016746,GO:0043687,GO:0043966,GO:0043966,GO:0045893,GO:0048522
comp33023_c0_seq3.p2	sp|Q338B9|GCN5_ORYSJ_Histone_acetyltransferase_GCN5_OS=Oryza_sativa_subsp._japonica_GN=GCN5_PE=2_SV=1	1.00E-29	GO:0000123,GO:0003677,GO:0004402,GO:0004402,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006351,GO:0006355,GO:0006355,GO:0008080,GO:0008080,GO:0009410,GO:0009416,GO:0009640,GO:0009908,GO:0010015,GO:0010388,GO:0010484,GO:0016567,GO:0016568,GO:0016568,GO:0016571,GO:0016573,GO:0016579,GO:0016740,GO:0016740,GO:0016746,GO:0016746,GO:0016746,GO:0043687,GO:0043966,GO:0043966,GO:0045893,GO:0048522
comp33023_c0_seq5.p2	sp|Q338B9|GCN5_ORYSJ_Histone_acetyltransferase_GCN5_OS=Oryza_sativa_subsp._japonica_GN=GCN5_PE=2_SV=1	2.00E-23	GO:0000123,GO:0003677,GO:0004402,GO:0004402,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006351,GO:0006355,GO:0006355,GO:0008080,GO:0008080,GO:0009410,GO:0009416,GO:0009640,GO:0009908,GO:0010015,GO:0010388,GO:0010484,GO:0016567,GO:0016568,GO:0016568,GO:0016571,GO:0016573,GO:0016579,GO:0016740,GO:0016740,GO:0016746,GO:0016746,GO:0016746,GO:0043687,GO:0043966,GO:0043966,GO:0045893,GO:0048522
comp33023_c0_seq6.p1			
comp33023_c1_seq6.p1	sp|Q338B9|GCN5_ORYSJ_Histone_acetyltransferase_GCN5_OS=Oryza_sativa_subsp._japonica_GN=GCN5_PE=2_SV=1	4.00E-13	GO:0000123,GO:0003677,GO:0004402,GO:0004402,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006351,GO:0006355,GO:0006355,GO:0008080,GO:0008080,GO:0009410,GO:0009416,GO:0009640,GO:0009908,GO:0010015,GO:0010388,GO:0010484,GO:0016567,GO:0016568,GO:0016568,GO:0016571,GO:0016573,GO:0016579,GO:0016740,GO:0016740,GO:0016746,GO:0016746,GO:0016746,GO:0043687,GO:0043966,GO:0043966,GO:0045893,GO:0048522
comp33023_c1_seq7.p1	sp|Q338B9|GCN5_ORYSJ_Histone_acetyltransferase_GCN5_OS=Oryza_sativa_subsp._japonica_GN=GCN5_PE=2_SV=1	3.00E-52	GO:0000123,GO:0003677,GO:0004402,GO:0004402,GO:0005634,GO:0005634,GO:0005634,GO:0006351,GO:0006351,GO:0006355,GO:0006355,GO:0008080,GO:0008080,GO:0009410,GO:0009416,GO:0009640,GO:0009908,GO:0010015,GO:0010388,GO:0010484,GO:0016567,GO:0016568,GO:0016568,GO:0016571,GO:0016573,GO:0016579,GO:0016740,GO:0016740,GO:0016746,GO:0016746,GO:0016746,GO:0043687,GO:0043966,GO:0043966,GO:0045893,GO:0048522
comp33024_c1_seq12.p2			
comp33024_c1_seq15.p1			
comp33024_c1_seq16.p1	sp|O22040|ANP1_ARATH_Mitogen-activated_protein_kinase_kinase_kinase_ANP1_OS=Arabidopsis_thaliana_GN=ANP1_PE=1_SV=2	2.00E-56	GO:0000165,GO:0000165,GO:0000165,GO:0000166,GO:0000186,GO:0000186,GO:0000186,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004709,GO:0004709,GO:0004709,GO:0005524,GO:0005524,GO:0005737,GO:0006468,GO:0006979,GO:0007155,GO:0009908,GO:0010090,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0035556,GO:0045010,GO:0046777,GO:0048765,GO:0071555
comp33024_c1_seq19.p1	sp|O22040|ANP1_ARATH_Mitogen-activated_protein_kinase_kinase_kinase_ANP1_OS=Arabidopsis_thaliana_GN=ANP1_PE=1_SV=2	2.00E-56	GO:0000165,GO:0000165,GO:0000165,GO:0000166,GO:0000186,GO:0000186,GO:0000186,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004709,GO:0004709,GO:0004709,GO:0005524,GO:0005524,GO:0005737,GO:0006468,GO:0006979,GO:0007155,GO:0009908,GO:0010090,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0035556,GO:0045010,GO:0046777,GO:0048765,GO:0071555
comp33024_c1_seq19.p2			
comp33024_c1_seq2.p1	sp|Q3TUD9|TMM18_MOUSE_Transmembrane_protein_18_OS=Mus_musculus_GN=Tmem18_PE=2_SV=1	5.00E-19	GO:0003674,GO:0003677,GO:0005634,GO:0005737,GO:0005737,GO:0006351,GO:0016020,GO:0016021,GO:0016477,GO:0016477,GO:0031965,GO:0031965,GO:0031965
comp33024_c1_seq22.p1	sp|O22040|ANP1_ARATH_Mitogen-activated_protein_kinase_kinase_kinase_ANP1_OS=Arabidopsis_thaliana_GN=ANP1_PE=1_SV=2	2.00E-56	GO:0000165,GO:0000165,GO:0000165,GO:0000166,GO:0000186,GO:0000186,GO:0000186,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004709,GO:0004709,GO:0004709,GO:0005524,GO:0005524,GO:0005737,GO:0006468,GO:0006979,GO:0007155,GO:0009908,GO:0010090,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0035556,GO:0045010,GO:0046777,GO:0048765,GO:0071555
comp33024_c1_seq22.p2			
comp33024_c1_seq23.p1	sp|O22040|ANP1_ARATH_Mitogen-activated_protein_kinase_kinase_kinase_ANP1_OS=Arabidopsis_thaliana_GN=ANP1_PE=1_SV=2	2.00E-56	GO:0000165,GO:0000165,GO:0000165,GO:0000166,GO:0000186,GO:0000186,GO:0000186,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004709,GO:0004709,GO:0004709,GO:0005524,GO:0005524,GO:0005737,GO:0006468,GO:0006979,GO:0007155,GO:0009908,GO:0010090,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0035556,GO:0045010,GO:0046777,GO:0048765,GO:0071555
comp33024_c1_seq25.p1	sp|Q9NPB0|SMDC1_HUMAN_SAYSvFN_domain-containing_protein_1_OS=Homo_sapiens_GN=SAYSD1_PE=2_SV=1	1.00E-12	GO:0016020,GO:0016021,GO:0030659,GO:0031410,GO:0043231
comp33024_c1_seq27.p1	sp|Q00004|SRP68_CANFA_Signal_recognition_particle_68_kDa_protein_OS=Canis_familiaris_GN=SRP68_PE=1_SV=1	8.00E-42	GO:0003723,GO:0005047,GO:0005634,GO:0005730,GO:0005737,GO:0005737,GO:0005786,GO:0005786,GO:0005829,GO:0006614,GO:0008312,GO:0030529,GO:0030942,GO:0042493,GO:0044822
comp33024_c1_seq28.p1			
comp33024_c1_seq3.p1	sp|Q90512|ODO2_TAKRU_Dihydrolipoyllysine-residue_succinyltransferase_component_of_2-oxoglutarate_dehydrogenase_complex,_mitochondrial_(Fragment)_OS=Takifugu_rubripes_GN=dlst_PE=3_SV=1	3.00E-92	GO:0004149,GO:0004149,GO:0005739,GO:0005739,GO:0006099,GO:0006099,GO:0008152,GO:0016740,GO:0016746,GO:0016746,GO:0033512,GO:0045252
comp33024_c1_seq31.p1			
comp33024_c1_seq32.p1			
comp33024_c1_seq34.p1	sp|O22040|ANP1_ARATH_Mitogen-activated_protein_kinase_kinase_kinase_ANP1_OS=Arabidopsis_thaliana_GN=ANP1_PE=1_SV=2	2.00E-56	GO:0000165,GO:0000165,GO:0000165,GO:0000166,GO:0000186,GO:0000186,GO:0000186,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004709,GO:0004709,GO:0004709,GO:0005524,GO:0005524,GO:0005737,GO:0006468,GO:0006979,GO:0007155,GO:0009908,GO:0010090,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0035556,GO:0045010,GO:0046777,GO:0048765,GO:0071555
comp33024_c1_seq34.p2			
comp33024_c1_seq35.p1			
comp33024_c1_seq37.p2	sp|P11179|ODO2_BOVIN_Dihydrolipoyllysine-residue_succinyltransferase_component_of_2-oxoglutarate_dehydrogenase_complex,_mitochondrial_OS=Bos_taurus_GN=DLST_PE=1_SV=2	3.00E-76	GO:0004149,GO:0004149,GO:0005739,GO:0005739,GO:0006099,GO:0006099,GO:0008152,GO:0016740,GO:0016746,GO:0016746,GO:0033512,GO:0045252
comp33024_c1_seq5.p1			
comp33024_c1_seq6.p1			
comp33024_c2_seq1.p1			
comp33024_c4_seq2.p1	sp|P25888|RHLE_ECOLI_ATP-dependent_RNA_helicase_rhlE_OS=Escherichia_coli_(strain_K12)_GN=rhlE_PE=1_SV=3	3.00E-43	GO:0000166,GO:0000166,GO:0003676,GO:0003723,GO:0004004,GO:0004004,GO:0004004,GO:0004386,GO:0004386,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0006200,GO:0006200,GO:0006200,GO:0008026,GO:0008152,GO:0008152,GO:0008152,GO:0009408,GO:0016787,GO:0016787,GO:0042254,GO:0042254,GO:0042255,GO:0042255
comp33024_c4_seq5.p1	sp|Q5VRY0|RH39_ORYSJ_DEAD-box_ATP-dependent_RNA_helicase_39_OS=Oryza_sativa_subsp._japonica_GN=Os01g0184500_PE=2_SV=1	1.00E-98	GO:0000166,GO:0000166,GO:0003676,GO:0003676,GO:0003723,GO:0003723,GO:0004386,GO:0004386,GO:0005524,GO:0005524,GO:0005524,GO:0006200,GO:0006364,GO:0006399,GO:0008026,GO:0009507,GO:0009658,GO:0016787,GO:0016787,GO:0016887,GO:0070180,GO:0080158,GO:1901259
comp33024_c4_seq6.p1			
comp33024_c5_seq1.p1	sp|Q9W6S5|ALLC_XENLA_Allantoicase_OS=Xenopus_laevis_GN=allc_PE=2_SV=1	1.00E-95	GO:0000256,GO:0000256,GO:0004037,GO:0004037,GO:0006144,GO:0016787
comp33024_c5_seq2.p1	sp|Q9W6S5|ALLC_XENLA_Allantoicase_OS=Xenopus_laevis_GN=allc_PE=2_SV=1	6.00E-119	GO:0000256,GO:0000256,GO:0004037,GO:0004037,GO:0006144,GO:0016787
comp33025_c0_seq1.p1			
comp33025_c0_seq1.p7			
comp33025_c0_seq1.p8			
comp33025_c0_seq2.p1			
comp33027_c0_seq16.p1	sp|Q9SM23|ACBP1_ARATH_Acyl-CoA-binding_domain-containing_protein_1_OS=Arabidopsis_thaliana_GN=ACBP1_PE=1_SV=2	1.00E-11	GO:0000062,GO:0000062,GO:0005515,GO:0005576,GO:0005618,GO:0005618,GO:0005783,GO:0005789,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006629,GO:0006629,GO:0006810,GO:0006869,GO:0008289,GO:0008289,GO:0009409,GO:0009505,GO:0009737,GO:0010029,GO:0010162,GO:0010288,GO:0010288,GO:0016020,GO:0016021,GO:0032791,GO:0046872,GO:0070300,GO:1900140
comp33027_c0_seq2.p1	sp|Q2MF22|DOIAD_STRSD_2-deoxy-scyllo-inosamine_dehydrogenase_OS=Streptomyces_sp._(strain_ATCC_17920_/_DSM_40477_/_NCIB_11028)_GN=tobE_PE=3_SV=1	2.00E-13	GO:0008270,GO:0016491,GO:0016491,GO:0046872,GO:0055114,GO:0055114
comp33027_c0_seq21.p1	sp|Q2MF22|DOIAD_STRSD_2-deoxy-scyllo-inosamine_dehydrogenase_OS=Streptomyces_sp._(strain_ATCC_17920_/_DSM_40477_/_NCIB_11028)_GN=tobE_PE=3_SV=1	2.00E-17	GO:0008270,GO:0016491,GO:0016491,GO:0046872,GO:0055114,GO:0055114
comp33027_c0_seq24.p1	sp|Q02357|ANK1_MOUSE_Ankyrin-1_OS=Mus_musculus_GN=Ank1_PE=1_SV=2	1.00E-26	GO:0005634,GO:0005737,GO:0005856,GO:0005856,GO:0005886,GO:0005886,GO:0006779,GO:0006888,GO:0007165,GO:0010638,GO:0014731,GO:0014731,GO:0015672,GO:0016020,GO:0016020,GO:0016020,GO:0016529,GO:0016529,GO:0016529,GO:0030018,GO:0030507,GO:0030673,GO:0030863,GO:0031430,GO:0031672,GO:0042383,GO:0043005,GO:0045211,GO:0048821,GO:0048821,GO:0051117,GO:0055072,GO:0072661
comp33027_c0_seq30.p1			
comp33027_c0_seq30.p2	sp|Q29B63|CARM1_DROPS_Histone-arginine_methyltransferase_CARMER_OS=Drosophila_pseudoobscura_pseudoobscura_GN=Art4_PE=3_SV=1	5.00E-109	GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0006338,GO:0006351,GO:0006355,GO:0006355,GO:0006479,GO:0008168,GO:0008168,GO:0008469,GO:0016568,GO:0016740,GO:0019919,GO:0032259,GO:0034969,GO:0035241,GO:0035242,GO:0042054
comp33027_c0_seq30.p3	sp|Q8ZWC4|Y1861_PYRAE_Putative_ankyrin_repeat_protein_PAE1861_OS=Pyrobaculum_aerophilum_(strain_ATCC_51768_/_IM2_/_DSM_7523_/_JCM_9630_/_NBRC_100827)_GN=PAE1861_PE=4_SV=1	3.00E-13	
comp33027_c0_seq37.p1			
comp33027_c0_seq40.p1			
comp33027_c0_seq41.p1			
comp33027_c0_seq42.p1			
comp33027_c0_seq42.p2	sp|Q7XI75|CARM1_ORYSJ_Probable_histone-arginine_methyltransferase_CARM1_OS=Oryza_sativa_subsp._japonica_GN=CARM1_PE=2_SV=1	1.00E-96	GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0006351,GO:0006355,GO:0006355,GO:0006479,GO:0008168,GO:0008168,GO:0008469,GO:0008469,GO:0016568,GO:0016740,GO:0019919,GO:0032259,GO:0034969,GO:0034969,GO:0035242,GO:0042054
comp33027_c0_seq42.p3	sp|Q8ZWC4|Y1861_PYRAE_Putative_ankyrin_repeat_protein_PAE1861_OS=Pyrobaculum_aerophilum_(strain_ATCC_51768_/_IM2_/_DSM_7523_/_JCM_9630_/_NBRC_100827)_GN=PAE1861_PE=4_SV=1	3.00E-13	
comp33027_c0_seq44.p1			
comp33027_c0_seq53.p1			
comp33027_c0_seq58.p1			
comp33027_c0_seq58.p2			
comp33027_c0_seq59.p1			
comp33027_c0_seq7.p1			
comp33027_c0_seq7.p2			
comp33027_c0_seq7.p3	sp|Q29B63|CARM1_DROPS_Histone-arginine_methyltransferase_CARMER_OS=Drosophila_pseudoobscura_pseudoobscura_GN=Art4_PE=3_SV=1	5.00E-109	GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0006338,GO:0006351,GO:0006355,GO:0006355,GO:0006479,GO:0008168,GO:0008168,GO:0008469,GO:0016568,GO:0016740,GO:0019919,GO:0032259,GO:0034969,GO:0035241,GO:0035242,GO:0042054
comp33027_c0_seq7.p4	sp|Q8ZWC4|Y1861_PYRAE_Putative_ankyrin_repeat_protein_PAE1861_OS=Pyrobaculum_aerophilum_(strain_ATCC_51768_/_IM2_/_DSM_7523_/_JCM_9630_/_NBRC_100827)_GN=PAE1861_PE=4_SV=1	3.00E-13	
comp33028_c0_seq2.p1			
comp33028_c0_seq3.p1			
comp33028_c0_seq6.p1			
comp33028_c0_seq6.p2			
comp33029_c0_seq1.p1			
comp33029_c0_seq10.p1			
comp33029_c0_seq3.p1			
comp33029_c0_seq5.p1			
comp33030_c1_seq13.p4			
comp33030_c1_seq15.p4			
comp33030_c1_seq17.p2			
comp33030_c1_seq9.p2			
comp33031_c0_seq10.p1			
comp33031_c0_seq10.p2	sp|Q9D273|MMAB_MOUSE_Cob(I)yrinic_acid_a,c-diamide_adenosyltransferase,_mitochondrial_OS=Mus_musculus_GN=Mmab_PE=2_SV=1	4.00E-36	GO:0000166,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0008817,GO:0008817,GO:0009235,GO:0009236,GO:0016740
comp33031_c0_seq13.p1			
comp33031_c0_seq13.p2	sp|Q9D273|MMAB_MOUSE_Cob(I)yrinic_acid_a,c-diamide_adenosyltransferase,_mitochondrial_OS=Mus_musculus_GN=Mmab_PE=2_SV=1	4.00E-36	GO:0000166,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0008817,GO:0008817,GO:0009235,GO:0009236,GO:0016740
comp33031_c0_seq17.p1			
comp33031_c0_seq23.p1			
comp33031_c0_seq26.p1	sp|Q9D273|MMAB_MOUSE_Cob(I)yrinic_acid_a,c-diamide_adenosyltransferase,_mitochondrial_OS=Mus_musculus_GN=Mmab_PE=2_SV=1	6.00E-14	GO:0000166,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0008817,GO:0008817,GO:0009235,GO:0009236,GO:0016740
comp33031_c0_seq27.p1			
comp33031_c0_seq27.p2			
comp33031_c0_seq29.p1	sp|Q9D273|MMAB_MOUSE_Cob(I)yrinic_acid_a,c-diamide_adenosyltransferase,_mitochondrial_OS=Mus_musculus_GN=Mmab_PE=2_SV=1	4.00E-19	GO:0000166,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0008817,GO:0008817,GO:0009235,GO:0009236,GO:0016740
comp33031_c0_seq30.p1			
comp33031_c0_seq32.p1			
comp33031_c0_seq32.p2	sp|Q9D273|MMAB_MOUSE_Cob(I)yrinic_acid_a,c-diamide_adenosyltransferase,_mitochondrial_OS=Mus_musculus_GN=Mmab_PE=2_SV=1	1.00E-24	GO:0000166,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0008817,GO:0008817,GO:0009235,GO:0009236,GO:0016740
comp33031_c0_seq33.p1			
comp33031_c0_seq33.p2			
comp33031_c0_seq35.p1			
comp33031_c0_seq5.p1	sp|Q9D273|MMAB_MOUSE_Cob(I)yrinic_acid_a,c-diamide_adenosyltransferase,_mitochondrial_OS=Mus_musculus_GN=Mmab_PE=2_SV=1	1.00E-24	GO:0000166,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0008817,GO:0008817,GO:0009235,GO:0009236,GO:0016740
comp33031_c0_seq7.p1			
comp33031_c0_seq7.p2	sp|Q9D273|MMAB_MOUSE_Cob(I)yrinic_acid_a,c-diamide_adenosyltransferase,_mitochondrial_OS=Mus_musculus_GN=Mmab_PE=2_SV=1	1.00E-24	GO:0000166,GO:0005524,GO:0005739,GO:0005739,GO:0005739,GO:0008817,GO:0008817,GO:0009235,GO:0009236,GO:0016740
comp33032_c1_seq1.p1			
comp33032_c2_seq1.p1	sp|Q4V8U5|ANO10_DANRE_Anoctamin-10_OS=Danio_rerio_GN=ano10_PE=2_SV=1	9.00E-41	GO:0016020,GO:0016020,GO:0016021
comp33032_c2_seq13.p1			
comp33032_c2_seq15.p1	sp|Q4V8U5|ANO10_DANRE_Anoctamin-10_OS=Danio_rerio_GN=ano10_PE=2_SV=1	2.00E-36	GO:0016020,GO:0016020,GO:0016021
comp33032_c2_seq19.p1	sp|Q4V8U5|ANO10_DANRE_Anoctamin-10_OS=Danio_rerio_GN=ano10_PE=2_SV=1	1.00E-46	GO:0016020,GO:0016020,GO:0016021
comp33032_c2_seq19.p2	sp|Q09833|YAD7_SCHPO_tRNA_(uracil(54)-C(5))-methyltransferase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC4G8.07c_PE=2_SV=1	3.00E-74	GO:0005634,GO:0005739,GO:0006396,GO:0008033,GO:0008033,GO:0008168,GO:0008173,GO:0016740,GO:0030488,GO:0030696,GO:0030697,GO:0030697,GO:0032259,GO:0046872,GO:0051536,GO:0051539
comp33032_c2_seq20.p1			
comp33032_c2_seq21.p2			
comp33032_c2_seq23.p1	sp|Q4V8U5|ANO10_DANRE_Anoctamin-10_OS=Danio_rerio_GN=ano10_PE=2_SV=1	9.00E-41	GO:0016020,GO:0016020,GO:0016021
comp33032_c2_seq24.p1	sp|Q4V8U5|ANO10_DANRE_Anoctamin-10_OS=Danio_rerio_GN=ano10_PE=2_SV=1	2.00E-36	GO:0016020,GO:0016020,GO:0016021
comp33032_c2_seq24.p2	sp|Q09833|YAD7_SCHPO_tRNA_(uracil(54)-C(5))-methyltransferase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC4G8.07c_PE=2_SV=1	3.00E-74	GO:0005634,GO:0005739,GO:0006396,GO:0008033,GO:0008033,GO:0008168,GO:0008173,GO:0016740,GO:0030488,GO:0030696,GO:0030697,GO:0030697,GO:0032259,GO:0046872,GO:0051536,GO:0051539
comp33032_c2_seq3.p1			
comp33033_c0_seq2.p1			
comp33033_c0_seq4.p1	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	8.00E-16	GO:0000166,GO:0003676,GO:0004190,GO:0005524,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016787,GO:0046872
comp33033_c0_seq6.p1			
comp33034_c0_seq2.p1			
comp33034_c1_seq11.p1			
comp33034_c1_seq14.p1			
comp33034_c1_seq2.p2			
comp33034_c1_seq4.p1			
comp33034_c1_seq8.p1			
comp33034_c1_seq8.p2			
comp33035_c0_seq1.p2			
comp33035_c0_seq10.p2			
comp33035_c0_seq2.p1			
comp33035_c0_seq33.p1			
comp33035_c0_seq9.p1			
comp33036_c0_seq1.p1			
comp33036_c0_seq10.p1			
comp33036_c0_seq14.p1			
comp33036_c0_seq9.p1			
comp33037_c0_seq5.p1	sp|Q505J3|WSCD1_RAT_WSC_domain-containing_protein_1_OS=Rattus_norvegicus_GN=Wscd1_PE=2_SV=1	7.00E-11	GO:0008146,GO:0008152,GO:0016020,GO:0016020,GO:0016021
comp33037_c0_seq9.p1	sp|A2BGL3|WSCD2_DANRE_WSC_domain-containing_protein_2_OS=Danio_rerio_GN=wscd2_PE=3_SV=1	3.00E-15	GO:0008146,GO:0008152,GO:0016020,GO:0016020,GO:0016021
comp33038_c0_seq15.p1			
comp33038_c0_seq18.p1			
comp33039_c0_seq1.p1			
comp33040_c0_seq1.p1			
comp33040_c0_seq1.p2			
comp33040_c0_seq10.p1	sp|Q15751|HERC1_HUMAN_Probable_E3_ubiquitin-protein_ligase_HERC1_OS=Homo_sapiens_GN=HERC1_PE=1_SV=2	5.00E-55	GO:0004842,GO:0005085,GO:0005086,GO:0005737,GO:0005737,GO:0005794,GO:0005794,GO:0005794,GO:0005829,GO:0006810,GO:0010507,GO:0016020,GO:0016020,GO:0016567,GO:0016874,GO:0021702,GO:0031175,GO:0043547,GO:0043547,GO:0050885
comp33040_c0_seq10.p2			
comp33040_c0_seq7.p1			
comp33040_c0_seq8.p1			
comp33040_c1_seq2.p1	sp|P11632|NHP6A_YEAST_Non-histone_chromosomal_protein_6A_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=NHP6A_PE=1_SV=1	3.00E-14	GO:0001195,GO:0003677,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0006281,GO:0006298,GO:0006338,GO:0006351,GO:0006355,GO:0006974,GO:0008301,GO:0008301,GO:0031491,GO:0031491,GO:0031491,GO:0034724,GO:0051123,GO:0070898,GO:0070898,GO:0070898,GO:0070898,GO:0032301
comp33040_c1_seq5.p3			
comp33041_c0_seq3.p1	sp|Q04692|SMRCD_MOUSE_SWI/SNF-related_matrix-associated_actin-dependent_regulator_of_chromatin_subfamily_A_containing_DEAD/H_box_1_OS=Mus_musculus_GN=Smarcad1_PE=1_SV=2	7.00E-123	GO:0000018,GO:0000018,GO:0000166,GO:0000729,GO:0000729,GO:0000792,GO:0003677,GO:0003677,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0006281,GO:0006974,GO:0016568,GO:0016787,GO:0035861,GO:0035861,GO:0043044,GO:0043044,GO:0043596,GO:0051304,GO:0051304,GO:0070932,GO:0070932,GO:0070933,GO:0070933
comp33041_c0_seq5.p1			
comp33042_c0_seq1.p1			
comp33043_c0_seq4.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	3.00E-17	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305
comp33044_c0_seq1.p1	sp|Q9GTN7|TAGA_DICDI_Serine_protease/ABC_transporter_B_family_protein_tagA_OS=Dictyostelium_discoideum_GN=tagA_PE=1_SV=2	1.00E-23	GO:0000166,GO:0004252,GO:0005524,GO:0005524,GO:0006200,GO:0006508,GO:0006508,GO:0006508,GO:0006810,GO:0006810,GO:0006810,GO:0008233,GO:0008236,GO:0008236,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016787,GO:0016887,GO:0030154,GO:0042626,GO:0042626,GO:0042626,GO:0045595,GO:0045595,GO:0055085,GO:0055085
comp33044_c0_seq4.p1	sp|Q9GTN7|TAGA_DICDI_Serine_protease/ABC_transporter_B_family_protein_tagA_OS=Dictyostelium_discoideum_GN=tagA_PE=1_SV=2	6.00E-22	GO:0000166,GO:0004252,GO:0005524,GO:0005524,GO:0006200,GO:0006508,GO:0006508,GO:0006508,GO:0006810,GO:0006810,GO:0006810,GO:0008233,GO:0008236,GO:0008236,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016787,GO:0016887,GO:0030154,GO:0042626,GO:0042626,GO:0042626,GO:0045595,GO:0045595,GO:0055085,GO:0055085
comp33044_c0_seq7.p1			
comp33044_c0_seq9.p1	sp|Q9GTN7|TAGA_DICDI_Serine_protease/ABC_transporter_B_family_protein_tagA_OS=Dictyostelium_discoideum_GN=tagA_PE=1_SV=2	1.00E-23	GO:0000166,GO:0004252,GO:0005524,GO:0005524,GO:0006200,GO:0006508,GO:0006508,GO:0006508,GO:0006810,GO:0006810,GO:0006810,GO:0008233,GO:0008236,GO:0008236,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0016787,GO:0016887,GO:0030154,GO:0042626,GO:0042626,GO:0042626,GO:0045595,GO:0045595,GO:0055085,GO:0055085
comp33045_c1_seq11.p1			
comp33045_c1_seq11.p2			
comp33045_c1_seq14.p1			
comp33045_c1_seq14.p2			
comp33045_c1_seq15.p1	sp|Q8LQJ8|FTSH5_ORYSJ_ATP-dependent_zinc_metalloprotease_FTSH_5,_mitochondrial_OS=Oryza_sativa_subsp._japonica_GN=FTSH5_PE=3_SV=1	0	GO:0000166,GO:0004222,GO:0005524,GO:0005524,GO:0005739,GO:0005739,GO:0006508,GO:0006508,GO:0008233,GO:0008237,GO:0016020,GO:0016787,GO:0046872
comp33045_c1_seq9.p1	sp|Q9GR88|ERF1_POLMI_Eukaryotic_peptide_chain_release_factor_subunit_1_OS=Polyandrocarpa_misakiensis_GN=ERF1_PE=2_SV=1	0	GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006415,GO:0016149
comp33046_c0_seq2.p1	sp|P49793|NUP98_RAT_Nuclear_pore_complex_protein_Nup98-Nup96_OS=Rattus_norvegicus_GN=Nup98_PE=1_SV=2	1.00E-14	GO:0000059,GO:0000776,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005635,GO:0005643,GO:0005643,GO:0005643,GO:0005643,GO:0005643,GO:0005654,GO:0006260,GO:0006810,GO:0006810,GO:0015031,GO:0016020,GO:0017056,GO:0017056,GO:0031080,GO:0031965,GO:0031965,GO:0031965,GO:0031965,GO:0034399,GO:0034399,GO:0034399,GO:0042277,GO:0042405,GO:0042405,GO:0044615,GO:0044615,GO:0051028,GO:0051292,GO:0051292
comp33046_c0_seq4.p1	sp|P49793|NUP98_RAT_Nuclear_pore_complex_protein_Nup98-Nup96_OS=Rattus_norvegicus_GN=Nup98_PE=1_SV=2	6.00E-11	GO:0000059,GO:0000776,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005635,GO:0005643,GO:0005643,GO:0005643,GO:0005643,GO:0005643,GO:0005654,GO:0006260,GO:0006810,GO:0006810,GO:0015031,GO:0016020,GO:0017056,GO:0017056,GO:0031080,GO:0031965,GO:0031965,GO:0031965,GO:0031965,GO:0034399,GO:0034399,GO:0034399,GO:0042277,GO:0042405,GO:0042405,GO:0044615,GO:0044615,GO:0051028,GO:0051292,GO:0051292
comp33046_c0_seq4.p6			
comp33046_c1_seq2.p1	sp|Q9QZ05|E2AK4_MOUSE_Eukaryotic_translation_initiation_factor_2-alpha_kinase_4_OS=Mus_musculus_GN=Eif2ak4_PE=1_SV=2	1.00E-41	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0004694,GO:0005524,GO:0005524,GO:0006446,GO:0006446,GO:0006468,GO:0006468,GO:0009267,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0017148,GO:0022626,GO:0030968,GO:0042803,GO:0043558
comp33047_c0_seq10.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-82	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305
comp33047_c0_seq6.p1			
comp33047_c0_seq8.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	2.00E-33	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305
comp33048_c0_seq10.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	6.00E-14	GO:0005576,GO:0005618,GO:0005618,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0019867
comp33048_c0_seq13.p1			
comp33048_c0_seq2.p1			
comp33048_c0_seq20.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	2.00E-13	GO:0005576,GO:0005618,GO:0005618,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0019867
comp33048_c0_seq24.p1			
comp33048_c0_seq26.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	7.00E-16	GO:0005576,GO:0005618,GO:0005618,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0019867
comp33048_c0_seq27.p1			
comp33048_c0_seq33.p1			
comp33048_c0_seq36.p1			
comp33048_c0_seq36.p2			
comp33048_c0_seq40.p1			
comp33048_c0_seq43.p1			
comp33048_c0_seq44.p1			
comp33048_c0_seq47.p1			
comp33048_c0_seq47.p2			
comp33048_c0_seq5.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	1.00E-15	GO:0005576,GO:0005618,GO:0005618,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0019867
comp33049_c0_seq10.p1			
comp33049_c0_seq10.p2			
comp33049_c0_seq12.p1	sp|Q55E58|PATS1_DICDI_Probable_serine/threonine-protein_kinase_pats1_OS=Dictyostelium_discoideum_GN=pats1_PE=3_SV=1	6.00E-17	GO:0000166,GO:0000281,GO:0004672,GO:0004674,GO:0004674,GO:0004721,GO:0005524,GO:0005524,GO:0005525,GO:0005525,GO:0005622,GO:0006468,GO:0006470,GO:0007264,GO:0016301,GO:0016310,GO:0016311,GO:0016740,GO:0016772,GO:0016791,GO:0035176,GO:0042641
comp33049_c0_seq12.p2			
comp33049_c0_seq14.p1			
comp33049_c0_seq17.p1			
comp33049_c0_seq17.p3			
comp33049_c0_seq21.p1			
comp33049_c0_seq21.p2			
comp33049_c0_seq24.p1			
comp33049_c0_seq27.p1	sp|Q55E58|PATS1_DICDI_Probable_serine/threonine-protein_kinase_pats1_OS=Dictyostelium_discoideum_GN=pats1_PE=3_SV=1	5.00E-16	GO:0000166,GO:0000281,GO:0004672,GO:0004674,GO:0004674,GO:0004721,GO:0005524,GO:0005524,GO:0005525,GO:0005525,GO:0005622,GO:0006468,GO:0006470,GO:0007264,GO:0016301,GO:0016310,GO:0016311,GO:0016740,GO:0016772,GO:0016791,GO:0035176,GO:0042641
comp33049_c0_seq30.p1			
comp33049_c0_seq8.p1			
comp33050_c0_seq1.p1			
comp33050_c0_seq2.p1			
comp33050_c0_seq3.p1	sp|Q86C65|TOR_DICDI_Target_of_rapamycin_OS=Dictyostelium_discoideum_GN=tor_PE=1_SV=1	4.00E-16	GO:0000166,GO:0000724,GO:0004674,GO:0005515,GO:0005524,GO:0005634,GO:0006468,GO:0006935,GO:0007049,GO:0008144,GO:0016301,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0016773,GO:0031932,GO:0044351
comp33050_c0_seq4.p1			
comp33050_c0_seq8.p1			
comp33050_c0_seq8.p2			
comp33050_c0_seq9.p1			
comp33051_c0_seq10.p1			
comp33051_c0_seq13.p1			
comp33051_c0_seq3.p1	sp|O94269|UBP3_SCHPO_Probable_ubiquitin_carboxyl-terminal_hydrolase_3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ubp3_PE=2_SV=1	2.00E-18	GO:0004197,GO:0004221,GO:0004843,GO:0005515,GO:0005634,GO:0005737,GO:0005829,GO:0006508,GO:0006511,GO:0008233,GO:0008234,GO:0016579,GO:0016787,GO:0036459,GO:0043161,GO:0060628,GO:0061136
comp33051_c0_seq7.p1			
comp33053_c0_seq2.p2			
comp33053_c0_seq4.p1			
comp33054_c0_seq1.p1			
comp33054_c0_seq4.p1			
comp33055_c0_seq12.p1	sp|O66682|LY41_AQUAE_Uncharacterized_AIPM/Hcit_synthase_family_transferase_aq_356_OS=Aquifex_aeolicus_(strain_VF5)_GN=aq_356_PE=3_SV=1	8.00E-50	GO:0003824,GO:0003852,GO:0008652,GO:0009082,GO:0009097,GO:0009097,GO:0009098,GO:0016740,GO:0019752,GO:0046912
comp33055_c0_seq14.p1			
comp33055_c0_seq3.p1	sp|O66682|LY41_AQUAE_Uncharacterized_AIPM/Hcit_synthase_family_transferase_aq_356_OS=Aquifex_aeolicus_(strain_VF5)_GN=aq_356_PE=3_SV=1	2.00E-146	GO:0003824,GO:0003852,GO:0008652,GO:0009082,GO:0009097,GO:0009097,GO:0009098,GO:0016740,GO:0019752,GO:0046912
comp33056_c0_seq1.p1			
comp33056_c0_seq3.p1	sp|Q8GWB7|GUX6_ARATH_Putative_glucuronosyltransferase_PGSIP6_OS=Arabidopsis_thaliana_GN=PGSIP6_PE=2_SV=1	9.00E-26	GO:0000139,GO:0005768,GO:0005794,GO:0005794,GO:0005794,GO:0005794,GO:0005802,GO:0015020,GO:0015020,GO:0016020,GO:0016020,GO:0016021,GO:0016740,GO:0016757,GO:0016757,GO:0046513,GO:0046872,GO:1990482
comp33056_c1_seq10.p1			
comp33056_c1_seq2.p1			
comp33056_c1_seq3.p1			
comp33056_c1_seq6.p1			
comp33056_c1_seq6.p2			
comp33056_c2_seq1.p1	sp|Q8R1C6|MET22_MOUSE_Methyltransferase-like_protein_22_OS=Mus_musculus_GN=Mettl22_PE=2_SV=1	1.00E-21	GO:0003674,GO:0005575,GO:0005634,GO:0005634,GO:0008150,GO:0008168,GO:0016740,GO:0032259
comp33056_c2_seq1.p2	sp|Q9SGA6|RS191_ARATH_40S_ribosomal_protein_S19-1_OS=Arabidopsis_thaliana_GN=RPS19A_PE=2_SV=1	1.00E-50	GO:0003735,GO:0005618,GO:0005622,GO:0005829,GO:0005840,GO:0005840,GO:0006412,GO:0009506,GO:0022626,GO:0022626,GO:0022627,GO:0030529
comp33057_c1_seq14.p1			
comp33057_c1_seq3.p1			
comp33057_c1_seq30.p1			
comp33058_c0_seq2.p1			
comp33058_c1_seq1.p1			
comp33058_c2_seq9.p1	sp|B8N7E5|RSP5_ASPFN_Probable_E3_ubiquitin-protein_ligase_hulA_OS=Aspergillus_flavus_(strain_ATCC_200026_/_FGSC_A1120_/_NRRL_3357_/_JCM_12722_/_SRRC_167)_GN=hulA_PE=3_SV=1	2.00E-12	GO:0004842,GO:0005737,GO:0005737,GO:0016567,GO:0016874
comp33059_c0_seq1.p1			
comp33059_c0_seq5.p2			
comp33059_c0_seq6.p2			
comp33060_c0_seq12.p1	sp|P63251|IRK3_RAT_G_protein-activated_inward_rectifier_potassium_channel_1_OS=Rattus_norvegicus_GN=Kcnj3_PE=2_SV=1	9.00E-17	GO:0005242,GO:0005244,GO:0005515,GO:0005887,GO:0006810,GO:0006811,GO:0006813,GO:0006813,GO:0009897,GO:0009986,GO:0010107,GO:0015467,GO:0015467,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0030315,GO:0034765,GO:0034765,GO:0051602
comp33060_c0_seq2.p1	sp|P53396|ACLY_HUMAN_ATP-citrate_synthase_OS=Homo_sapiens_GN=ACLY_PE=1_SV=3	0	GO:0000166,GO:0003824,GO:0003878,GO:0003878,GO:0003878,GO:0003878,GO:0004775,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005654,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0005829,GO:0005829,GO:0005886,GO:0006101,GO:0006112,GO:0006200,GO:0006629,GO:0008152,GO:0008610,GO:0009346,GO:0015936,GO:0016020,GO:0016740,GO:0019432,GO:0031325,GO:0035338,GO:0044255,GO:0044262,GO:0044281,GO:0046872,GO:0046912,GO:0048037,GO:0070062,GO:0070062,GO:0070062
comp33060_c0_seq9.p1	sp|Q9P7W3|ACL1_SCHPO_Probable_ATP-citrate_synthase_subunit_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC1703.07_PE=1_SV=1	6.00E-58	GO:0000166,GO:0003824,GO:0003878,GO:0005524,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0006085,GO:0006099,GO:0006101,GO:0006629,GO:0006633,GO:0008152,GO:0016740,GO:0044262,GO:0046872,GO:0046912,GO:0048037,GO:0003878
comp33061_c0_seq13.p1			
comp33061_c0_seq16.p1	sp|Q9Z0H8|CLIP2_MOUSE_CAP-Gly_domain-containing_linker_protein_2_OS=Mus_musculus_GN=Clip2_PE=1_SV=2	9.00E-13	GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005874,GO:0051010,GO:0005881,GO:0035371
comp33061_c0_seq17.p1	sp|Q01397|DYNA_NEUCR_Dynactin,_150_kDa_isoform_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=ro-3_PE=3_SV=3	2.00E-12	GO:0003774,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005869,GO:0005874,GO:0008152,GO:0010970,GO:0030286,GO:0045502
comp33061_c0_seq19.p1	sp|Q9Z0H8|CLIP2_MOUSE_CAP-Gly_domain-containing_linker_protein_2_OS=Mus_musculus_GN=Clip2_PE=1_SV=2	1.00E-12	GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005874,GO:0051010,GO:0005881,GO:0035371
comp33061_c0_seq20.p1	sp|Q9Z0H8|CLIP2_MOUSE_CAP-Gly_domain-containing_linker_protein_2_OS=Mus_musculus_GN=Clip2_PE=1_SV=2	8.00E-13	GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005874,GO:0051010,GO:0005881,GO:0035371
comp33061_c0_seq23.p1	sp|Q01397|DYNA_NEUCR_Dynactin,_150_kDa_isoform_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=ro-3_PE=3_SV=3	2.00E-12	GO:0003774,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005869,GO:0005874,GO:0008152,GO:0010970,GO:0030286,GO:0045502
comp33061_c0_seq24.p1	sp|Q9Z0H8|CLIP2_MOUSE_CAP-Gly_domain-containing_linker_protein_2_OS=Mus_musculus_GN=Clip2_PE=1_SV=2	8.00E-13	GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005874,GO:0051010,GO:0005881,GO:0035371
comp33061_c0_seq4.p1	sp|Q9Z0H8|CLIP2_MOUSE_CAP-Gly_domain-containing_linker_protein_2_OS=Mus_musculus_GN=Clip2_PE=1_SV=2	1.00E-14	GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005737,GO:0005737,GO:0005856,GO:0005856,GO:0005874,GO:0051010,GO:0005881,GO:0035371
comp33061_c0_seq5.p1			
comp33061_c0_seq7.p1			
comp33062_c0_seq4.p1			
comp33063_c0_seq2.p1	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	2.00E-114	GO:0003824,GO:0004601,GO:0004601,GO:0016020,GO:0016491,GO:0046872,GO:0055114,GO:0055114
comp33063_c0_seq3.p1	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	4.00E-73	GO:0003824,GO:0004601,GO:0004601,GO:0016020,GO:0016491,GO:0046872,GO:0055114,GO:0055114
comp33063_c0_seq5.p1	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	1.00E-146	GO:0003824,GO:0004601,GO:0004601,GO:0016020,GO:0016491,GO:0046872,GO:0055114,GO:0055114
comp33065_c0_seq11.p1	sp|Q6DEY7|EPAB_XENTR_Embryonic_polyadenylate-binding_protein_OS=Xenopus_tropicalis_GN=epabp_PE=2_SV=1	4.00E-150	GO:0000166,GO:0003676,GO:0003723,GO:0003723,GO:0005737,GO:0005737,GO:0005737,GO:0006397,GO:0006412,GO:0008143,GO:0031370,GO:0043009,GO:0043621,GO:0048255,GO:0060212
comp33065_c0_seq14.p1	sp|Q6DEY7|EPAB_XENTR_Embryonic_polyadenylate-binding_protein_OS=Xenopus_tropicalis_GN=epabp_PE=2_SV=1	2.00E-148	GO:0000166,GO:0003676,GO:0003723,GO:0003723,GO:0005737,GO:0005737,GO:0005737,GO:0006397,GO:0006412,GO:0008143,GO:0031370,GO:0043009,GO:0043621,GO:0048255,GO:0060212
comp33065_c0_seq22.p1			
comp33065_c0_seq24.p1	sp|Q6DEY7|EPAB_XENTR_Embryonic_polyadenylate-binding_protein_OS=Xenopus_tropicalis_GN=epabp_PE=2_SV=1	1.00E-148	GO:0000166,GO:0003676,GO:0003723,GO:0003723,GO:0005737,GO:0005737,GO:0005737,GO:0006397,GO:0006412,GO:0008143,GO:0031370,GO:0043009,GO:0043621,GO:0048255,GO:0060212
comp33066_c0_seq11.p1			
comp33066_c0_seq19.p1	sp|Q8NEZ3|WDR19_HUMAN_WD_repeat-containing_protein_19_OS=Homo_sapiens_GN=WDR19_PE=2_SV=2	3.00E-62	GO:0000902,GO:0001701,GO:0005654,GO:0005737,GO:0005856,GO:0005929,GO:0005929,GO:0005929,GO:0005929,GO:0007224,GO:0030030,GO:0030326,GO:0030991,GO:0031076,GO:0031513,GO:0031513,GO:0031514,GO:0031514,GO:0032391,GO:0032391,GO:0035721,GO:0042384,GO:0042384,GO:0042471,GO:0042995,GO:0048701,GO:0050877,GO:0055123,GO:0060271,GO:0060830,GO:0060831,GO:0061055
comp33066_c0_seq27.p1	sp|Q8NEZ3|WDR19_HUMAN_WD_repeat-containing_protein_19_OS=Homo_sapiens_GN=WDR19_PE=2_SV=2	3.00E-62	GO:0000902,GO:0001701,GO:0005654,GO:0005737,GO:0005856,GO:0005929,GO:0005929,GO:0005929,GO:0005929,GO:0007224,GO:0030030,GO:0030326,GO:0030991,GO:0031076,GO:0031513,GO:0031513,GO:0031514,GO:0031514,GO:0032391,GO:0032391,GO:0035721,GO:0042384,GO:0042384,GO:0042471,GO:0042995,GO:0048701,GO:0050877,GO:0055123,GO:0060271,GO:0060830,GO:0060831,GO:0061055
comp33066_c0_seq29.p1	sp|Q3UGF1|WDR19_MOUSE_WD_repeat-containing_protein_19_OS=Mus_musculus_GN=Wdr19_PE=1_SV=1	3.00E-52	GO:0000902,GO:0001701,GO:0003674,GO:0005737,GO:0005856,GO:0005929,GO:0005929,GO:0005929,GO:0007224,GO:0030030,GO:0030326,GO:0030991,GO:0030991,GO:0031076,GO:0031513,GO:0031514,GO:0032391,GO:0035721,GO:0035721,GO:0035721,GO:0042384,GO:0042384,GO:0042471,GO:0042995,GO:0048701,GO:0050877,GO:0055123,GO:0060271,GO:0060271,GO:0060830,GO:0060831,GO:0060831,GO:0061055
comp33066_c0_seq34.p1			

comp33066_c0_seq8.p1	sp|Q3UGF1|WDR19_MOUSE_WD_repeat-containing_protein_19_OS=Mus_musculus_GN=Wdr19_PE=1_SV=1	3.00E-52	[illegible]	[illegible]
comp33066_c0_seq9.p1				
comp33068_c1_seq1.p2				
comp33068_c1_seq5.p1				
comp33068_c1_seq6.p1				
comp33069_c0_seq10.p1	sp|Q05754|DOPO_RAT_Dopamine_beta-hydroxylase_OS=Rattus_norvegicus_GN=Dbh_PE=1_SV=1	2.00E-18	[illegible]	[illegible]
comp33069_c0_seq12.p1	sp|Q08CS6|MOXD2_DANRE_DBH-like_monooxygenase_protein_2_homolog_OS=Danio_rerio_GN=moxd2_PE=2_SV=2	5.00E-17	[illegible]	[illegible]
comp33069_c0_seq18.p1	sp|Q08CS6|MOXD2_DANRE_DBH-like_monooxygenase_protein_2_homolog_OS=Danio_rerio_GN=moxd2_PE=2_SV=2	5.00E-17	[illegible]	[illegible]
comp33069_c0_seq3.p1	sp|Q08CS6|MOXD2_DANRE_DBH-like_monooxygenase_protein_2_homolog_OS=Danio_rerio_GN=moxd2_PE=2_SV=2	2.00E-16	[illegible]	[illegible]
comp33070_c0_seq1.p1	sp|Q9YGN6|SMUG1_XENLA_Single-strand_selective_monofunctional_uracil_DNA_glycosylase_OS=Xenopus_laevis_GN=smug1_PE=1_SV=1	6.00E-53	[illegible]	[illegible]
comp33070_c0_seq2.p1	sp|Q9YGN6|SMUG1_XENLA_Single-strand_selective_monofunctional_uracil_DNA_glycosylase_OS=Xenopus_laevis_GN=smug1_PE=1_SV=1	9.00E-51	[illegible]	[illegible]
comp33070_c1_seq1.p1				
comp33070_c1_seq4.p1				
comp33071_c0_seq6.p2	sp|Q8LFJ5|T112A_ARATH_TRM112-like_protein_At1g22270_OS=Arabidopsis_thaliana_GN=At1g22270_PE=2_SV=1	9.00E-46	[illegible]	[illegible]
comp33071_c0_seq7.p1	sp|Q54TA1|DRKC_DICDI_Probable_serine/threonine-protein_kinase_drkC_OS=Dictyostelium_discoideum_GN=drkC_PE=3_SV=1	3.00E-30	[illegible]	[illegible]
comp33071_c0_seq8.p1				
comp33071_c0_seq8.p9	sp|Q8LFJ5|T112A_ARATH_TRM112-like_protein_At1g22270_OS=Arabidopsis_thaliana_GN=At1g22270_PE=2_SV=1	5.00E-47	[illegible]	[illegible]
comp33072_c0_seq1.p1				
comp33072_c0_seq2.p1	sp|P52178|TPT2_BRAOB_Triose_phosphate/phosphate_translocator,_non-green_plastid,_chloroplastic_OS=Brassica_oleracea_var._botrytis_GN=NGTPT_PE=2_SV=1	2.00E-12	[illegible]	[illegible]
comp33072_c0_seq26.p1				
comp33072_c0_seq27.p1				
comp33072_c0_seq35.p1				
comp33072_c0_seq41.p1				
comp33072_c0_seq42.p1				
comp33072_c0_seq43.p1	sp|Q8RXN3|PPT1_ARATH_Phosphoenolpyruvate/phosphate_translocator_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=PPT1_PE=1_SV=1	2.00E-12	[illegible]	[illegible]
comp33072_c0_seq48.p1				
comp33073_c0_seq11.p1				
comp33073_c0_seq13.p1				
comp33073_c0_seq13.p3				
comp33073_c0_seq14.p1				
comp33073_c0_seq3.p1				
comp33073_c0_seq7.p1				
comp33073_c0_seq9.p1				
comp33073_c0_seq9.p3				
comp33074_c0_seq3.p1	sp|Q69ZU8|ANKR6_MOUSE_Ankyrin_repeat_domain-containing_protein_6_OS=Mus_musculus_GN=Ankrd6_PE=1_SV=2	8.00E-18	[illegible]	[illegible]
comp33074_c3_seq1.p1				
comp33074_c3_seq13.p1	sp|B9DTJ5|TIG_STRU0_Trigger_factor_OS=Streptococcus_uberis_(strain_ATCC_BAA-854_/_0140J)_GN=tig_PE=3_SV=1	1.00E-13	[illegible]	[illegible]
comp33074_c3_seq15.p1				
comp33074_c3_seq16.p1	sp|O04928|CDS1_ARATH_Phosphatidate_cytidylyltransferase_OS=Arabidopsis_thaliana_GN=CDS1_PE=2_SV=1	4.00E-54	[illegible]	[illegible]
comp33074_c3_seq17.p1	sp|P45245|Y1544_HAEIN_Uncharacterized_NAD(P)H_oxidoreductase_HI_1544_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=HI_1544_PE=3_SV=1	5.00E-13	GO:0016491,GO:0055114	[illegible]
comp33074_c3_seq21.p1	sp|Q6DDU8|FIGL1_XENLA_Fidgetin-like_protein_1_OS=Xenopus_laevis_GN=fignl1_PE=2_SV=1	7.00E-80	[illegible]	[illegible]
comp33074_c3_seq22.p1	sp|Q54XQ2|RCKA_DICDI_RGS_domain-containing_serine/threonine-protein_kinase_A_OS=Dictyostelium_discoideum_GN=rckA_PE=1_SV=1	7.00E-28	[illegible]	[illegible]
comp33074_c3_seq24.p1	sp|Q55CU8|RSC5_DICDI_Random_slug_protein_5_OS=Dictyostelium_discoideum_GN=rsc5_PE=2_SV=1	7.00E-32	GO:0003674,GO:0005575,GO:0008150	[illegible]
comp33074_c3_seq25.p1	sp|Q54XQ2|RCKA_DICDI_RGS_domain-containing_serine/threonine-protein_kinase_A_OS=Dictyostelium_discoideum_GN=rckA_PE=1_SV=1	8.00E-28	[illegible]	[illegible]
comp33074_c3_seq28.p1	sp|B9DTJ5|TIG_STRU0_Trigger_factor_OS=Streptococcus_uberis_(strain_ATCC_BAA-854_/_0140J)_GN=tig_PE=3_SV=1	5.00E-14	[illegible]	[illegible]
comp33074_c3_seq31.p1				
comp33074_c3_seq35.p1	sp|Q6DDU8|FIGL1_XENLA_Fidgetin-like_protein_1_OS=Xenopus_laevis_GN=fignl1_PE=2_SV=1	4.00E-95	[illegible]	[illegible]
comp33074_c3_seq36.p1	sp|P45245|Y1544_HAEIN_Uncharacterized_NAD(P)H_oxidoreductase_HI_1544_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=HI_1544_PE=3_SV=1	3.00E-13	GO:0016491,GO:0055114	[illegible]
comp33074_c3_seq8.p1				
comp33075_c0_seq1.p1	sp|Q02224|CENPE_HUMAN_Centromere-associated_protein_E_OS=Homo_sapiens_GN=CENPE_PE=1_SV=2	2.00E-62	[illegible]	[illegible]
comp33075_c0_seq2.p1	sp|Q6RT24|CENPE_MOUSE_Centromere-associated_protein_E_OS=Mus_musculus_GN=Cenpe_PE=1_SV=1	2.00E-76	[illegible]	[illegible]
comp33075_c0_seq2.p5				
comp33075_c0_seq3.p1	sp|Q6RT24|CENPE_MOUSE_Centromere-associated_protein_E_OS=Mus_musculus_GN=Cenpe_PE=1_SV=1	2.00E-76	[illegible]	[illegible]
comp33075_c0_seq3.p2				
comp33075_c0_seq6.p1	sp|Q54NP8|KIF4_DICDI_Kinesin-related_protein_4_OS=Dictyostelium_discoideum_GN=kif4_PE=2_SV=1	6.00E-32	[illegible]	[illegible]
comp33075_c0_seq8.p1				
comp33076_c0_seq1.p2				
comp33076_c0_seq18.p1				
comp33076_c0_seq24.p1				
comp33076_c0_seq28.p1	sp|Q6PBT5|PYRD1_DANRE_Pyridine_nucleotide-disulfide_oxidoreductase_domain-containing_protein_1_OS=Danio_rerio_GN=pyroxd1_PE=2_SV=1	1.00E-42	[illegible]	[illegible]
comp33076_c0_seq28.p2	sp|Q9FEA2|SYE_ARATH_Glutamate--tRNA_ligase,_chloroplastic/mitochondrial_OS=Arabidopsis_thaliana_GN=At5g64050_PE=1_SV=1	0	[illegible]	[illegible]
comp33076_c0_seq34.p1				
comp33076_c0_seq36.p1	sp|Q6PBT5|PYRD1_DANRE_Pyridine_nucleotide-disulfide_oxidoreductase_domain-containing_protein_1_OS=Danio_rerio_GN=pyroxd1_PE=2_SV=1	2.00E-42	[illegible]	[illegible]
comp33076_c0_seq5.p1				
comp33076_c0_seq9.p1	sp|Q6PBT5|PYRD1_DANRE_Pyridine_nucleotide-disulfide_oxidoreductase_domain-containing_protein_1_OS=Danio_rerio_GN=pyroxd1_PE=2_SV=1	4.00E-43	[illegible]	[illegible]
comp33076_c0_seq9.p2	sp|Q5REJ2|PYRD1_PONAB_Pyridine_nucleotide-disulfide_oxidoreductase_domain-containing_protein_1_OS=Pongo_abelii_GN=PYROXD1_PE=2_SV=1	2.00E-11	[illegible]	[illegible]
comp33077_c0_seq10.p2				
comp33077_c0_seq12.p1				
comp33077_c0_seq2.p1				
comp33077_c0_seq6.p1				
comp33077_c0_seq8.p1				
comp33078_c0_seq14.p1				
comp33078_c0_seq2.p1				
comp33078_c0_seq27.p2				
comp33078_c0_seq27.p4				
comp33078_c0_seq28.p1				
comp33078_c0_seq38.p1				
comp33078_c0_seq39.p2				
comp33078_c0_seq42.p1				
comp33078_c0_seq42.p2				
comp33078_c0_seq43.p1				
comp33078_c0_seq46.p1				
comp33078_c0_seq50.p1				
comp33079_c1_seq1.p1	sp|A4VRK4|TRMB_PSEU5_tRNA_(guanine-N(7)-)-methyltransferase_OS=Pseudomonas_stutzeri_(strain_A1501)_GN=trmB_PE=3_SV=1	6.00E-32	[illegible]	[illegible]
comp33079_c2_seq12.p1	sp|Q9LYZ7|UPL4_ARATH_E3_ubiquitin-protein_ligase_UPL4_OS=Arabidopsis_thaliana_GN=UPL4_PE=1_SV=1	3.00E-14	[illegible]	[illegible]
comp33079_c2_seq14.p1				
comp33079_c2_seq14.p2	sp|Q10435|YDE1_SCHPO_Probable_ubiquitin_fusion_degradation_protein_C12B10.01c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC12B10.01c_PE=2_SV=2	1.00E-29	[illegible]	[illegible]
comp33079_c2_seq15.p1				
comp33079_c2_seq16.p1	sp|Q9LYZ7|UPL4_ARATH_E3_ubiquitin-protein_ligase_UPL4_OS=Arabidopsis_thaliana_GN=UPL4_PE=1_SV=1	3.00E-14	[illegible]	[illegible]
comp33079_c2_seq20.p2				
comp33079_c2_seq5.p1	sp|Q6WWW4|UPL3_ARATH_E3_ubiquitin-protein_ligase_UPL3_OS=Arabidopsis_thaliana_GN=UPL3_PE=1_SV=1	2.00E-36	[illegible]	[illegible]
comp33080_c0_seq1.p1				
comp33080_c0_seq4.p1				
comp33080_c0_seq8.p1				
comp33081_c0_seq10.p2				
comp33081_c0_seq12.p1				
comp33081_c0_seq14.p1				
comp33081_c0_seq18.p1				
comp33081_c0_seq20.p1				
comp33081_c0_seq21.p1				
comp33082_c0_seq2.p1				
comp33082_c0_seq6.p1				
comp33082_c1_seq1.p1				
comp33083_c0_seq3.p1				
comp33084_c0_seq1.p1				
comp33084_c0_seq10.p1				
comp33084_c0_seq13.p1	sp|Q62073|M3K7_MOUSE_Mitogen-activated_protein_kinase_kinase_kinase_7_OS=Mus_musculus_GN=Map3k7_PE=1_SV=1	4.00E-25	[illegible]	[illegible]
comp33084_c0_seq14.p1				
comp33084_c0_seq20.p1				
comp33085_c0_seq1.p1				
comp33086_c0_seq11.p1				
comp33086_c0_seq12.p2				
comp33086_c0_seq5.p1				
comp33086_c0_seq7.p1				
comp33086_c0_seq8.p1				
comp33088_c0_seq11.p1				
comp33088_c0_seq13.p1				
comp33088_c0_seq14.p1				
comp33088_c0_seq21.p1				
comp33088_c0_seq23.p1	sp|Q502K3|ANR52_DANRE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_C_OS=Danio_rerio_GN=ankrd52_PE=2_SV=1	2.00E-14	GO:0003674,GO:0005575,GO:0008150	[illegible]
comp33088_c0_seq25.p1				
comp33088_c0_seq29.p1				
comp33088_c0_seq33.p1				
comp33088_c0_seq34.p1	sp|Q502K3|ANR52_DANRE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_C_OS=Danio_rerio_GN=ankrd52_PE=2_SV=1	2.00E-14	GO:0003674,GO:0005575,GO:0008150	[illegible]
comp33088_c0_seq37.p1				
comp33088_c0_seq4.p1				
comp33088_c0_seq4.p2				
comp33088_c0_seq48.p1	sp|Q502K3|ANR52_DANRE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_C_OS=Danio_rerio_GN=ankrd52_PE=2_SV=1	2.00E-14	GO:0003674,GO:0005575,GO:0008150	[illegible]
comp33088_c0_seq50.p1				
comp33088_c0_seq52.p1				
comp33088_c0_seq55.p1				
comp33088_c0_seq59.p1				
comp33088_c0_seq59.p2	sp|Q9LYC2|NPL41_ARATH_NPL4-like_protein_1_OS=Arabidopsis_thaliana_GN=At3g63000_PE=1_SV=1	1.00E-37	[illegible]	[illegible]
comp33088_c0_seq61.p1				
comp33088_c0_seq66.p1				
comp33088_c0_seq71.p1				
comp33088_c0_seq72.p1				
comp33088_c0_seq72.p2				
comp33089_c0_seq1.p1				
comp33089_c0_seq1.p2				
comp33089_c0_seq11.p1				
comp33089_c0_seq14.p1	sp|O94580|YQ77_SCHPO_Ubiquitin_and_WLM_domain-containing_protein_C1442.07c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC1442.07c_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp33089_c0_seq14.p2				
comp33089_c0_seq14.p4				
comp33089_c0_seq15.p1				
comp33089_c0_seq3.p1				
comp33089_c0_seq4.p1	sp|O94580|YQ77_SCHPO_Ubiquitin_and_WLM_domain-containing_protein_C1442.07c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC1442.07c_PE=2_SV=1	2.00E-23	[illegible]	[illegible]
comp33089_c0_seq4.p2	sp|Q54T82|Y1931_DICDI_Putative_leucine-rich_repeat-containing_protein_DDB_G0281931_OS=Dictyostelium_discoideum_GN=DDB_G0281931_PE=4_SV=1	2.00E-12	[illegible]	[illegible]
comp33089_c0_seq5.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	5.00E-15	[illegible]	[illegible]
comp33092_c0_seq17.p1				
comp33092_c0_seq18.p1	sp|Q0JKV1|AKT1_ORYSJ_Potassium_channel_AKT1_OS=Oryza_sativa_subsp._japonica_GN=AKT1_PE=2_SV=1	2.00E-34	[illegible]	[illegible]
comp33093_c0_seq7.p2				
comp33093_c0_seq8.p1				
comp33093_c0_seq9.p1				
comp33096_c0_seq19.p1				
comp33096_c0_seq8.p1				
comp33097_c0_seq11.p1				
comp33097_c0_seq11.p3				
comp33097_c0_seq11.p8				
comp33097_c0_seq12.p1				
comp33097_c0_seq12.p2				
comp33097_c0_seq12.p7				
comp33097_c0_seq14.p1				
comp33097_c0_seq14.p2				
comp33097_c0_seq17.p1				
comp33097_c0_seq2.p2				
comp33097_c0_seq2.p7				
comp33097_c0_seq2.p8				
comp33098_c0_seq1.p1				
comp33098_c1_seq1.p1				
comp33098_c1_seq11.p1				
comp33098_c1_seq15.p1				
comp33098_c1_seq18.p1				
comp33098_c1_seq19.p1				
comp33098_c1_seq2.p1				
comp33098_c1_seq22.p1				
comp33098_c1_seq23.p1				
comp33098_c1_seq25.p1				
comp33098_c1_seq3.p1				
comp33099_c0_seq1.p1	sp|Q10126|YSM6_CAEEL_Putative_uncharacterized_transposon-derived_protein_F52C9.6_OS=Caenorhabditis_elegans_GN=F52C9.6_PE=5_SV=1	4.00E-12		
comp33099_c0_seq12.p1				
comp33099_c0_seq12.p3				
comp33099_c0_seq13.p1	sp|Q9BHM6|OCDH_PECMA_Octopine_dehydrogenase_OS=Pecten_maximus_GN=odh1_PE=1_SV=1	7.00E-48	[illegible]	[illegible]
comp33099_c0_seq2.p1				
comp33099_c0_seq4.p1				
comp33099_c0_seq7.p1				
comp33100_c0_seq1.p1				
comp33101_c0_seq10.p2				
comp33101_c0_seq12.p1	sp|Q5ZKI0|KCC2D_CHICK_Calcium/calmodulin-dependent_protein_kinase_type_II_delta_chain_OS=Gallus_gallus_GN=CAMK2D_PE=2_SV=1	2.00E-42	[illegible]	[illegible]
comp33101_c0_seq4.p1				
comp33101_c0_seq6.p1	sp|Q8IBS5|CDPK4_PLAF7_Calcium-dependent_protein_kinase_4_OS=Plasmodium_falciparum_(isolate_3D7)_GN=CPK4_PE=1_SV=3	6.00E-14	[illegible]	[illegible]
comp33102_c0_seq2.p1				
comp33102_c3_seq1.p1	sp|P87172|GPI3_SCHPO_Phosphatidylinositol_N-acetylglucosaminyltransferase_gpi3_subunit_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=gpi3_PE=2_SV=1	5.00E-147	[illegible]	[illegible]
comp33102_c3_seq10.p1	sp|Q64323|PIGA_MOUSE_N-acetylglucosaminyl-phosphatidylinositol_biosynthetic_protein_OS=Mus_musculus_GN=Piga_PE=2_SV=1	8.00E-134	[illegible]	[illegible]
comp33102_c3_seq2.p1	sp|P87172|GPI3_SCHPO_Phosphatidylinositol_N-acetylglucosaminyltransferase_gpi3_subunit_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=gpi3_PE=2_SV=1	4.00E-147	[illegible]	[illegible]
comp33102_c3_seq5.p1	sp|Q4ZIN3|MBRL_HUMAN_Membralin_OS=Homo_sapiens_GN=C19orf6_PE=1_SV=1	1.00E-22	[illegible]	[illegible]
comp33102_c3_seq5.p2	sp|A0A8M2|L14AA_XENLA_Protein_LSM14_homolog_A-A_OS=Xenopus_laevis_GN=lsm14a-a_PE=1_SV=1	8.00E-13	[illegible]	[illegible]
comp33102_c3_seq6.p1	sp|Q64323|PIGA_MOUSE_N-acetylglucosaminyl-phosphatidylinositol_biosynthetic_protein_OS=Mus_musculus_GN=Piga_PE=2_SV=1	6.00E-134	[illegible]	[illegible]
comp33102_c3_seq8.p1	sp|Q8VC85|LSM1_MOUSE_U6_snRNA-associated_Sm-like_protein_LSm1_OS=Mus_musculus_GN=Lsm1_PE=2_SV=1	2.00E-19	[illegible]	[illegible]
comp33103_c0_seq5.p1				
comp33103_c1_seq3.p1				
comp33103_c1_seq7.p1				
comp33104_c0_seq1.p1	sp|Q9URX8|NG06_SCHPO_Probable_nucleoporin_C890.06_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC890.06_PE=2_SV=3	5.00E-23	[illegible]	[illegible]
comp33104_c0_seq3.p1	sp|Q9URX8|NG06_SCHPO_Probable_nucleoporin_C890.06_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC890.06_PE=2_SV=3	4.00E-17	[illegible]	[illegible]
comp33104_c0_seq5.p1	sp|Q9URX8|NG06_SCHPO_Probable_nucleoporin_C890.06_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC890.06_PE=2_SV=3	6.00E-25	[illegible]	[illegible]
comp33104_c0_seq6.p1	sp|O75694|NU155_HUMAN_Nuclear_pore_complex_protein_Nup155_OS=Homo_sapiens_GN=NUP155_PE=1_SV=1	3.00E-25	[illegible]	[illegible]
comp33105_c1_seq10.p1	sp|Q24799|MYPH_ECHGR_Myophilin_OS=Echinococcus_granulosus_PE=2_SV=1	5.00E-15		
comp33105_c1_seq11.p2	sp|Q9P2K5|MYEF2_HUMAN_Myelin_expression_factor_2_OS=Homo_sapiens_GN=MYEF2_PE=1_SV=3	3.00E-13	[illegible]	[illegible]
comp33105_c1_seq13.p1				
comp33105_c1_seq16.p1				
comp33105_c1_seq2.p1				
comp33105_c1_seq20.p1	sp|Q24799|MYPH_ECHGR_Myophilin_OS=Echinococcus_granulosus_PE=2_SV=1	5.00E-15		
comp33105_c1_seq21.p1	sp|O13853|ITS3_SCHPO_Phosphatidylinositol_4-phosphate_5-kinase_its3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=its3_PE=1_SV=3	2.00E-52	[illegible]	[illegible]
comp33105_c1_seq24.p1	sp|Q8H0W1|PLSP1_ARATH_Chloroplast_processing_peptidase_OS=Arabidopsis_thaliana_GN=PLSP1_PE=2_SV=2	3.00E-11	[illegible]	[illegible]
comp33105_c1_seq7.p1	sp|O13853|ITS3_SCHPO_Phosphatidylinositol_4-phosphate_5-kinase_its3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=its3_PE=1_SV=3	2.00E-52	[illegible]	[illegible]
comp33105_c1_seq8.p1	sp|Q51876|LEP_PHOLA_Signal_peptidase_I_OS=Phormidium_laminosum_GN=lepB_PE=3_SV=1	2.00E-47	[illegible]	[illegible]
comp33105_c1_seq9.p1				
comp33106_c0_seq12.p1				
comp33106_c0_seq2.p1				
comp33106_c0_seq2.p2				
comp33106_c0_seq2.p4				
comp33106_c0_seq5.p1				
comp33106_c0_seq5.p2				
comp33107_c2_seq1.p1	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	8.00E-24	[illegible]	[illegible]
comp33107_c2_seq1.p2				
comp33107_c2_seq14.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	6.00E-19	[illegible]	[illegible]
comp33107_c2_seq3.p1	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	4.00E-27	[illegible]	[illegible]
comp33107_c2_seq5.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	3.00E-13	[illegible]	[illegible]
comp33108_c0_seq1.p1				
comp33109_c0_seq1.p1	sp|Q88NC9|ALGG_PSEPK_Poly(beta-D-mannuronate)_C5_epimerase_OS=Pseudomonas_putida_(strain_KT2440)_GN=algG_PE=3_SV=2	2.00E-16	[illegible]	[illegible]
comp33109_c0_seq3.p1				
comp33109_c0_seq7.p1				
comp33110_c1_seq4.p1				
comp33110_c1_seq5.p1				
comp33112_c0_seq1.p1	sp|Q0IIF7|UBP14_BOVIN_Ubiquitin_carboxyl-terminal_hydrolase_14_OS=Bos_taurus_GN=USP14_PE=2_SV=3	2.00E-69	[illegible]	[illegible]
comp33112_c1_seq2.p1	sp|P23506|PIMT_MOUSE_Protein-L-isoaspartate(D-aspartate)_O-methyltransferase_OS=Mus_musculus_GN=Pcmt1_PE=1_SV=3	3.00E-70	[illegible]	[illegible]
comp33112_c3_seq17.p1	sp|P79003|RER1_SACPS_Protein_RER1_OS=Saccharomyces_pastorianus_GN=RER1_PE=3_SV=1	1.00E-15	[illegible]	[illegible]
comp33113_c1_seq10.p2				
comp33113_c1_seq5.p1				
comp33113_c1_seq9.p1				
comp33114_c0_seq13.p1				
comp33114_c0_seq16.p1				
comp33114_c0_seq17.p2				
comp33114_c0_seq17.p6				
comp33115_c0_seq11.p1				
comp33115_c0_seq3.p1				
comp33115_c0_seq3.p2				
comp33115_c0_seq9.p1				
comp33116_c0_seq3.p1				
comp33116_c0_seq4.p1				
comp33117_c0_seq6.p1	sp|Q54SY2|NVL_DICDI_Putative_ribosome_biogenesis_ATPase_nvl_OS=Dictyostelium_discoideum_GN=nvl_PE=3_SV=1	4.00E-102	[illegible]	[illegible]
comp33117_c0_seq9.p1				
comp33118_c0_seq1.p1				
comp33118_c0_seq5.p3				
comp33119_c0_seq12.p1				
comp33119_c0_seq15.p3				
comp33119_c0_seq8.p1				
comp33119_c0_seq9.p3				
comp33120_c1_seq1.p1				
comp33120_c1_seq3.p2				
comp33123_c0_seq14.p2				
comp33123_c0_seq14.p4				
comp33123_c0_seq3.p1				
comp33123_c0_seq4.p1				
comp33123_c0_seq5.p1				
comp33123_c0_seq7.p1	sp|Q9Z2G9|HTAI2_MOUSE_Oxidoreductase_HTATIP2_OS=Mus_musculus_GN=Htatip2_PE=1_SV=2	2.00E-14	[illegible]	[illegible]
comp33124_c0_seq1.p1				
comp33124_c0_seq10.p1	sp|Q12168|ENG2_YEAST_Endo-1,3(4)-beta-glucanase_2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=ACF2_PE=1_SV=1	2.00E-47	[illegible]	[illegible]
comp33124_c0_seq6.p1	sp|Q9UT45|ENG1_SCHPO_Endo-1,3(4)-beta-glucanase_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=eng1_PE=2_SV=1	2.00E-74	[illegible]	[illegible]
comp33125_c0_seq21.p1				
comp33125_c0_seq5.p1				
comp33126_c0_seq1.p1				
comp33126_c0_seq11.p1				
comp33126_c0_seq15.p1				
comp33126_c0_seq4.p1				
comp33126_c0_seq7.p1				
comp33127_c0_seq1.p1				
comp33127_c0_seq5.p1				
comp33127_c0_seq6.p1				
comp33127_c0_seq6.p2				
comp33127_c0_seq6.p3				
comp33127_c0_seq8.p1				
comp33128_c0_seq16.p1				
comp33130_c0_seq11.p1	sp|O02751|CFDP2_BOVIN_Craniofacial_development_protein_2_OS=Bos_taurus_GN=CFDP2_PE=1_SV=2	2.00E-15	[illegible]	[illegible]
comp33130_c0_seq4.p1	sp|O02751|CFDP2_BOVIN_Craniofacial_development_protein_2_OS=Bos_taurus_GN=CFDP2_PE=1_SV=2	1.00E-20	[illegible]	[illegible]
comp33130_c0_seq6.p1				
comp33130_c0_seq7.p1	sp|Q05086|UBE3A_HUMAN_Ubiquitin-protein_ligase_E3A_OS=Homo_sapiens_GN=UBE3A_PE=1_SV=4	3.00E-78	[illegible]	[illegible]
comp33131_c0_seq11.p1	sp|Q940M4|OCT7_ARATH_Organic_cation/carnitine_transporter_7_OS=Arabidopsis_thaliana_GN=OCT7_PE=2_SV=1	5.00E-36	[illegible]	[illegible]
comp33131_c0_seq13.p1	sp|D3ZJP6|MYO10_RAT_Unconventional_myosin-X_OS=Rattus_norvegicus_GN=Myo10_PE=1_SV=1	6.00E-25	[illegible]	[illegible]
comp33131_c0_seq14.p1	sp|Q940M4|OCT7_ARATH_Organic_cation/carnitine_transporter_7_OS=Arabidopsis_thaliana_GN=OCT7_PE=2_SV=1	2.00E-36	[illegible]	[illegible]
comp33131_c0_seq16.p1				
comp33131_c0_seq7.p1	sp|P0DH79|Y5064_ARATH_CBS_domain-containing_protein_CBSCBSPB5_OS=Arabidopsis_thaliana_GN=CBSCBSPB5_PE=2_SV=1	4.00E-48	[illegible]	[illegible]
comp33132_c0_seq3.p1				
comp33132_c0_seq5.p1				
comp33132_c0_seq7.p1				
comp33132_c0_seq9.p1				
comp33133_c0_seq10.p1	sp|Q5UPD5|YL059_MIMIV_Putative_ankyrin_repeat_protein_L59_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L59_PE=4_SV=1	5.00E-13		
comp33133_c0_seq17.p1	sp|Q9UUK2|GCN5_SCHPO_Histone_acetyltransferase_gcn5_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=gcn5_PE=1_SV=1	8.00E-13	[illegible]	[illegible]
comp33133_c0_seq4.p1	sp|Q9ZUA5|VIT1_ARATH_Vacuolar_iron_transporter_1_OS=Arabidopsis_thaliana_GN=VIT1_PE=2_SV=1	1.00E-22	[illegible]	[illegible]
comp33133_c0_seq7.p1	sp|Q9UUK2|GCN5_SCHPO_Histone_acetyltransferase_gcn5_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=gcn5_PE=1_SV=1	8.00E-13	[illegible]	[illegible]
comp33133_c1_seq3.p1				
comp33133_c1_seq5.p1				
comp33133_c3_seq1.p1				
comp33133_c7_seq1.p1				
comp33133_c8_seq1.p1	sp|Q54CS7|JMJCE_DICDI_JmjC_domain-containing_protein_E_OS=Dictyostelium_discoideum_GN=jcdE_PE=4_SV=2	2.00E-63	GO:0003674,GO:0005575,GO:0008150	[illegible]
comp33134_c0_seq10.p1				
comp33134_c0_seq10.p2				
comp33134_c0_seq19.p1				
comp33134_c0_seq2.p1				
comp33134_c0_seq4.p1				
comp33134_c0_seq4.p3				
comp33134_c0_seq5.p1				
comp33134_c0_seq6.p1				
comp33134_c0_seq6.p3				
comp33134_c0_seq8.p1				
comp33134_c0_seq9.p1				
comp33136_c0_seq3.p1				
comp33136_c0_seq6.p1	sp|Q8L7M4|SDN5_ARATH_Small_RNA_degrading_nuclease_5_OS=Arabidopsis_thaliana_GN=SDN5_PE=2_SV=2	2.00E-44	[illegible]	[illegible]
comp33136_c0_seq7.p1	sp|Q8L7M4|SDN5_ARATH_Small_RNA_degrading_nuclease_5_OS=Arabidopsis_thaliana_GN=SDN5_PE=2_SV=2	2.00E-44	[illegible]	[illegible]
comp33137_c0_seq13.p1	sp|Q2A121|FTO_RAT_Alpha-ketoglutarate-dependent_dioxygenase_FTO_OS=Rattus_norvegicus_GN=Fto_PE=2_SV=1	6.00E-40	[illegible]	[illegible]
comp33137_c0_seq19.p1				
comp33137_c0_seq7.p2				
comp33138_c0_seq13.p1	sp|B2GU58|KIF11_XENTR_Kinesin-like_protein_KIF11_OS=Xenopus_tropicalis_GN=kif11_PE=2_SV=1	2.00E-70	[illegible]	[illegible]
comp33138_c0_seq15.p1				
comp33138_c0_seq18.p3	sp|O96952|THIO_GEOCY_Thioredoxin_OS=Geodia_cydonium_GN=THIO_PE=3_SV=1	2.00E-26	[illegible]	[illegible]
comp33138_c0_seq2.p1				
comp33138_c0_seq21.p1				
comp33138_c0_seq23.p1				
comp33138_c0_seq5.p1	sp|B1ZJ42|APAG_METPB_Protein_ApaG_OS=Methylobacterium_populi_(strain_ATCC_BAA-705_/_NCIMB_13946_/_BJ001)_GN=apaG_PE=3_SV=1	6.00E-12		
comp33138_c0_seq8.p1				
comp33139_c0_seq10.p1	sp|Q54D08|LST8_DICDI_Protein_LST8_homolog_OS=Dictyostelium_discoideum_GN=lst8_PE=1_SV=1	1.00E-25	[illegible]	[illegible]
comp33139_c0_seq12.p1				
comp33139_c0_seq14.p1	sp|Q7ZYC4|ACBG2_XENLA_Long-chain-fatty-acid--CoA_ligase_ACSBG2_OS=Xenopus_laevis_GN=acsbg2_PE=2_SV=1	0	[illegible]	[illegible]
comp33139_c0_seq21.p1				
comp33139_c0_seq24.p1				
comp33139_c0_seq25.p1				
comp33139_c0_seq26.p1	sp|Q54D08|LST8_DICDI_Protein_LST8_homolog_OS=Dictyostelium_discoideum_GN=lst8_PE=1_SV=1	2.00E-104	[illegible]	[illegible]
comp33139_c0_seq27.p1				
comp33139_c0_seq3.p1				
comp33139_c0_seq30.p1	sp|Q54D08|LST8_DICDI_Protein_LST8_homolog_OS=Dictyostelium_discoideum_GN=lst8_PE=1_SV=1	5.00E-111	[illegible]	[illegible]
comp33139_c0_seq33.p1				
comp33139_c0_seq6.p1				
comp33139_c0_seq7.p1				
comp33139_c0_seq9.p1	sp|Q7ZYC4|ACBG2_XENLA_Long-chain-fatty-acid--CoA_ligase_ACSBG2_OS=Xenopus_laevis_GN=acsbg2_PE=2_SV=1	1.00E-176	[illegible]	[illegible]
comp33140_c2_seq17.p1				
comp33140_c2_seq17.p2				
comp33140_c2_seq25.p1				
comp33140_c2_seq3.p1				
comp33140_c2_seq6.p1				
comp33140_c2_seq7.p1				
comp33140_c2_seq8.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	7.00E-17	[illegible]	[illegible]
comp33141_c0_seq11.p1				

comp33141_c0_seq13.p3		
comp33142_c0_seq1.p1	sp|P53273|YG35_YEAST_Uncharacterized_vacuolar_membrane_protein_YGR125W_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YGR125W_PE=1_SV=1	9.00E-21
comp33142_c0_seq5.p1	sp|P53273|YG35_YEAST_Uncharacterized_vacuolar_membrane_protein_YGR125W_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YGR125W_PE=1_SV=1	8.00E-21
comp33143_c0_seq2.p1		
comp33143_c0_seq4.p1		
comp33143_c0_seq5.p1		
comp33143_c0_seq7.p1	sp|Q9WUU9|MCM3A_MOUSE_80_kDa_MCM3-associated_protein_OS=Mus_musculus_GN=Mcm3ap_PE=2_SV=2	8.00E-15
comp33143_c0_seq9.p1		
comp33143_c2_seq1.p1	sp|Q9NUJ7|PLCX1_HUMAN_PI-PLC_X_domain-containing_protein_1_OS=Homo_sapiens_GN=PLCXD1_PE=2_SV=1	3.00E-12
comp33144_c0_seq10.p1	sp|Q9P7J8|GAD8_SCHPO_Serine/threonine-protein_kinase_gad8_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=gad8_PE=1_SV=1	3.00E-59
comp33144_c0_seq10.p2		
comp33144_c0_seq15.p1	sp|Q9P7J8|GAD8_SCHPO_Serine/threonine-protein_kinase_gad8_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=gad8_PE=1_SV=1	3.00E-59
comp33144_c0_seq15.p2		
comp33144_c0_seq16.p1	sp|P54644|KRAC_DICDI_RAC_family_serine/threonine-protein_kinase_homolog_OS=Dictyostelium_discoideum_GN=pkbA_PE=1_SV=1	2.00E-32
comp33144_c0_seq7.p1		
comp33144_c2_seq1.p1	sp|P38529|HSF1_CHICK_Heat_shock_factor_protein_1_OS=Gallus_gallus_GN=HSF1_PE=2_SV=1	4.00E-13
comp33145_c0_seq10.p1		
comp33145_c0_seq3.p2		
comp33145_c0_seq5.p1		
comp33145_c1_seq2.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	2.00E-29
comp33145_c1_seq3.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	6.00E-19
comp33147_c0_seq4.p1		
comp33147_c0_seq5.p1		
comp33147_c0_seq6.p1		
comp33147_c0_seq7.p1		
comp33148_c0_seq8.p1		
comp33148_c0_seq9.p1	sp|P0CQ67|RAD5_CRYNB_DNA_repair_protein_RAD5_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_B-3501A)_GN=RAD5_PE=3_SV=1	6.00E-14
comp33149_c0_seq14.p1		
comp33149_c0_seq16.p1		
comp33149_c0_seq19.p1		
comp33149_c0_seq19.p2		
comp33149_c0_seq19.p3		
comp33149_c0_seq24.p1		
comp33149_c0_seq26.p1		
comp33149_c0_seq7.p1	sp|A2BGR3|ERC6L_DANRE_DNA_excision_repair_protein_ERCC-6-like_OS=Danio_rerio_GN=ercc6l_PE=1_SV=1	4.00E-81
comp33151_c0_seq1.p1	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	0
comp33151_c0_seq10.p1	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	9.00E-82
comp33151_c0_seq4.p1	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	1.00E-127
comp33151_c0_seq7.p1	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	2.00E-180
comp33151_c0_seq7.p2	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	1.00E-127
comp33152_c1_seq1.p1		
comp33152_c1_seq1.p2		
comp33152_c1_seq11.p1		
comp33152_c1_seq13.p1	sp|O74343|YH2X_SCHPO_Putative_pseudouridine_synthase_C1A4.09_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC1A4.09_PE=2_SV=1	7.00E-37
comp33152_c1_seq20.p1	sp|P72740|DLDH_SYNY3_Dihydrolipoyl_dehydrogenase_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=lpdA_PE=1_SV=3	2.00E-175
comp33152_c1_seq21.p2		
comp33152_c1_seq4.p1	sp|P72740|DLDH_SYNY3_Dihydrolipoyl_dehydrogenase_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=lpdA_PE=1_SV=3	4.00E-66
comp33152_c1_seq43.p1		
comp33152_c1_seq43.p2		
comp33152_c1_seq46.p1		
comp33152_c1_seq8.p2		
comp33153_c0_seq10.p1		
comp33153_c0_seq10.p2	sp|O22494|GSHB_SOLLC_Glutathione_synthetase,_chloroplastic_OS=Solanum_lycopersicum_GN=GSH2_PE=2_SV=1	1.00E-105
comp33153_c0_seq2.p1		
comp33153_c0_seq2.p2	sp|O22494|GSHB_SOLLC_Glutathione_synthetase,_chloroplastic_OS=Solanum_lycopersicum_GN=GSH2_PE=2_SV=1	2.00E-84
comp33154_c0_seq1.p1		
comp33154_c1_seq12.p1	sp|P54676|PI3K4_DICDI_Phosphatidylinositol_3-kinase_VPS34-like_OS=Dictyostelium_discoideum_GN=pikE_PE=3_SV=2	7.00E-76
comp33154_c1_seq16.p1		
comp33154_c1_seq16.p3		
comp33155_c0_seq10.p7		
comp33155_c0_seq15.p1		
comp33155_c0_seq6.p7		
comp33156_c0_seq10.p1		
comp33156_c0_seq2.p1		
comp33156_c0_seq24.p1		
comp33156_c0_seq25.p1		
comp33156_c0_seq29.p2		
comp33156_c0_seq35.p1		
comp33157_c1_seq20.p1		
comp33157_c1_seq22.p1	sp|Q2QRX6|DRTS_ORYSJ_Putative_bifunctional_dihydrofolate_reductase-thymidylate_synthase_OS=Oryza_sativa_subsp._japonica_GN=Os12g0446900_PE=3_SV=2	8.00E-143
comp33157_c1_seq25.p1		
comp33157_c1_seq27.p1	sp|O35509|RB11B_RAT_Ras-related_protein_Rab-11B_OS=Rattus_norvegicus_GN=Rab11b_PE=2_SV=4	3.00E-102
comp33157_c1_seq9.p1		
comp33157_c2_seq1.p1		
comp33158_c0_seq4.p1	sp|Q5U3S1|KATL1_DANRE_Katanin_p60_ATPase-containing_subunit_A-like_1_OS=Danio_rerio_GN=katnal1_PE=2_SV=1	3.00E-111
comp33158_c0_seq8.p1		
comp33159_c0_seq1.p1		
comp33159_c0_seq1.p2		
comp33159_c0_seq1.p3		
comp33159_c0_seq10.p1	sp|Q9LIE5|FHY3_ARATH_Protein_FAR-RED_ELONGATED_HYPOCOTYL_3_OS=Arabidopsis_thaliana_GN=FHY3_PE=1_SV=1	4.00E-15
comp33159_c0_seq10.p3		
comp33159_c0_seq10.p4		
comp33159_c0_seq16.p1		
comp33159_c0_seq17.p1		
comp33159_c0_seq4.p1		
comp33159_c0_seq4.p2		
comp33159_c0_seq5.p1		
comp33159_c0_seq8.p1	sp|Q9LIE5|FHY3_ARATH_Protein_FAR-RED_ELONGATED_HYPOCOTYL_3_OS=Arabidopsis_thaliana_GN=FHY3_PE=1_SV=1	5.00E-15
comp33159_c0_seq8.p3		
comp33160_c0_seq2.p2		
comp33160_c0_seq4.p2	sp|P10394|POL4_DROME_Retrovirus-related_Pol_polyprotein_from_transposon_412_OS=Drosophila_melanogaster_GN=POL_PE=4_SV=1	7.00E-11
comp33161_c0_seq1.p1	sp|Q6VN19|RBP10_MOUSE_Ran-binding_protein_10_OS=Mus_musculus_GN=Ranbp10_PE=1_SV=2	1.00E-16
comp33161_c2_seq1.p1	sp|P26988|G3P_PHYIN_Glyceraldehyde-3-phosphate_dehydrogenase_OS=Phytophthora_infestans_GN=GPDA_PE=3_SV=1	5.00E-168
comp33161_c3_seq16.p1		
comp33161_c3_seq17.p1		
comp33161_c3_seq5.p1		
comp33162_c0_seq12.p1		
comp33162_c0_seq8.p1		
comp33163_c0_seq8.p1		
comp33164_c0_seq11.p1		
comp33164_c0_seq19.p2		
comp33164_c0_seq2.p1		
comp33164_c0_seq35.p1		
comp33165_c0_seq1.p1		
comp33165_c0_seq2.p3		
comp33165_c0_seq3.p1		
comp33165_c0_seq6.p1		
comp33166_c0_seq12.p1		
comp33166_c0_seq15.p1	sp|Q0D576|HPT2_ORYSJ_Probable_homogentisate_phytyltransferase_2,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=HPT2_PE=3_SV=2	4.00E-85
comp33167_c0_seq15.p1		
comp33167_c0_seq16.p2		
comp33167_c0_seq3.p1		
comp33167_c0_seq8.p2		
comp33167_c1_seq1.p1		
comp33167_c1_seq3.p1		
comp33167_c1_seq4.p1		
comp33168_c0_seq10.p1		
comp33168_c0_seq2.p1		
comp33169_c0_seq14.p1		
comp33169_c0_seq17.p1		
comp33169_c0_seq19.p1		
comp33169_c0_seq20.p1		
comp33169_c0_seq23.p1		
comp33169_c0_seq9.p1		
comp33170_c0_seq1.p1	sp|Q9Y2Q3|GSTK1_HUMAN_Glutathione_S-transferase_kappa_1_OS=Homo_sapiens_GN=GSTK1_PE=1_SV=3	4.00E-60
comp33170_c0_seq2.p1	sp|Q9Y2Q3|GSTK1_HUMAN_Glutathione_S-transferase_kappa_1_OS=Homo_sapiens_GN=GSTK1_PE=1_SV=3	1.00E-44
comp33171_c0_seq17.p1		
comp33171_c0_seq18.p1		
comp33171_c0_seq3.p1		
comp33171_c0_seq8.p1		
comp33172_c0_seq3.p1	sp|Q621J7|ZYG1_CAEBR_Probable_serine/threonine-protein_kinase_zyg-1_OS=Caenorhabditis_briggsae_GN=zyg-1_PE=3_SV=1	4.00E-13
comp33172_c0_seq4.p1		
comp33172_c0_seq5.p1		
comp33172_c0_seq6.p1		
comp33172_c0_seq7.p1	sp|Q621J7|ZYG1_CAEBR_Probable_serine/threonine-protein_kinase_zyg-1_OS=Caenorhabditis_briggsae_GN=zyg-1_PE=3_SV=1	4.00E-12
comp33174_c1_seq13.p1		
comp33174_c1_seq18.p1		
comp33174_c1_seq30.p1		
comp33174_c1_seq4.p1		
comp33174_c1_seq6.p1		
comp33174_c1_seq9.p1		
comp33175_c0_seq10.p1		
comp33175_c0_seq11.p1	sp|Q14204|DYHC1_HUMAN_Cytoplasmic_dynein_1_heavy_chain_1_OS=Homo_sapiens_GN=DYNC1H1_PE=1_SV=5	0
comp33175_c0_seq11.p2		
comp33175_c0_seq2.p1		
comp33175_c0_seq4.p1		
comp33175_c0_seq5.p1		
comp33175_c0_seq6.p2		
comp33176_c0_seq10.p1		
comp33176_c0_seq12.p1		
comp33176_c0_seq2.p1		
comp33176_c0_seq5.p1		
comp33176_c0_seq7.p1		
comp33177_c0_seq2.p1		
comp33177_c1_seq1.p1		
comp33177_c1_seq12.p1		
comp33178_c2_seq15.p1	sp|Q3EAQ5|PTR36_ARATH_Probable_peptide/nitrate_transporter_At3g43790_OS=Arabidopsis_thaliana_GN=ZIFL2_PE=2_SV=2	2.00E-37
comp33178_c2_seq15.p2		
comp33178_c2_seq18.p1	sp|Q3EAQ5|PTR36_ARATH_Probable_peptide/nitrate_transporter_At3g43790_OS=Arabidopsis_thaliana_GN=ZIFL2_PE=2_SV=2	4.00E-43
comp33178_c2_seq4.p1	sp|Q3EAQ5|PTR36_ARATH_Probable_peptide/nitrate_transporter_At3g43790_OS=Arabidopsis_thaliana_GN=ZIFL2_PE=2_SV=2	2.00E-37
comp33178_c2_seq4.p2		
comp33179_c0_seq1.p1		
comp33179_c0_seq1.p3	sp|P29687|RAB5_TOBAC_Ras-related_protein_Rab5_OS=Nicotiana_tabacum_GN=RAB5_PE=2_SV=1	2.00E-61
comp33179_c0_seq10.p1		
comp33179_c0_seq10.p2	sp|P29687|RAB5_TOBAC_Ras-related_protein_Rab5_OS=Nicotiana_tabacum_GN=RAB5_PE=2_SV=1	2.00E-61
comp33179_c0_seq12.p1		
comp33179_c0_seq12.p3	sp|P29687|RAB5_TOBAC_Ras-related_protein_Rab5_OS=Nicotiana_tabacum_GN=RAB5_PE=2_SV=1	2.00E-61
comp33179_c0_seq2.p1		
comp33179_c0_seq2.p2	sp|P29687|RAB5_TOBAC_Ras-related_protein_Rab5_OS=Nicotiana_tabacum_GN=RAB5_PE=2_SV=1	2.00E-61
comp33179_c0_seq3.p1		
comp33179_c0_seq6.p1	sp|Q6GQP4|RAB31_RAT_Ras-related_protein_Rab-31_OS=Rattus_norvegicus_GN=Rab31_PE=2_SV=2	1.00E-43
comp33181_c0_seq2.p1		
comp33181_c0_seq6.p1		
comp33182_c0_seq1.p1		
comp33183_c0_seq2.p1		
comp33184_c0_seq16.p1		
comp33185_c0_seq3.p1		
comp33185_c0_seq4.p1		
comp33185_c0_seq6.p1		
comp33186_c0_seq5.p1		
comp33186_c2_seq1.p1		
comp33187_c0_seq4.p1	sp|Q6NUF4|TPX2A_XENLA_Targeting_protein_for_Xklp2-A_OS=Xenopus_laevis_GN=tpx2-a_PE=1_SV=1	2.00E-15
comp33188_c0_seq16.p2		
comp33188_c0_seq17.p1		
comp33188_c0_seq22.p1		
comp33188_c0_seq7.p1		
comp33188_c1_seq5.p1		
comp33190_c0_seq1.p1		
comp33191_c0_seq1.p1		
comp33191_c0_seq12.p1		
comp33191_c0_seq14.p1		
comp33191_c0_seq16.p1		
comp33191_c0_seq21.p2		
comp33191_c0_seq6.p1		
comp33191_c0_seq6.p4		
comp33192_c0_seq13.p1		
comp33192_c0_seq2.p1		
comp33193_c0_seq1.p1	sp|Q9LT31|VPS9A_ARATH_Vacuolar_protein_sorting-associated_protein_9A_OS=Arabidopsis_thaliana_GN=VPS9A_PE=1_SV=1	1.00E-28
comp33193_c1_seq1.p1		
comp33193_c1_seq1.p2		
comp33193_c1_seq3.p1		
comp33193_c1_seq3.p2		
comp33194_c1_seq4.p1		
comp33194_c1_seq6.p1		
comp33194_c1_seq7.p1		
comp33195_c0_seq1.p1	sp|Q9K7A0|CSD_BACHD_Probable_cysteine_desulfurase_OS=Bacillus_halodurans_(strain_ATCC_BAA-125_/_DSM_18197_/_FERM_7344_/_JCM_9153_/_C-125)_GN=csd_PE=3_SV=2	6.00E-18
comp33195_c0_seq1.p5		
comp33195_c0_seq1.p7		
comp33195_c0_seq14.p1		
comp33195_c0_seq8.p1		
comp33196_c0_seq13.p1		
comp33197_c0_seq10.p1		
comp33198_c0_seq2.p1		
comp33198_c0_seq2.p2		
comp33198_c0_seq2.p4		
comp33198_c0_seq2.p6		
comp33198_c0_seq2.p7		
comp33198_c0_seq6.p1		
comp33198_c0_seq6.p2		
comp33198_c0_seq6.p4		
comp33198_c0_seq6.p6		
comp33198_c0_seq6.p7		
comp33200_c1_seq12.p4		
comp33201_c0_seq10.p1		
comp33201_c0_seq27.p1		
comp33201_c0_seq28.p1		
comp33201_c0_seq33.p1		
comp33201_c0_seq9.p1		
comp33202_c2_seq11.p4		
comp33202_c2_seq2.p1	sp|P34065|PSB5_CHICK_Proteasome_subunit_beta_type-5_(Fragment)_OS=Gallus_gallus_GN=PSMB5_PE=2_SV=2	1.00E-55
comp33202_c2_seq7.p1	sp|P34065|PSB5_CHICK_Proteasome_subunit_beta_type-5_(Fragment)_OS=Gallus_gallus_GN=PSMB5_PE=2_SV=2	3.00E-59
comp33203_c0_seq14.p1		
comp33203_c0_seq3.p2		
comp33203_c0_seq4.p1		
comp33203_c0_seq5.p1		
comp33203_c0_seq6.p2		
comp33204_c0_seq1.p1		
comp33205_c0_seq25.p1		
comp33205_c0_seq27.p1		
comp33205_c0_seq41.p3		
comp33206_c0_seq1.p2		
comp33206_c0_seq13.p2		
comp33206_c0_seq17.p1		
comp33206_c0_seq9.p2		
comp33207_c0_seq15.p1		
comp33208_c0_seq1.p1		
comp33208_c0_seq4.p1		
comp33208_c0_seq5.p1		
comp33209_c1_seq1.p1		
comp33209_c2_seq6.p1		
comp33209_c3_seq1.p1	sp|A4QNN3|UBP30_XENTR_Ubiquitin_carboxyl-terminal_hydrolase_30_OS=Xenopus_tropicalis_GN=usp30_PE=2_SV=1	2.00E-23
comp33209_c3_seq1.p2		
comp33210_c2_seq5.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	7.00E-36
comp33210_c2_seq6.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	7.00E-41
comp33210_c2_seq6.p2	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	3.00E-36
comp33211_c0_seq4.p1		
comp33212_c0_seq17.p1		
comp33213_c0_seq1.p1		
comp33213_c0_seq12.p2		
comp33213_c0_seq13.p1		
comp33213_c0_seq3.p1		
comp33213_c0_seq4.p1		
comp33213_c0_seq5.p1		
comp33214_c0_seq29.p2		
comp33214_c0_seq30.p1	sp|Q71A39|PHLP1_DICDI_Phosducin-like_protein_1_OS=Dictyostelium_discoideum_GN=phlp1_PE=2_SV=1	2.00E-24
comp33214_c0_seq4.p1		
comp33215_c1_seq1.p1		
comp33215_c1_seq10.p1		
comp33215_c1_seq2.p1	sp|Q96JK4|HIPL1_HUMAN_HHIP-like_protein_1_OS=Homo_sapiens_GN=HHIPL1_PE=2_SV=2	4.00E-31
comp33215_c1_seq21.p1		
comp33215_c1_seq4.p1		
comp33215_c1_seq7.p1	sp|Q96JK4|HIPL1_HUMAN_HHIP-like_protein_1_OS=Homo_sapiens_GN=HHIPL1_PE=2_SV=2	6.00E-16
comp33215_c1_seq9.p1		
comp33216_c0_seq6.p1		
comp33216_c0_seq8.p1	sp|Q1ECX4|TLK2_DANRE_Serine/threonine-protein_kinase_tousled-like_2_OS=Danio_rerio_GN=tlk2_PE=2_SV=2	3.00E-119
comp33216_c0_seq8.p2		
comp33216_c0_seq9.p1		
comp33217_c0_seq14.p1		
comp33217_c0_seq14.p2		
comp33217_c0_seq14.p3		
comp33217_c0_seq16.p2		
comp33217_c0_seq16.p4		
comp33217_c0_seq2.p1		
comp33217_c0_seq2.p2		
comp33217_c0_seq2.p4		
comp33217_c0_seq24.p1		
comp33217_c0_seq24.p3		
comp33217_c0_seq34.p2		
comp33217_c0_seq34.p4		
comp33217_c0_seq37.p1		
comp33217_c0_seq39.p1		
comp33217_c0_seq4.p1		
comp33217_c0_seq46.p1		
comp33217_c0_seq46.p2		
comp33217_c0_seq46.p4		
comp33217_c0_seq49.p1		
comp33217_c0_seq49.p3		
comp33217_c0_seq51.p1		
comp33217_c0_seq51.p3		
comp33217_c0_seq53.p1		
comp33217_c0_seq53.p2		
comp33217_c0_seq53.p4		
comp33217_c0_seq9.p1		
comp33217_c0_seq9.p2		
comp33218_c0_seq13.p1	sp|Q9QXE5|TSSP_MOUSE_Thymus-specific_serine_protease_OS=Mus_musculus_GN=Prss16_PE=2_SV=1	2.00E-69
comp33218_c0_seq13.p2		
comp33218_c0_seq21.p1		
comp33218_c0_seq21.p2	sp|P34528|YM67_CAEEL_Putative_serine_protease_K12H4.7_OS=Caenorhabditis_elegans_GN=K12H4.7_PE=2_SV=2	4.00E-35
comp33218_c0_seq21.p3	sp|Q9QXE5|TSSP_MOUSE_Thymus-specific_serine_protease_OS=Mus_musculus_GN=Prss16_PE=2_SV=1	4.00E-31
comp33219_c0_seq2.p1	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	1.00E-15
comp33219_c0_seq4.p1	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	1.00E-13
comp33219_c0_seq4.p2		
comp33219_c0_seq5.p2		
comp33220_c0_seq1.p1	sp|P34036|DYHC_DICDI_Dynein_heavy_chain,_cytoplasmic_OS=Dictyostelium_discoideum_GN=dhcA_PE=1_SV=2	0
comp33221_c0_seq2.p1		
comp33222_c0_seq1.p1		
comp33222_c0_seq3.p1		
comp33222_c0_seq34.p1		
comp33222_c0_seq39.p1		
comp33222_c0_seq5.p1		
comp33223_c0_seq10.p1		
comp33223_c0_seq11.p1		
comp33223_c0_seq11.p3		
comp33223_c1_seq1.p1		
comp33223_c3_seq1.p2		
comp33224_c0_seq2.p1	sp|O75132|ZBED4_HUMAN_Zinc_finger_BED_domain-containing_protein_4_OS=Homo_sapiens_GN=ZBED4_PE=1_SV=2	2.00E-11
comp33225_c0_seq1.p1	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	3.00E-37
comp33225_c0_seq1.p3		
comp33226_c0_seq1.p2		
comp33226_c0_seq1.p3		
comp33226_c0_seq2.p1		
comp33226_c0_seq4.p1		
comp33227_c0_seq3.p1		
comp33228_c0_seq1.p1		
comp33228_c0_seq1.p2		
comp33229_c0_seq14.p2		
comp33229_c0_seq23.p1	sp|Q24574|UBPE_DROME_Ubiquitin_carboxyl-terminal_hydrolase_64E_OS=Drosophila_melanogaster_GN=Ubp64E_PE=1_SV=2	1.00E-13
comp33229_c0_seq8.p1		
comp33229_c0_seq9.p1	sp|Q24574|UBPE_DROME_Ubiquitin_carboxyl-terminal_hydrolase_64E_OS=Drosophila_melanogaster_GN=Ubp64E_PE=1_SV=2	2.00E-15
comp33230_c0_seq16.p1	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	5.00E-11
comp33230_c0_seq17.p2	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	3.00E-16
comp33230_c0_seq4.p1		
comp33230_c0_seq5.p3	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	3.00E-16
comp33230_c0_seq9.p1		
comp33231_c0_seq2.p1		
comp33231_c0_seq2.p2		
comp33232_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	3.00E-12
comp33232_c0_seq15.p1		
comp33232_c0_seq9.p1		
comp33233_c0_seq15.p2		
comp33233_c0_seq18.p1		
comp33233_c0_seq4.p1		
comp33233_c0_seq5.p1		
comp33233_c1_seq2.p1		
comp33233_c1_seq3.p1		
comp33233_c1_seq7.p1		
comp33234_c0_seq16.p1		
comp33234_c0_seq17.p1		
comp33234_c0_seq19.p1		
comp33234_c0_seq24.p1		
comp33234_c0_seq26.p1		
comp33234_c0_seq28.p1		
comp33234_c0_seq3.p1		
comp33234_c0_seq33.p1		
comp33234_c0_seq35.p1		
comp33234_c0_seq36.p1		
comp33234_c0_seq37.p1		
comp33234_c0_seq38.p1		
comp33234_c0_seq42.p1		
comp33234_c0_seq43.p1		
comp33234_c0_seq47.p1		
comp33234_c0_seq47.p2	sp|O82251|TI202_ARATH_Protein_TIC_20-II,_chloroplastic_OS=Arabidopsis_thaliana_GN=TIC20-II_PE=2_SV=1	5.00E-12
comp33234_c0_seq48.p1		
comp33234_c0_seq7.p1		
comp33235_c0_seq2.p1		
comp33235_c0_seq2.p3		
comp33236_c0_seq2.p1		
comp33236_c1_seq5.p1		
comp33236_c1_seq5.p3		
comp33236_c1_seq7.p1		
comp33236_c1_seq7.p3		
comp33237_c0_seq14.p2		
comp33237_c0_seq2.p1		
comp33237_c0_seq3.p2		
comp33237_c0_seq9.p1		
comp33238_c0_seq6.p1	sp|Q9NZM1|MYOF_HUMAN_Myoferlin_OS=Homo_sapiens_GN=MYOF_PE=1_SV=1	8.00E-22
comp33239_c0_seq1.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	7.00E-81
comp33239_c0_seq1.p4		
comp33240_c0_seq7.p1		
comp33240_c2_seq2.p1		
comp33241_c0_seq1.p1		
comp33241_c0_seq1.p2		

comp33241_c0_seq10.p1				
comp33241_c0_seq10.p2				
comp33241_c0_seq11.p1				
comp33241_c0_seq3.p1				
comp33241_c0_seq4.p1				
comp33241_c0_seq7.p1				
comp33241_c0_seq8.p1				
comp33241_c0_seq8.p2				
comp33241_c0_seq9.p1				
comp33241_c0_seq9.p3				
comp33242_c0_seq2.p1				
comp33242_c0_seq2.p2				
comp33242_c0_seq2.p7				
comp33242_c0_seq2.p8				
comp33243_c0_seq18.p1				
comp33243_c0_seq2.p1				
comp33243_c0_seq26.p1				
comp33243_c0_seq7.p1				
comp33244_c0_seq10.p1				
comp33244_c0_seq22.p1				
comp33244_c0_seq22.p4				
comp33244_c0_seq25.p2				
comp33244_c0_seq28.p1				
comp33244_c0_seq9.p1				
comp33245_c0_seq1.p1				
comp33245_c0_seq1.p2				
comp33245_c3_seq1.p1	sp|B5X0N6|KEA6_ARATH_K(+)_efflux_antiporter_6_OS=Arabidopsis_thaliana_GN=KEA6_PE=2_SV=1	2.00E-35	GO:0006810,GO:0006811,GO:0006812,GO:0006813,GO:0006814,GO:0010351,GO:0015297,GO:0015299,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0055085,GO:1902600	transport,ion transport,cation transport,potassium ion transport,sodium ion transport,lithium ion transport,antiporter activity,solute:proton antiporter activity,membrane,membrane,membrane,integral component of membrane,integral component of membrane,transmembrane transport,hydrogen ion transmembrane transport
comp33245_c9_seq13.p1	sp|P18496|ATP10_YEAST_Mitochondrial_ATPase_complex_subunit_ATP10_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=ATP10_PE=1_SV=2	5.00E-11	GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0005743,GO:0016020,GO:0032592,GO:0033615,GO:0033615,GO:0033615,GO:0051082	mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,membrane,integral component of mitochondrial membrane,mitochondrial proton-transporting ATP synthase complex assembly,mitochondrial proton-transporting ATP synthase complex assembly,mitochondrial proton-transporting ATP synthase complex assembly,unfolded protein binding
comp33245_c9_seq13.p3				
comp33245_c9_seq17.p1	sp|P18496|ATP10_YEAST_Mitochondrial_ATPase_complex_subunit_ATP10_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=ATP10_PE=1_SV=2	5.00E-11	GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0005743,GO:0016020,GO:0032592,GO:0033615,GO:0033615,GO:0033615,GO:0051082	mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,membrane,integral component of mitochondrial membrane,mitochondrial proton-transporting ATP synthase complex assembly,mitochondrial proton-transporting ATP synthase complex assembly,mitochondrial proton-transporting ATP synthase complex assembly,unfolded protein binding
comp33245_c9_seq20.p2				
comp33245_c9_seq22.p1	sp|P18496|ATP10_YEAST_Mitochondrial_ATPase_complex_subunit_ATP10_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=ATP10_PE=1_SV=2	5.00E-11	GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0005743,GO:0016020,GO:0032592,GO:0033615,GO:0033615,GO:0033615,GO:0051082	mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,membrane,integral component of mitochondrial membrane,mitochondrial proton-transporting ATP synthase complex assembly,mitochondrial proton-transporting ATP synthase complex assembly,mitochondrial proton-transporting ATP synthase complex assembly,unfolded protein binding
comp33245_c9_seq22.p3				
comp33245_c9_seq27.p1				
comp33245_c9_seq3.p1				
comp33245_c9_seq30.p1				
comp33245_c9_seq5.p1	sp|Q8H110|XCT_ARATH_Protein_XAP5_CIRCADIAN_TIMEKEEPER_OS=Arabidopsis_thaliana_GN=XCT_PE=1_SV=1	2.00E-83	GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0009637,GO:0009640,GO:0009793,GO:0009845,GO:0009873,GO:0009909,GO:0009933,GO:0010099,GO:0010114,GO:0010162,GO:0010182,GO:0010228,GO:0016567,GO:0019915,GO:0042752,GO:0048511,GO:0050826	nucleus,nucleus,nucleus,nucleus,response to blue light,photomorphogenesis,embryo development ending in seed dormancy,seed germination,ethylene-activated signaling pathway,regulation of flower development,meristem structural organization,regulation of photomorphogenesis,response to red light,seed dormancy process,sugar mediated signaling pathway,vegetative to reproductive phase transition of meristem,protein ubiquitination,lipid storage,regulation of circadian rhythm,rhythmic process,response to freezing
comp33245_c9_seq7.p1	sp|P18496|ATP10_YEAST_Mitochondrial_ATPase_complex_subunit_ATP10_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=ATP10_PE=1_SV=2	5.00E-11	GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0005743,GO:0016020,GO:0032592,GO:0033615,GO:0033615,GO:0033615,GO:0051082	mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,membrane,integral component of mitochondrial membrane,mitochondrial proton-transporting ATP synthase complex assembly,mitochondrial proton-transporting ATP synthase complex assembly,mitochondrial proton-transporting ATP synthase complex assembly,unfolded protein binding
comp33246_c0_seq5.p1				
comp33246_c0_seq8.p1				
comp33247_c0_seq3.p1				
comp33247_c0_seq6.p1				
comp33248_c0_seq3.p1				
comp33249_c0_seq10.p1				
comp33249_c0_seq10.p5				
comp33249_c0_seq13.p1				
comp33249_c0_seq13.p5				
comp33249_c0_seq6.p1				
comp33250_c0_seq10.p2				
comp33250_c0_seq11.p1				
comp33250_c0_seq4.p1				
comp33250_c0_seq6.p1				
comp33250_c0_seq7.p1				
comp33251_c0_seq5.p1				
comp33252_c0_seq1.p1				
comp33252_c0_seq9.p1				
comp33253_c0_seq22.p1				
comp33253_c0_seq26.p1				
comp33253_c0_seq6.p1				
comp33254_c0_seq1.p1	sp|Q9UR07|RTF23_SCHPO_Retrotransposable_element_Tf2_155_kDa_protein_type_3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=Tf2-11_PE=4_SV=1	1.00E-17	GO:0003676,GO:0003677,GO:0003723,GO:0003824,GO:0003887,GO:0003964,GO:0004190,GO:0004190,GO:0004518,GO:0004519,GO:0005634,GO:0006278,GO:0006310,GO:0006508,GO:0006508,GO:0008152,GO:0008233,GO:0015074,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0071897,GO:0090305,GO:0090305	nucleic acid binding,DNA binding,RNA binding,catalytic activity,DNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,nucleus,RNA-dependent DNA replication,DNA recombination,proteolysis,proteolysis,metabolic process,peptidase activity,DNA integration,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,DNA biosynthetic process,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33254_c0_seq1.p2				
comp33254_c0_seq4.p1				
comp33254_c0_seq5.p1	sp|Q05654|RTF21_SCHPO_Retrotransposable_element_Tf2_155_kDa_protein_type_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=Tf2-1_PE=2_SV=1	1.00E-29		
comp33254_c0_seq5.p2				
comp33254_c0_seq6.p1	sp|Q05654|RTF21_SCHPO_Retrotransposable_element_Tf2_155_kDa_protein_type_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=Tf2-1_PE=2_SV=1	1.00E-29		
comp33254_c0_seq6.p2				
comp33254_c0_seq8.p1	sp|Q9UR07|RTF23_SCHPO_Retrotransposable_element_Tf2_155_kDa_protein_type_3_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=Tf2-11_PE=4_SV=1	1.00E-17	GO:0003676,GO:0003677,GO:0003723,GO:0003824,GO:0003887,GO:0003964,GO:0004190,GO:0004190,GO:0004518,GO:0004519,GO:0005634,GO:0006278,GO:0006310,GO:0006508,GO:0006508,GO:0008152,GO:0008233,GO:0015074,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0071897,GO:0090305,GO:0090305	nucleic acid binding,DNA binding,RNA binding,catalytic activity,DNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,nucleus,RNA-dependent DNA replication,DNA recombination,proteolysis,proteolysis,metabolic process,peptidase activity,DNA integration,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,DNA biosynthetic process,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33254_c0_seq8.p2				
comp33255_c0_seq1.p1				
comp33255_c0_seq13.p1				
comp33255_c0_seq15.p1				
comp33255_c0_seq2.p1				
comp33255_c0_seq8.p1				
comp33256_c0_seq2.p1				
comp33256_c0_seq3.p1				
comp33256_c0_seq3.p3				
comp33257_c0_seq20.p1				
comp33258_c0_seq1.p1				
comp33258_c0_seq1.p3				
comp33258_c0_seq2.p1				
comp33258_c0_seq2.p2				
comp33258_c0_seq4.p1				
comp33258_c0_seq5.p1				
comp33259_c0_seq1.p1				
comp33259_c0_seq9.p1				
comp33260_c0_seq2.p2	sp|P32794|AFG2_YEAST_ATPase_family_gene_2_protein_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=AFG2_PE=1_SV=1	4.00E-28	GO:0000166,GO:0005524,GO:0005524,GO:0005622,GO:0006200,GO:0016887,GO:0030687,GO:0030687,GO:0042273,GO:0042493	nucleotide binding,ATP binding,ATP binding,intracellular,ATP catabolic process,ATPase activity,preribosome, large subunit precursor,preribosome, large subunit precursor,ribosomal large subunit biogenesis,response to drug
comp33260_c2_seq1.p1				
comp33260_c2_seq15.p1	sp|Q8CJ27|ASPM_MOUSE_Abnormal_spindle-like_microcephaly-associated_protein_homolog_OS=Mus_musculus_GN=Aspm_PE=2_SV=2	6.00E-85	GO:0000922,GO:0000922,GO:0001764,GO:0001764,GO:0002052,GO:0002052,GO:0005516,GO:0005516,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005819,GO:0005856,GO:0005874,GO:0007049,GO:0007067,GO:0007283,GO:0007420,GO:0008584,GO:0021873,GO:0021987,GO:0030496,GO:0045665,GO:0045769,GO:0048477,GO:0048589,GO:0051301,GO:0051661,GO:0072687,GO:0090263,GO:0090306,GO:0097150,GO:0097431,GO:0097431	spindle pole,spindle pole,neuron migration,neuron migration,positive regulation of neuroblast proliferation,positive regulation of neuroblast proliferation,calmodulin binding,calmodulin binding,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,spindle,cytoskeleton,microtubule,cell cycle,mitotic nuclear division,spermatogenesis,brain development,male gonad development,forebrain neuroblast division,cerebral cortex development,midbody,negative regulation of neuron differentiation,negative regulation of asymmetric cell division,oogenesis,developmental growth,cell division,maintenance of centrosome location,meiotic spindle,positive regulation of canonical Wnt signaling pathway,spindle assembly involved in meiosis,neuronal stem cell maintenance,mitotic spindle pole,mitotic spindle pole
comp33260_c2_seq23.p1	sp|Q8CJ27|ASPM_MOUSE_Abnormal_spindle-like_microcephaly-associated_protein_homolog_OS=Mus_musculus_GN=Aspm_PE=2_SV=2	6.00E-79	GO:0000922,GO:0000922,GO:0001764,GO:0001764,GO:0002052,GO:0002052,GO:0005516,GO:0005516,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005819,GO:0005856,GO:0005874,GO:0007049,GO:0007067,GO:0007283,GO:0007420,GO:0008584,GO:0021873,GO:0021987,GO:0030496,GO:0045665,GO:0045769,GO:0048477,GO:0048589,GO:0051301,GO:0051661,GO:0072687,GO:0090263,GO:0090306,GO:0097150,GO:0097431,GO:0097431	spindle pole,spindle pole,neuron migration,neuron migration,positive regulation of neuroblast proliferation,positive regulation of neuroblast proliferation,calmodulin binding,calmodulin binding,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,spindle,cytoskeleton,microtubule,cell cycle,mitotic nuclear division,spermatogenesis,brain development,male gonad development,forebrain neuroblast division,cerebral cortex development,midbody,negative regulation of neuron differentiation,negative regulation of asymmetric cell division,oogenesis,developmental growth,cell division,maintenance of centrosome location,meiotic spindle,positive regulation of canonical Wnt signaling pathway,spindle assembly involved in meiosis,neuronal stem cell maintenance,mitotic spindle pole,mitotic spindle pole
comp33260_c2_seq32.p1	sp|P62289|ASPM_GORGO_Abnormal_spindle-like_microcephaly-associated_protein_homolog_OS=Gorilla_gorilla_gorilla_GN=ASPM_PE=2_SV=1	8.00E-60	GO:0005516,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005819,GO:0005856,GO:0007049,GO:0007067,GO:0051301	calmodulin binding,nucleus,nucleus,cytoplasm,cytoplasm,spindle,cytoskeleton,cell cycle,mitotic nuclear division,cell division
comp33260_c2_seq33.p1	sp|Q8CJ27|ASPM_MOUSE_Abnormal_spindle-like_microcephaly-associated_protein_homolog_OS=Mus_musculus_GN=Aspm_PE=2_SV=2	1.00E-50	GO:0000922,GO:0000922,GO:0001764,GO:0001764,GO:0002052,GO:0002052,GO:0005516,GO:0005516,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005819,GO:0005856,GO:0005874,GO:0007049,GO:0007067,GO:0007283,GO:0007420,GO:0008584,GO:0021873,GO:0021987,GO:0030496,GO:0045665,GO:0045769,GO:0048477,GO:0048589,GO:0051301,GO:0051661,GO:0072687,GO:0090263,GO:0090306,GO:0097150,GO:0097431,GO:0097431	spindle pole,spindle pole,neuron migration,neuron migration,positive regulation of neuroblast proliferation,positive regulation of neuroblast proliferation,calmodulin binding,calmodulin binding,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,spindle,cytoskeleton,microtubule,cell cycle,mitotic nuclear division,spermatogenesis,brain development,male gonad development,forebrain neuroblast division,cerebral cortex development,midbody,negative regulation of neuron differentiation,negative regulation of asymmetric cell division,oogenesis,developmental growth,cell division,maintenance of centrosome location,meiotic spindle,positive regulation of canonical Wnt signaling pathway,spindle assembly involved in meiosis,neuronal stem cell maintenance,mitotic spindle pole,mitotic spindle pole
comp33260_c2_seq33.p4	sp|P62289|ASPM_GORGO_Abnormal_spindle-like_microcephaly-associated_protein_homolog_OS=Gorilla_gorilla_gorilla_GN=ASPM_PE=2_SV=1	4.00E-11	GO:0005516,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005819,GO:0005856,GO:0007049,GO:0007067,GO:0051301	calmodulin binding,nucleus,nucleus,cytoplasm,cytoplasm,spindle,cytoskeleton,cell cycle,mitotic nuclear division,cell division
comp33260_c2_seq6.p1	sp|Q8CJ27|ASPM_MOUSE_Abnormal_spindle-like_microcephaly-associated_protein_homolog_OS=Mus_musculus_GN=Aspm_PE=2_SV=2	9.00E-45	GO:0000922,GO:0000922,GO:0001764,GO:0001764,GO:0002052,GO:0002052,GO:0005516,GO:0005516,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005819,GO:0005856,GO:0005874,GO:0007049,GO:0007067,GO:0007283,GO:0007420,GO:0008584,GO:0021873,GO:0021987,GO:0030496,GO:0045665,GO:0045769,GO:0048477,GO:0048589,GO:0051301,GO:0051661,GO:0072687,GO:0090263,GO:0090306,GO:0097150,GO:0097431,GO:0097431	spindle pole,spindle pole,neuron migration,neuron migration,positive regulation of neuroblast proliferation,positive regulation of neuroblast proliferation,calmodulin binding,calmodulin binding,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,spindle,cytoskeleton,microtubule,cell cycle,mitotic nuclear division,spermatogenesis,brain development,male gonad development,forebrain neuroblast division,cerebral cortex development,midbody,negative regulation of neuron differentiation,negative regulation of asymmetric cell division,oogenesis,developmental growth,cell division,maintenance of centrosome location,meiotic spindle,positive regulation of canonical Wnt signaling pathway,spindle assembly involved in meiosis,neuronal stem cell maintenance,mitotic spindle pole,mitotic spindle pole
comp33260_c2_seq6.p4	sp|P62289|ASPM_GORGO_Abnormal_spindle-like_microcephaly-associated_protein_homolog_OS=Gorilla_gorilla_gorilla_GN=ASPM_PE=2_SV=1	4.00E-11	GO:0005516,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005819,GO:0005856,GO:0007049,GO:0007067,GO:0051301	calmodulin binding,nucleus,nucleus,cytoplasm,cytoplasm,spindle,cytoskeleton,cell cycle,mitotic nuclear division,cell division
comp33260_c2_seq7.p1				
comp33261_c0_seq6.p3				
comp33261_c0_seq8.p4				
comp33262_c0_seq12.p1				
comp33262_c0_seq12.p2				
comp33262_c0_seq12.p3				
comp33262_c0_seq12.p4	sp|Q86UV5|UBP48_HUMAN_Ubiquitin_carboxyl-terminal_hydrolase_48_OS=Homo_sapiens_GN=USP48_PE=1_SV=1	9.00E-19	GO:0004197,GO:0004221,GO:0004843,GO:0004843,GO:0005634,GO:0005634,GO:0005654,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0006508,GO:0006511,GO:0008233,GO:0008234,GO:0016579,GO:0016787,GO:0036459,GO:0043161,GO:0061136	cysteine-type endopeptidase activity,ubiquitin thiolesterase activity,ubiquitin-specific protease activity,ubiquitin-specific protease activity,nucleus,nucleus,nucleoplasm,cytoplasm,cytoplasm,cytoplasm,mitochondrion,proteolysis,ubiquitin-dependent protein catabolic process,peptidase activity,cysteine-type peptidase activity,protein deubiquitination,hydrolase activity,ubiquitinyl hydrolase activity,proteasome-mediated ubiquitin-dependent protein catabolic process,regulation of proteasomal protein catabolic process
comp33262_c0_seq12.p8				
comp33262_c0_seq24.p1				
comp33262_c0_seq24.p2				
comp33262_c0_seq24.p3	sp|Q86UV5|UBP48_HUMAN_Ubiquitin_carboxyl-terminal_hydrolase_48_OS=Homo_sapiens_GN=USP48_PE=1_SV=1	9.00E-19	GO:0004197,GO:0004221,GO:0004843,GO:0004843,GO:0005634,GO:0005634,GO:0005654,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0006508,GO:0006511,GO:0008233,GO:0008234,GO:0016579,GO:0016787,GO:0036459,GO:0043161,GO:0061136	cysteine-type endopeptidase activity,ubiquitin thiolesterase activity,ubiquitin-specific protease activity,ubiquitin-specific protease activity,nucleus,nucleus,nucleoplasm,cytoplasm,cytoplasm,cytoplasm,mitochondrion,proteolysis,ubiquitin-dependent protein catabolic process,peptidase activity,cysteine-type peptidase activity,protein deubiquitination,hydrolase activity,ubiquitinyl hydrolase activity,proteasome-mediated ubiquitin-dependent protein catabolic process,regulation of proteasomal protein catabolic process
comp33262_c0_seq24.p5				
comp33262_c0_seq24.p7				
comp33262_c0_seq5.p1	sp|Q86UV5|UBP48_HUMAN_Ubiquitin_carboxyl-terminal_hydrolase_48_OS=Homo_sapiens_GN=USP48_PE=1_SV=1	2.00E-18	GO:0004197,GO:0004221,GO:0004843,GO:0004843,GO:0005634,GO:0005634,GO:0005654,GO:0005737,GO:0005737,GO:0005737,GO:0005739,GO:0006508,GO:0006511,GO:0008233,GO:0008234,GO:0016579,GO:0016787,GO:0036459,GO:0043161,GO:0061136	cysteine-type endopeptidase activity,ubiquitin thiolesterase activity,ubiquitin-specific protease activity,ubiquitin-specific protease activity,nucleus,nucleus,nucleoplasm,cytoplasm,cytoplasm,cytoplasm,mitochondrion,proteolysis,ubiquitin-dependent protein catabolic process,peptidase activity,cysteine-type peptidase activity,protein deubiquitination,hydrolase activity,ubiquitinyl hydrolase activity,proteasome-mediated ubiquitin-dependent protein catabolic process,regulation of proteasomal protein catabolic process
comp33262_c0_seq5.p2				
comp33262_c0_seq5.p5				
comp33263_c0_seq11.p1				
comp33263_c0_seq16.p1	sp|Q46189|YHG1_CLOPA_Uncharacterized_protein_in_hydrogenase_1_5'region_(Fragment)_OS=Clostridium_pasteurianum_PE=3_SV=1	3.00E-35	GO:0008152,GO:0016772	metabolic process,transferase activity, transferring phosphorus-containing groups
comp33263_c0_seq8.p1				
comp33264_c1_seq16.p2				
comp33264_c1_seq19.p1				
comp33264_c1_seq23.p1				
comp33264_c1_seq28.p1				
comp33264_c1_seq36.p2				
comp33264_c1_seq44.p1				
comp33264_c1_seq44.p2				
comp33265_c0_seq2.p1				
comp33265_c0_seq3.p1	sp|Q9VLF6|U585_DROME_UPF0585_protein_CG18661_OS=Drosophila_melanogaster_GN=CG18661_PE=2_SV=2	2.00E-34	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp33265_c1_seq6.p1				
comp33266_c0_seq6.p1				
comp33267_c0_seq2.p1				
comp33268_c0_seq3.p1				
comp33268_c0_seq4.p1				
comp33269_c0_seq12.p1				
comp33269_c0_seq12.p3				
comp33269_c0_seq3.p1				
comp33269_c0_seq8.p1				
comp3327_c0_seq1.p1				
comp33270_c0_seq25.p1				
comp33270_c0_seq26.p1	sp|Q8GYM6|CCT14_ARATH_Cyclin-T1-4_OS=Arabidopsis_thaliana_GN=CYCT1-4_PE=1_SV=1	7.00E-16	GO:0000079,GO:0000394,GO:0005634,GO:0006355,GO:0006366,GO:0007049,GO:0008284,GO:0009615,GO:0010090,GO:0019901,GO:0048366,GO:0051301	regulation of cyclin-dependent protein serine/threonine kinase activity,RNA splicing, via endonucleolytic cleavage and ligation,nucleus,regulation of transcription, DNA-templated,transcription from RNA polymerase II promoter,cell cycle,positive regulation of cell proliferation,response to virus,trichome morphogenesis,protein kinase binding,leaf development,cell division
comp33270_c0_seq27.p1				
comp33270_c0_seq30.p1				
comp33270_c0_seq40.p1				
comp33271_c0_seq3.p1				
comp33271_c1_seq1.p1				
comp33271_c1_seq2.p1				
comp33271_c2_seq3.p1				
comp33271_c2_seq6.p1	sp|Q8BZ25|ANKK1_MOUSE_Ankyrin_repeat_and_protein_kinase_domain-containing_protein_1_OS=Mus_musculus_GN=Ankk1_PE=2_SV=1	8.00E-17	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005575,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772	nucleotide binding,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,ATP binding,ATP binding,cellular_component,protein phosphorylation,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups
comp33271_c2_seq6.p5				
comp33272_c0_seq2.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-13	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33273_c0_seq2.p1				
comp33273_c0_seq4.p1				
comp33273_c0_seq7.p1				
comp33274_c0_seq2.p1				
comp33274_c0_seq3.p2				
comp33274_c0_seq4.p1				
comp33275_c0_seq11.p1				
comp33275_c0_seq11.p2				
comp33275_c0_seq11.p3				
comp33275_c0_seq11.p5				
comp33275_c0_seq9.p1				
comp33275_c0_seq9.p2				
comp33275_c0_seq9.p4				
comp33276_c0_seq1.p1				
comp33276_c0_seq3.p1				
comp33277_c1_seq2.p2				
comp33277_c1_seq2.p5				
comp33277_c1_seq3.p1				
comp33277_c1_seq3.p2				
comp33278_c0_seq3.p1				
comp33278_c1_seq1.p1				
comp33278_c2_seq5.p1				
comp33278_c2_seq6.p1				
comp33278_c2_seq9.p1				
comp33279_c1_seq1.p1	sp|P20825|POL2_DROME_Retrovirus-related_Pol_polyprotein_from_transposon_297_OS=Drosophila_melanogaster_GN=pol_PE=4_SV=1	1.00E-43	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0006508,GO:0008233,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,proteolysis,peptidase activity,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33280_c0_seq2.p1				
comp33280_c0_seq2.p2	sp|Q9M060|IF62_ARATH_Eukaryotic_translation_initiation_factor_6-2_OS=Arabidopsis_thaliana_GN=EIF6-2_PE=2_SV=1	8.00E-120	GO:0003743,GO:0003743,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0005730,GO:0005737,GO:0005737,GO:0005829,GO:0006412,GO:0006413,GO:0006413,GO:0009793,GO:0042254,GO:0042256,GO:0042256,GO:0042273,GO:0043022,GO:0043023,GO:0071215	translation initiation factor activity,translation initiation factor activity,nucleus,nucleus,nucleolus,nucleolus,nucleolus,cytoplasm,cytoplasm,cytoplasm,cytosol,translation,translational initiation,translational initiation,embryo development ending in seed dormancy,ribosome biogenesis,mature ribosome assembly,mature ribosome assembly,ribosomal large subunit biogenesis,ribosome binding,ribosomal large subunit binding,cellular response to abscisic acid stimulus
comp33280_c0_seq2.p3				
comp33280_c0_seq4.p1				
comp33280_c0_seq6.p5				
comp33280_c1_seq1.p1				
comp33281_c0_seq2.p1	sp|Q54LN2|VP13D_DICDI_Putative_vacuolar_protein_sorting-associated_protein_13D_OS=Dictyostelium_discoideum_GN=vps13D_PE=3_SV=1	6.00E-37	GO:0003674,GO:0005575,GO:0005622,GO:0005794,GO:0005794,GO:0006623,GO:0006810,GO:0015031,GO:0019898,GO:0045053	molecular_function,cellular_component,intracellular,Golgi apparatus,Golgi apparatus,protein targeting to vacuole,transport,protein transport,extrinsic component of membrane,protein retention in Golgi apparatus
comp33281_c0_seq3.p1				
comp33281_c0_seq4.p1				
comp33281_c0_seq7.p1	sp|Q54LN2|VP13D_DICDI_Putative_vacuolar_protein_sorting-associated_protein_13D_OS=Dictyostelium_discoideum_GN=vps13D_PE=3_SV=1	6.00E-37	GO:0003674,GO:0005575,GO:0005622,GO:0005794,GO:0005794,GO:0006623,GO:0006810,GO:0015031,GO:0019898,GO:0045053	molecular_function,cellular_component,intracellular,Golgi apparatus,Golgi apparatus,protein targeting to vacuole,transport,protein transport,extrinsic component of membrane,protein retention in Golgi apparatus
comp33282_c0_seq4.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-23	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33282_c0_seq5.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	8.00E-68	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33282_c0_seq5.p2	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	9.00E-12	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33282_c0_seq5.p4				
comp33283_c0_seq4.p1				
comp33283_c0_seq4.p2				
comp33284_c0_seq1.p1	sp|E1C5V0|SMYD2_CHICK_N-lysine_methyltransferase_SMYD2_OS=Gallus_gallus_GN=SMYD2_PE=3_SV=1	5.00E-36	GO:0000122,GO:0000993,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0006351,GO:0006355,GO:0008168,GO:0008285,GO:0010452,GO:0016279,GO:0016568,GO:0016740,GO:0018024,GO:0018026,GO:0018027,GO:0032259,GO:0034968,GO:0043516,GO:0046872,GO:0046975	negative regulation of transcription from RNA polymerase II promoter,RNA polymerase II core binding,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytosol,cytosol,transcription, DNA-templated,regulation of transcription, DNA-templated,methyltransferase activity,negative regulation of cell proliferation,histone H3-K36 methylation,protein-lysine N-methyltransferase activity,chromatin modification,transferase activity,histone-lysine N-methyltransferase activity,peptidyl-lysine monomethylation,peptidyl-lysine dimethylation,methylation,histone lysine methylation,regulation of DNA damage response, signal transduction by p53 class mediator,metal ion binding,histone methyltransferase activity (H3-K36 specific)
comp33284_c0_seq1.p2				
comp33284_c0_seq1.p4				
comp33285_c0_seq8.p1	sp|O02751|CFDP2_BOVIN_Craniofacial_development_protein_2_OS=Bos_taurus_GN=CFDP2_PE=1_SV=2	7.00E-20	GO:0005634,GO:0005634,GO:0005737,GO:0005737	nucleus,nucleus,cytoplasm,cytoplasm
comp33286_c0_seq12.p1				
comp33286_c0_seq12.p2				
comp33286_c0_seq13.p2				
comp33287_c0_seq1.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	4.00E-13	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33287_c0_seq6.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	2.00E-103	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33287_c0_seq7.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	6.00E-96	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33287_c0_seq9.p1				
comp33287_c1_seq1.p1	sp|P54774|CDC48_SOYBN_Cell_division_cycle_protein_48_homolog_OS=Glycine_max_GN=CDC48_PE=2_SV=1	0	GO:0000166,GO:0005524,GO:0005524,GO:0005886,GO:0005886,GO:0007049,GO:0008152,GO:0016020,GO:0016787	nucleotide binding,ATP binding,ATP binding,plasma membrane,plasma membrane,cell cycle,metabolic process,membrane,hydrolase activity
comp33288_c0_seq1.p1				
comp33288_c0_seq3.p1	sp|Q6PC19|SSU72_DANRE_RNA_polymerase_II_subunit_A_C-terminal_domain_phosphatase_SSU72_OS=Danio_rerio_GN=ssu72_PE=2_SV=1	6.00E-39	GO:0004721,GO:0004721,GO:0004721,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006397,GO:0006397,GO:0016311,GO:0016311,GO:0016311,GO:0016787	phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,mRNA processing,mRNA processing,dephosphorylation,dephosphorylation,dephosphorylation,hydrolase activity
comp33288_c0_seq3.p2				
comp33289_c0_seq1.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	8.00E-43	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33289_c0_seq1.p3				
comp33289_c0_seq1.p5				
comp33290_c0_seq1.p1				
comp33290_c0_seq1.p2				
comp33290_c0_seq3.p1				
comp33290_c0_seq5.p1				
comp33291_c0_seq1.p1				
comp33291_c1_seq1.p3				
comp33291_c4_seq1.p1				
comp33292_c1_seq1.p1				
comp33292_c1_seq1.p4				
comp33292_c1_seq6.p1				
comp33292_c1_seq6.p4				
comp33292_c1_seq8.p1				
comp33292_c2_seq1.p2				
comp33292_c3_seq1.p1				
comp33293_c2_seq19.p1				
comp33293_c2_seq5.p1	sp|P11369|POL2_MOUSE_Retrovirus-related_Pol_polyprotein_LINE-1_OS=Mus_musculus_GN=Pol_PE=1_SV=2	3.00E-22	GO:0003824,GO:0003964,GO:0003964,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006310,GO:0008152,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	catalytic activity,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,DNA recombination,metabolic process,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33294_c0_seq2.p1				
comp33294_c0_seq6.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	2.00E-24	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33294_c0_seq6.p2	sp|P04146|COPIA_DROME_Copia_protein_OS=Drosophila_melanogaster_GN=GIP_PE=1_SV=3	2.00E-29	GO:0000166,GO:0003676,GO:0004190,GO:0005524,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016787,GO:0046872	nucleotide binding,nucleic acid binding,aspartic-type endopeptidase activity,ATP binding,proteolysis,peptidase activity,zinc ion binding,DNA integration,hydrolase activity,metal ion binding
comp33294_c0_seq6.p3	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	5.00E-20	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33295_c0_seq2.p11				
comp33295_c0_seq2.p2	sp|Q95SX7|RTBS_DROME_Probable_RNA-directed_DNA_polymerase_from_transposon_BS_OS=Drosophila_melanogaster_GN=RTase_PE=2_SV=1	3.00E-12	GO:0003964,GO:0003964,GO:0003964,GO:0005575,GO:0006278,GO:0006278,GO:0006278,GO:0006313,GO:0016740,GO:0016779	RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,cellular_component,RNA-dependent DNA replication,RNA-dependent DNA replication,RNA-dependent DNA replication,transposition, DNA-mediated,transferase activity,nucleotidyltransferase activity
comp33295_c0_seq2.p3				
comp33296_c0_seq1.p1	sp|A2WTA0|PLA3_ORYSI_Phospholipase_A1-II_3_OS=Oryza_sativa_subsp._indica_GN=OsI_03088_PE=3_SV=1	9.00E-20	GO:0005576,GO:0005576,GO:0006629,GO:0006629,GO:0008970,GO:0016042,GO:0016787	extracellular region,extracellular region,lipid metabolic process,lipid metabolic process,phosphatidylcholine 1-acylhydrolase activity,lipid catabolic process,hydrolase activity
comp33296_c1_seq1.p10	sp|P10394|POL4_DROME_Retrovirus-related_Pol_polyprotein_from_transposon_412_OS=Drosophila_melanogaster_GN=POL_PE=4_SV=1	4.00E-16	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0006508,GO:0008233,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,proteolysis,peptidase activity,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33296_c1_seq1.p2				
comp33296_c1_seq1.p3				
comp33296_c1_seq3.p1	sp|Q7LHG5|YI31B_YEAST_Transposon_Ty3-I_Gag-Pol_polyprotein_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TY3B-I_PE=3_SV=2	2.00E-24	GO:0000166,GO:0000943,GO:0003676,GO:0003677,GO:0003723,GO:0003723,GO:0003824,GO:0003887,GO:0003887,GO:0003887,GO:0003964,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0004523,GO:0004540,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006278,GO:0006278,GO:0006278,GO:0006310,GO:0006508,GO:0008152,GO:0008233,GO:0008233,GO:0008270,GO:0015074,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0019076,GO:0032197,GO:0046872,GO:0071897,GO:0071897,GO:0071897,GO:0090305,GO:0090305,GO:0090501,GO:0090502	nucleotide binding,retrotransposon nucleocapsid,nucleic acid binding,DNA binding,RNA binding,RNA binding,catalytic activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-DNA hybrid ribonuclease activity,ribonuclease activity,ATP binding,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,RNA-dependent DNA replication,RNA-dependent DNA replication,RNA-dependent DNA replication,DNA recombination,proteolysis,metabolic process,peptidase activity,peptidase activity,zinc ion binding,DNA integration,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,viral release from host cell,transposition, RNA-mediated,metal ion binding,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis,RNA phosphodiester bond hydrolysis,RNA phosphodiester bond hydrolysis, endonucleolytic
comp33296_c1_seq3.p11	sp|P10394|POL4_DROME_Retrovirus-related_Pol_polyprotein_from_transposon_412_OS=Drosophila_melanogaster_GN=POL_PE=4_SV=1	4.00E-16	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0006508,GO:0008233,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,proteolysis,peptidase activity,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33296_c1_seq3.p2				
comp33296_c1_seq3.p3				
comp33296_c1_seq6.p10	sp|P10394|POL4_DROME_Retrovirus-related_Pol_polyprotein_from_transposon_412_OS=Drosophila_melanogaster_GN=POL_PE=4_SV=1	4.00E-16	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0006508,GO:0008233,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,proteolysis,peptidase activity,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33296_c1_seq6.p2				
comp33296_c1_seq6.p3				
comp33296_c1_seq7.p1	sp|Q7LHG5|YI31B_YEAST_Transposon_Ty3-I_Gag-Pol_polyprotein_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TY3B-I_PE=3_SV=2	2.00E-24	GO:0000166,GO:0000943,GO:0003676,GO:0003677,GO:0003723,GO:0003723,GO:0003824,GO:0003887,GO:0003887,GO:0003887,GO:0003964,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0004523,GO:0004540,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006278,GO:0006278,GO:0006278,GO:0006310,GO:0006508,GO:0008152,GO:0008233,GO:0008233,GO:0008270,GO:0015074,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0019076,GO:0032197,GO:0046872,GO:0071897,GO:0071897,GO:0071897,GO:0090305,GO:0090305,GO:0090501,GO:0090502	nucleotide binding,retrotransposon nucleocapsid,nucleic acid binding,DNA binding,RNA binding,RNA binding,catalytic activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-DNA hybrid ribonuclease activity,ribonuclease activity,ATP binding,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,RNA-dependent DNA replication,RNA-dependent DNA replication,RNA-dependent DNA replication,DNA recombination,proteolysis,metabolic process,peptidase activity,peptidase activity,zinc ion binding,DNA integration,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,viral release from host cell,transposition, RNA-mediated,metal ion binding,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis,RNA phosphodiester bond hydrolysis,RNA phosphodiester bond hydrolysis, endonucleolytic
comp33296_c1_seq7.p11	sp|P10394|POL4_DROME_Retrovirus-related_Pol_polyprotein_from_transposon_412_OS=Drosophila_melanogaster_GN=POL_PE=4_SV=1	4.00E-16	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0006508,GO:0008233,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,proteolysis,peptidase activity,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp33296_c1_seq7.p2				
comp33296_c1_seq7.p3				
comp33299_c0_seq1.p1	sp|Q7XZQ8|FNSI_PETCR_Flavone_synthase_OS=Petroselinum_crispum_GN=FNSI_PE=1_SV=1	2.00E-37	GO:0005737,GO:0005737,GO:0009813,GO:0009813,GO:0016491,GO:0016491,GO:0016706,GO:0031418,GO:0033759,GO:0046872,GO:0051553,GO:0055114,GO:0055114	cytoplasm,cytoplasm,flavonoid biosynthetic process,flavonoid biosynthetic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,L-ascorbic acid binding,flavone synthase activity,metal ion binding,flavone biosynthetic process,oxidation-reduction process,oxidation-reduction process
comp33315_c0_seq1.p1				
comp33316_c0_seq1.p1				
comp33320_c0_seq1.p1	sp|Q54HW1|PSD10_DICDI_26S_proteasome_non-ATPase_regulatory_subunit_10_OS=Dictyostelium_discoideum_GN=psmD10_PE=2_SV=1	2.00E-17	GO:0003674,GO:0008150	molecular_function,biological_process
comp33331_c0_seq1.p1				
comp33340_c0_seq1.p2				
comp33351_c0_seq1.p2				
comp33358_c0_seq1.p1	sp|P46283|S17P_ARATH_Sedoheptulose-1,7-bisphosphatase,_chloroplastic_OS=Arabidopsis_thaliana_GN=At3g55800_PE=1_SV=1	1.00E-82	GO:0000023,GO:0000165,GO:0005975,GO:0005975,GO:0005986,GO:0006098,GO:0006364,GO:0006612,GO:0009409,GO:0009507,GO:0009507,GO:0009507,GO:0009507,GO:0009536,GO:0009570,GO:0009570,GO:0009570,GO:0009579,GO:0009595,GO:0009657,GO:0009697,GO:0009773,GO:0009814,GO:0009862,GO:0009867,GO:0009941,GO:0010103,GO:0010200,GO:0010207,GO:0010310,GO:0010363,GO:0016051,GO:0016311,GO:0016311,GO:0016311,GO:0016787,GO:0019252,GO:0019252,GO:0019253,GO:0019253,GO:0019253,GO:0019288,GO:0019344,GO:0019684,GO:0019760,GO:0019761,GO:0031348,GO:0035304,GO:0042132,GO:0042578,GO:0042742,GO:0042742,GO:0043085,GO:0043900,GO:0046872,GO:0048046,GO:0050278,GO:0050278,GO:0050832	maltose metabolic process,MAPK cascade,carbohydrate metabolic process,carbohydrate metabolic process,sucrose biosynthetic process,pentose-phosphate shunt,rRNA processing,protein targeting to membrane,response to cold,chloroplast,chloroplast,chloroplast,chloroplast,plastid,chloroplast stroma,chloroplast stroma,chloroplast stroma,thylakoid,detection of biotic stimulus,plastid organization,salicylic acid biosynthetic process,photosynthetic electron transport in photosystem I,defense response, incompatible interaction,systemic acquired resistance, salicylic acid mediated signaling pathway,jasmonic acid mediated signaling pathway,chloroplast envelope,stomatal complex morphogenesis,response to chitin,photosystem II assembly,regulation of hydrogen peroxide metabolic process,regulation of plant-type hypersensitive response,carbohydrate biosynthetic process,dephosphorylation,dephosphorylation,dephosphorylation,hydrolase activity,starch biosynthetic process,starch biosynthetic process,reductive pentose-phosphate cycle,reductive pentose-phosphate cycle,reductive pentose-phosphate cycle,isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway,cysteine biosynthetic process,photosynthesis, light reaction,glucosinolate metabolic process,glucosinolate biosynthetic process,negative regulation of defense response,regulation of protein dephosphorylation,fructose 1,6-bisphosphate 1-phosphatase activity,phosphoric ester hydrolase activity,defense response to bacterium,defense response to bacterium,positive regulation of catalytic activity,regulation of multi-organism process,metal ion binding,apoplast,sedoheptulose-bisphosphatase activity,sedoheptulose-bisphosphatase activity,defense response to fungus
comp33360_c0_seq1.p2				
comp33361_c0_seq1.p1	sp|Q3SZD7|CBR1_BOVIN_Carbonyl_reductase_[NADPH]_1_OS=Bos_taurus_GN=CBR1_PE=2_SV=1	2.00E-72	GO:0004090,GO:0004090,GO:0005737,GO:0005737,GO:0008152,GO:0016491,GO:0016491,GO:0017144,GO:0042373,GO:0047021,GO:0050221,GO:0055114	carbonyl reductase (NADPH) activity,carbonyl reductase (NADPH) activity,cytoplasm,cytoplasm,metabolic process,oxidoreductase activity,oxidoreductase activity,drug metabolic process,vitamin K metabolic process,15-hydroxyprostaglandin dehydrogenase (NADP+) activity,prostaglandin-E2 9-reductase activity,oxidation-reduction process
comp33367_c0_seq1.p2				
comp33389_c0_seq1.p1				
comp33390_c0_seq1.p1				
comp33392_c0_seq1.p1				
comp33399_c0_seq1.p1				
comp3341_c0_seq1.p1				
comp33417_c0_seq1.p1	sp|P52012|CYP4_CAEEL_Peptidyl-prolyl_cis-trans_isomerase_4_OS=Caenorhabditis_elegans_GN=cyn-4_PE=1_SV=3	6.00E-96	GO:0000209,GO:0000413,GO:0000413,GO:0003755,GO:0003755,GO:0003755,GO:0003755,GO:0004842,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0006457,GO:0007275,GO:0007548,GO:0016567,GO:0016567,GO:0016853,GO:0016874,GO:0030154,GO:0034450,GO:0040022	protein polyubiquitination,protein peptidyl-prolyl isomerization,protein peptidyl-prolyl isomerization,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,ubiquitin-protein transferase activity,protein binding,protein binding,nucleus,nucleus,nucleus,protein folding,multicellular organismal development,sex differentiation,protein ubiquitination,protein ubiquitination,isomerase activity,ligase activity,cell differentiation,ubiquitin-ubiquitin ligase activity,feminization of hermaphroditic germ-line
comp33424_c0_seq1.p1				
comp33425_c0_seq1.p1	sp|Q6PEI7|PYRG1_DANRE_CTP_synthase_1_OS=Danio_rerio_GN=ctps_PE=1_SV=1	0	GO:0000166,GO:0003883,GO:0003883,GO:0003883,GO:0005524,GO:0006221,GO:0006221,GO:0006241,GO:0006541,GO:0016874,GO:0044210	nucleotide binding,CTP synthase activity,CTP synthase activity,CTP synthase activity,ATP binding,pyrimidine nucleotide biosynthetic process,pyrimidine nucleotide biosynthetic process,CTP biosynthetic process,glutamine metabolic process,ligase activity,'de novo' CTP biosynthetic process
comp33437_c0_seq1.p1				
comp33450_c0_seq1.p1				
comp33451_c0_seq1.p1	sp|A8KBL5|S38AB_DANRE_Putative_sodium-coupled_neutral_amino_acid_transporter_11_OS=Danio_rerio_GN=slc38a11_PE=2_SV=2	1.00E-35	GO:0003333,GO:0005783,GO:0006810,GO:0006811,GO:0006814,GO:0006865,GO:0015171,GO:0016020,GO:0016020,GO:0016021	amino acid transmembrane transport,endoplasmic reticulum,transport,ion transport,sodium ion transport,amino acid transport,amino acid transmembrane transporter activity,membrane,membrane,integral component of membrane
comp33451_c0_seq1.p3				
comp33458_c0_seq1.p2	sp|P50567|H2A_CHLRE_Histone_H2A_OS=Chlamydomonas_reinhardtii_GN=H2A-II_PE=3_SV=1	6.00E-57	GO:0000786,GO:0000786,GO:0003677,GO:0003677,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0046982	nucleosome,nucleosome,DNA binding,DNA binding,nucleus,nucleus,nucleus,chromosome,chromosome,protein heterodimerization activity
comp33461_c0_seq1.p1	sp|Q9FJX2|RL262_ARATH_60S_ribosomal_protein_L26-2_OS=Arabidopsis_thaliana_GN=RPL26B_PE=2_SV=1	2.00E-54	GO:0003735,GO:0005515,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0015934,GO:0022625,GO:0022626,GO:0030529	structural constituent of ribosome,protein binding,intracellular,ribosome,ribosome,translation,large ribosomal subunit,cytosolic large ribosomal subunit,cytosolic ribosome,ribonucleoprotein complex
comp33468_c0_seq1.p1				
comp33478_c0_seq1.p1				
comp33488_c0_seq1.p1				
comp33492_c0_seq1.p1	sp|P82887|H2B_OLILU_Histone_H2B_OS=Olisthodiscus_luteus_PE=1_SV=2	4.00E-52	GO:0000786,GO:0000786,GO:0003677,GO:0003677,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0046982	nucleosome,nucleosome,DNA binding,DNA binding,nucleus,nucleus,nucleus,chromosome,chromosome,protein heterodimerization activity
comp33494_c0_seq1.p2	sp|P31753|RS27A_ASPOF_Ubiquitin-40S_ribosomal_protein_S27a_(Fragment)_OS=Asparagus_officinalis_PE=3_SV=2	8.00E-20	GO:0003735,GO:0005622,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005840,GO:0005840,GO:0006412,GO:0030529,GO:0046872	structural constituent of ribosome,intracellular,nucleus,nucleus,cytoplasm,cytoplasm,ribosome,ribosome,translation,ribonucleoprotein complex,metal ion binding
comp33496_c0_seq1.p2	sp|B4EY52|GPMB_PROMH_Probable_phosphoglycerate_mutase_GpmB_OS=Proteus_mirabilis_(strain_HI4320)_GN=gpmB_PE=3_SV=1	7.00E-13	GO:0003824,GO:0004619,GO:0004619,GO:0006096,GO:0006096,GO:0006096,GO:0006096,GO:0008152,GO:0016853	catalytic activity,phosphoglycerate mutase activity,phosphoglycerate mutase activity,glycolytic process,glycolytic process,glycolytic process,glycolytic process,metabolic process,isomerase activity
comp33497_c0_seq1.p1	sp|P0AEZ6|MIND_SHIFL_Septum_site-determining_protein_MinD_OS=Shigella_flexneri_GN=minD_PE=3_SV=2	3.00E-92	GO:0000166,GO:0000917,GO:0000918,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0006200,GO:0007049,GO:0016020,GO:0016887,GO:0051301	nucleotide binding,barrier septum assembly,barrier septum site selection,ATP binding,plasma membrane,plasma membrane,plasma membrane,ATP catabolic process,cell cycle,membrane,ATPase activity,cell division
comp33498_c0_seq1.p1	sp|Q3SYZ6|XYLB_BOVIN_Xylulose_kinase_OS=Bos_taurus_GN=XYLB_PE=2_SV=1	5.00E-102	GO:0000166,GO:0004856,GO:0004856,GO:0004856,GO:0005524,GO:0005975,GO:0005975,GO:0005997,GO:0005997,GO:0016301,GO:0016310,GO:0016740,GO:0016773,GO:0042732,GO:0046835,GO:0046835,GO:0046835,GO:0070062	nucleotide binding,xylulokinase activity,xylulokinase activity,xylulokinase activity,ATP binding,carbohydrate metabolic process,carbohydrate metabolic process,xylulose metabolic process,xylulose metabolic process,kinase activity,phosphorylation,transferase activity,phosphotransferase activity, alcohol group as acceptor,D-xylose metabolic process,carbohydrate phosphorylation,carbohydrate phosphorylation,carbohydrate phosphorylation,extracellular vesicular exosome
comp33508_c0_seq1.p1				
comp33509_c0_seq1.p1				
comp33513_c0_seq1.p1	sp|P18426|SCR11_OMMSL_S-crystallin_SL11_OS=Ommastrephes_sloanei_PE=2_SV=1	1.00E-11	GO:0005212	structural constituent of eye lens
comp33515_c0_seq1.p1				
comp3352_c0_seq1.p1				
comp33524_c0_seq1.p1				
comp33525_c0_seq1.p1				
comp33526_c0_seq1.p1	sp|P07742|RIR1_MOUSE_Ribonucleoside-diphosphate_reductase_large_subunit_OS=Mus_musculus_GN=Rrm1_PE=1_SV=2	0	GO:0000166,GO:0000278,GO:0003824,GO:0004748,GO:0004748,GO:0004748,GO:0005515,GO:0005524,GO:0005524,GO:0005635,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006206,GO:0006260,GO:0006260,GO:0006260,GO:0008152,GO:0008584,GO:0009263,GO:0010212,GO:0016491,GO:0017076,GO:0021846,GO:0042995,GO:0043025,GO:0051259,GO:0051290,GO:0055114,GO:0055114,GO:0060041,GO:0070062,GO:0004748	nucleotide binding,mitotic cell cycle,catalytic activity,ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor,ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor,ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor,protein binding,ATP binding,ATP binding,nuclear envelope,cytoplasm,cytoplasm,cytoplasm,cytoplasm,pyrimidine nucleobase metabolic process,DNA replication,DNA replication,DNA replication,metabolic process,male gonad development,deoxyribonucleotide biosynthetic process,response to ionizing radiation,oxidoreductase activity,purine nucleotide binding,cell proliferation in forebrain,cell projection,neuronal cell body,protein oligomerization,protein heterotetramerization,oxidation-reduction process,oxidation-reduction process,retina development in camera-type eye,extracellular vesicular exosome,ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor
comp33527_c0_seq1.p1				
comp33540_c0_seq1.p1				
comp33542_c0_seq1.p1				
comp33543_c0_seq1.p1				
comp33546_c0_seq1.p1				
comp33547_c0_seq1.p2				
comp33551_c0_seq1.p1				
comp33552_c0_seq1.p1	sp|O05389|YRBE_BACSU_Uncharacterized_oxidoreductase_yrbE_OS=Bacillus_subtilis_GN=yrbE_PE=3_SV=2	2.00E-89	GO:0008152,GO:0016491,GO:0016491,GO:0055114,GO:0055114	metabolic process,oxidoreductase activity,oxidoreductase activity,oxidation-reduction process,oxidation-reduction process
comp33555_c0_seq1.p1	sp|B5DE73|ASPH2_XENTR_Aspartate_beta-hydroxylase_domain-containing_protein_2_OS=Xenopus_tropicalis_GN=asphd2_PE=2_SV=1	6.00E-14	GO:0016020,GO:0016020,GO:0016021,GO:0016491,GO:0018193,GO:0046872,GO:0051213,GO:0055114	membrane,membrane,integral component of membrane,oxidoreductase activity,peptidyl-amino acid modification,metal ion binding,dioxygenase activity,oxidation-reduction process
comp33559_c0_seq1.p1	sp|Q2W4C4|EFTS_MAGSA_Elongation_factor_Ts_OS=Magnetospirillum_magneticum_(strain_AMB-1_/_ATCC_700264)_GN=tsf_PE=3_SV=1	4.00E-54	GO:0003746,GO:0003746,GO:0003746,GO:0005622,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006414,GO:0006414,GO:0006414	translation elongation factor activity,translation elongation factor activity,translation elongation factor activity,intracellular,cytoplasm,cytoplasm,cytoplasm,translation,translational elongation,translational elongation,translational elongation
comp33563_c0_seq1.p1				
comp33564_c0_seq1.p1				
comp33565_c0_seq1.p1				
comp33568_c0_seq1.p1	sp|Q58536|Y1136_METJA_Uncharacterized_protein_MJ1136_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ1136_PE=4_SV=1	1.00E-89	GO:0003824,GO:0008080,GO:0008152,GO:0008152,GO:0051536	catalytic activity,N-acetyltransferase activity,metabolic process,metabolic process,iron-sulfur cluster binding
comp3357_c0_seq1.p2	sp|Q9I2V5|ACON2_PSEAE_Aconitate_hydratase_2_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=acnB_PE=3_SV=1	3.00E-99	GO:0003994,GO:0003994,GO:0005829,GO:0006099,GO:0006099,GO:0006099,GO:0008152,GO:0016829,GO:0046872,GO:0047456,GO:0051536,GO:0051539,GO:0051539	aconitate hydratase activity,aconitate hydratase activity,cytosol,tricarboxylic acid cycle,tricarboxylic acid cycle,tricarboxylic acid cycle,metabolic process,lyase activity,metal ion binding,2-methylisocitrate dehydratase activity,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,4 iron, 4 sulfur cluster binding
comp33570_c0_seq1.p1	sp|P43156|CYSP_HEMSP_Thiol_protease_SEN102_OS=Hemerocallis_sp._GN=SEN102_PE=2_SV=1	5.00E-81	GO:0005783,GO:0005788,GO:0006508,GO:0006508,GO:0008233,GO:0008234,GO:0008234,GO:0016787	endoplasmic reticulum,endoplasmic reticulum lumen,proteolysis,proteolysis,peptidase activity,cysteine-type peptidase activity,cysteine-type peptidase activity,hydrolase activity
comp33572_c0_seq1.p1				
comp33576_c0_seq1.p1				
comp33577_c0_seq1.p1				
comp33579_c0_seq1.p2				
comp33581_c0_seq1.p1	sp|P40940|ARF3_ARATH_ADP-ribosylation_factor_3_OS=Arabidopsis_thaliana_GN=ARF3_PE=1_SV=2	6.00E-77	GO:0000166,GO:0005515,GO:0005515,GO:0005515,GO:0005525,GO:0005525,GO:0005622,GO:0005794,GO:0005794,GO:0005795,GO:0005886,GO:0005886,GO:0006810,GO:0007264,GO:0015031,GO:0016020,GO:0016192,GO:0030244,GO:0046686,GO:0048193	nucleotide binding,protein binding,protein binding,protein binding,GTP binding,GTP binding,intracellular,Golgi apparatus,Golgi apparatus,Golgi stack,plasma membrane,plasma membrane,transport,small GTPase mediated signal transduction,protein transport,membrane,vesicle-mediated transport,cellulose biosynthetic process,response to cadmium ion,Golgi vesicle transport
comp33584_c0_seq1.p1	sp|Q9LT08|PSDE_ARATH_26S_proteasome_non-ATPase_regulatory_subunit_14_OS=Arabidopsis_thaliana_GN=RPN11_PE=1_SV=1	3.00E-165	GO:0000502,GO:0000502,GO:0005634,GO:0005829,GO:0006096,GO:0006499,GO:0006508,GO:0006511,GO:0006623,GO:0006635,GO:0006833,GO:0006972,GO:0007030,GO:0008233,GO:0008237,GO:0009266,GO:0009407,GO:0009640,GO:0009651,GO:0009651,GO:0009853,GO:0010388,GO:0016787,GO:0030163,GO:0043161,GO:0043248,GO:0046686,GO:0046872,GO:0051788,GO:0080129	proteasome complex,proteasome complex,nucleus,cytosol,glycolytic process,N-terminal protein myristoylation,proteolysis,ubiquitin-dependent protein catabolic process,protein targeting to vacuole,fatty acid beta-oxidation,water transport,hyperosmotic response,Golgi organization,peptidase activity,metallopeptidase activity,response to temperature stimulus,toxin catabolic process,photomorphogenesis,response to salt stress,response to salt stress,photorespiration,cullin deneddylation,hydrolase activity,protein catabolic process,proteasome-mediated ubiquitin-dependent protein catabolic process,proteasome assembly,response to cadmium ion,metal ion binding,response to misfolded protein,proteasome core complex assembly
comp33590_c0_seq1.p1	sp|P41753|HSP70_ACHKL_Heat_shock_70_kDa_protein_OS=Achlya_klebsiana_GN=HSP70_PE=2_SV=1	6.00E-61	GO:0000166,GO:0005524	nucleotide binding,ATP binding
comp33593_c0_seq1.p1	sp|Q9P7F1|YKK5_SCHPO_Carbohydrate-binding_domain-containing_protein_C2E1P3.05c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC2E1P3.05c_PE=2_SV=1	8.00E-14	GO:0004553,GO:0005576,GO:0005576,GO:0005576,GO:0005975,GO:0009986,GO:0030248,GO:0046379	hydrolase activity, hydrolyzing O-glycosyl compounds,extracellular region,extracellular region,extracellular region,carbohydrate metabolic process,cell surface,cellulose binding,extracellular polysaccharide metabolic process
comp33598_c0_seq1.p1				
comp33599_c0_seq1.p1				
comp33600_c0_seq1.p1				
comp33605_c0_seq1.p1	sp|Q5RDP9|AP3S2_PONAB_AP-3_complex_subunit_sigma-2_OS=Pongo_abelii_GN=AP3S2_PE=2_SV=1	3.00E-63	GO:0005794,GO:0005794,GO:0006810,GO:0006810,GO:0006886,GO:0008089,GO:0008089,GO:0008565,GO:0015031,GO:0015031,GO:0016020,GO:0016192,GO:0030117,GO:0030123,GO:0030659,GO:0031410,GO:0048490,GO:0048490	Golgi apparatus,Golgi apparatus,transport,transport,intracellular protein transport,anterograde axon cargo transport,anterograde axon cargo transport,protein transporter activity,protein transport,protein transport,membrane,vesicle-mediated transport,membrane coat,AP-3 adaptor complex,cytoplasmic vesicle membrane,cytoplasmic vesicle,anterograde synaptic vesicle transport,anterograde synaptic vesicle transport
comp33608_c0_seq1.p1	sp|P36958|RPB9_DROME_DNA-directed_RNA_polymerase_II_subunit_RPB9_OS=Drosophila_melanogaster_GN=RpII15_PE=2_SV=2	9.00E-32	GO:0001193,GO:0003676,GO:0003677,GO:0003899,GO:0003899,GO:0003899,GO:0005634,GO:0005634,GO:0005634,GO:0005665,GO:0005665,GO:0005665,GO:0006283,GO:0006351,GO:0006366,GO:0006367,GO:0007067,GO:0007095,GO:0008270,GO:0022008,GO:0046872	maintenance of transcriptional fidelity during DNA-templated transcription elongation from RNA polymerase II promoter,nucleic acid binding,DNA binding,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,nucleus,nucleus,nucleus,DNA-directed RNA polymerase II, core complex,DNA-directed RNA polymerase II, core complex,DNA-directed RNA polymerase II, core complex,transcription-coupled nucleotide-excision repair,transcription, DNA-templated,transcription from RNA polymerase II promoter,transcription initiation from RNA polymerase II promoter,mitotic nuclear division,mitotic G2 DNA damage checkpoint,zinc ion binding,neurogenesis,metal ion binding
comp33610_c0_seq1.p1	sp|O60551|NMT2_HUMAN_Glycylpeptide_N-tetradecanoyltransferase_2_OS=Homo_sapiens_GN=NMT2_PE=1_SV=1	2.00E-149	GO:0004379,GO:0004379,GO:0004379,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005794,GO:0005829,GO:0005829,GO:0005886,GO:0006499,GO:0007603,GO:0016032,GO:0016032,GO:0016032,GO:0016056,GO:0016740,GO:0016746,GO:0018008,GO:0019068,GO:0019082,GO:0019898,GO:0022400,GO:0075733	glycylpeptide N-tetradecanoyltransferase activity,glycylpeptide N-tetradecanoyltransferase activity,glycylpeptide N-tetradecanoyltransferase activity,cytoplasm,cytoplasm,cytoplasm,cytoplasm,Golgi apparatus,cytosol,cytosol,plasma membrane,N-terminal protein myristoylation,phototransduction, visible light,viral process,viral process,viral process,rhodopsin mediated signaling pathway,transferase activity,transferase activity, transferring acyl groups,N-terminal peptidyl-glycine N-myristoylation,virion assembly,viral protein processing,extrinsic component of membrane,regulation of rhodopsin mediated signaling pathway,intracellular transport of virus
comp33613_c0_seq1.p1	sp|Q5F457|WBP4_CHICK_WW_domain-binding_protein_4_OS=Gallus_gallus_GN=WBP4_PE=2_SV=1	5.00E-12	GO:0003676,GO:0005634,GO:0005634,GO:0005681,GO:0006397,GO:0008270,GO:0008380,GO:0016607,GO:0046872	nucleic acid binding,nucleus,nucleus,spliceosomal complex,mRNA processing,zinc ion binding,RNA splicing,nuclear speck,metal ion binding
comp33614_c0_seq1.p1	sp|Q56ZQ3|VSR4_ARATH_Vacuolar-sorting_receptor_4_OS=Arabidopsis_thaliana_GN=VSR4_PE=2_SV=2	2.00E-62	GO:0000139,GO:0005509,GO:0005768,GO:0005773,GO:0005794,GO:0005794,GO:0005794,GO:0005802,GO:0006623,GO:0006810,GO:0015031,GO:0016020,GO:0016020,GO:0016021,GO:0030665,GO:0031410,GO:0031902	Golgi membrane,calcium ion binding,endosome,vacuole,Golgi apparatus,Golgi apparatus,Golgi apparatus,trans-Golgi network,protein targeting to vacuole,transport,protein transport,membrane,membrane,integral component of membrane,clathrin-coated vesicle membrane,cytoplasmic vesicle,late endosome membrane
comp33616_c0_seq1.p1	sp|Q9Y2E8|SL9A8_HUMAN_Sodium/hydrogen_exchanger_8_OS=Homo_sapiens_GN=SLC9A8_PE=1_SV=4	3.00E-70	GO:0000139,GO:0000139,GO:0005794,GO:0005794,GO:0006810,GO:0006811,GO:0006811,GO:0006812,GO:0006813,GO:0006814,GO:0006814,GO:0006814,GO:0006885,GO:0015297,GO:0015299,GO:0015385,GO:0015385,GO:0015386,GO:0016020,GO:0016021,GO:0016021,GO:0035725,GO:0035725,GO:0051453,GO:0055085,GO:0055085,GO:0055085,GO:0071805,GO:1902600	Golgi membrane,Golgi membrane,Golgi apparatus,Golgi apparatus,transport,ion transport,ion transport,cation transport,potassium ion transport,sodium ion transport,sodium ion transport,sodium ion transport,regulation of pH,antiporter activity,solute:proton antiporter activity,sodium:proton antiporter activity,sodium:proton antiporter activity,potassium:proton antiporter activity,membrane,integral component of membrane,integral component of membrane,sodium ion transmembrane transport,sodium ion transmembrane transport,regulation of intracellular pH,transmembrane transport,transmembrane transport,transmembrane transport,potassium ion transmembrane transport,hydrogen ion transmembrane transport
comp33618_c0_seq1.p1				
comp33619_c0_seq1.p1	sp|A4FV84|MRT4_BOVIN_mRNA_turnover_protein_4_homolog_OS=Bos_taurus_GN=MRTO4_PE=2_SV=1	3.00E-58	GO:0005622,GO:0005634,GO:0005634,GO:0005730,GO:0005730,GO:0005737,GO:0005737,GO:0031965,GO:0042254,GO:0042254,GO:0044822	intracellular,nucleus,nucleus,nucleolus,nucleolus,cytoplasm,cytoplasm,nuclear membrane,ribosome biogenesis,ribosome biogenesis,poly(A) RNA binding
comp33620_c0_seq1.p1				
comp33621_c0_seq1.p1	sp|P67779|PHB_RAT_Prohibitin_OS=Rattus_norvegicus_GN=Phb_PE=1_SV=1	5.00E-89	GO:0000122,GO:0000981,GO:0001541,GO:0001552,GO:0003674,GO:0005634,GO:0005634,GO:0005737,GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005743,GO:0006366,GO:0008285,GO:0016020,GO:0016020,GO:0030061,GO:0031100,GO:0031315,GO:0034097,GO:0035902,GO:0042493,GO:0043066,GO:0043434,GO:0045471,GO:0071897,GO:0071897	negative regulation of transcription from RNA polymerase II promoter,sequence-specific DNA binding RNA polymerase II transcription factor activity,ovarian follicle development,ovarian follicle atresia,molecular_function,nucleus,nucleus,cytoplasm,mitochondrion,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial inner membrane,transcription from RNA polymerase II promoter,negative regulation of cell proliferation,membrane,membrane,mitochondrial crista,organ regeneration,extrinsic component of mitochondrial outer membrane,response to cytokine,response to immobilization stress,response to drug,negative regulation of apoptotic process,response to peptide hormone,response to ethanol,DNA biosynthetic process,DNA biosynthetic process
comp33624_c0_seq1.p1	sp|O36032|GLRX1_SCHPO_Glutaredoxin-1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=grx1_PE=2_SV=1	1.00E-25	GO:0004364,GO:0004602,GO:0005634,GO:0005829,GO:0005829,GO:0009055,GO:0015035,GO:0015035,GO:0019430,GO:0045454,GO:0055114,GO:0071294,GO:0034605	glutathione transferase activity,glutathione peroxidase activity,nucleus,cytosol,cytosol,electron carrier activity,protein disulfide oxidoreductase activity,protein disulfide oxidoreductase activity,removal of superoxide radicals,cell redox homeostasis,oxidation-reduction process,cellular response to zinc ion,cellular response to heat
comp33629_c0_seq1.p1	sp|O00835|ERCC3_DICDI_TFIIH_basal_transcription_factor_complex_helicase_repB_subunit_OS=Dictyostelium_discoideum_GN=repB_PE=2_SV=1	0	GO:0000166,GO:0003677,GO:0003677,GO:0004003,GO:0004386,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005675,GO:0006281,GO:0006289,GO:0006289,GO:0006351,GO:0006355,GO:0006366,GO:0006974,GO:0006974,GO:0006974,GO:0009650,GO:0016787,GO:0016787,GO:0032508	nucleotide binding,DNA binding,DNA binding,ATP-dependent DNA helicase activity,helicase activity,ATP binding,ATP binding,nucleus,nucleus,holo TFIIH complex,DNA repair,nucleotide-excision repair,nucleotide-excision repair,transcription, DNA-templated,regulation of transcription, DNA-templated,transcription from RNA polymerase II promoter,cellular response to DNA damage stimulus,cellular response to DNA damage stimulus,cellular response to DNA damage stimulus,UV protection,hydrolase activity,hydrolase activity,DNA duplex unwinding
comp33633_c0_seq1.p1				
comp33635_c0_seq1.p2				
comp33636_c0_seq1.p1				
comp33638_c0_seq1.p1				
comp33640_c0_seq1.p1				
comp33641_c0_seq1.p1				
comp33642_c0_seq1.p1	sp|Q6UB99|ANR11_HUMAN_Ankyrin_repeat_domain-containing_protein_11_OS=Homo_sapiens_GN=ANKRD11_PE=1_SV=3	2.00E-17	GO:0001701,GO:0001894,GO:0005634,GO:0005634,GO:0005634,GO:0005634,GO:0005654,GO:0005737,GO:0005886,GO:0035264,GO:0042475,GO:0048705,GO:0048705,GO:0060323,GO:0060325,GO:0060348	in utero embryonic development,tissue homeostasis,nucleus,nucleus,nucleus,nucleus,nucleoplasm,cytoplasm,plasma membrane,multicellular organism growth,odontogenesis of dentin-containing tooth,skeletal system morphogenesis,skeletal system morphogenesis,head morphogenesis,face morphogenesis,bone development
comp33643_c0_seq1.p1	sp|Q4QQW1|REEP4_RAT_Receptor_expression-enhancing_protein_4_OS=Rattus_norvegicus_GN=Reep4_PE=2_SV=1	1.00E-25	GO:0005783,GO:0005783,GO:0005783,GO:0005789,GO:0005874,GO:0006998,GO:0006998,GO:0007049,GO:0007067,GO:0007084,GO:0007084,GO:0008017,GO:0016020,GO:0016021,GO:0051301	endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,microtubule,nuclear envelope organization,nuclear envelope organization,cell cycle,mitotic nuclear division,mitotic nuclear envelope reassembly,mitotic nuclear envelope reassembly,microtubule binding,membrane,integral component of membrane,cell division
comp33644_c0_seq1.p1				
comp33645_c0_seq1.p1	sp|Q08DT6|RM47_BOVIN_39S_ribosomal_protein_L47,_mitochondrial_OS=Bos_taurus_GN=MRPL47_PE=2_SV=1	2.00E-15	GO:0003735,GO:0005739,GO:0005739,GO:0005761,GO:0005840,GO:0006412,GO:0030529	structural constituent of ribosome,mitochondrion,mitochondrion,mitochondrial ribosome,ribosome,translation,ribonucleoprotein complex
comp33646_c0_seq1.p1				
comp33647_c0_seq1.p1	sp|Q6Z829|WEE1_ORYSJ_Wee1-like_protein_kinase_OS=Oryza_sativa_subsp._japonica_GN=WEE1_PE=2_SV=1	3.00E-59	GO:0000166,GO:0000166,GO:0000278,GO:0000280,GO:0000724,GO:0000911,GO:0004672,GO:0004672,GO:0004674,GO:0004674,GO:0004713,GO:0004713,GO:0004715,GO:0004715,GO:0005524,GO:0005524,GO:0005524,GO:0005634,GO:0006260,GO:0006261,GO:0006270,GO:0006275,GO:0006306,GO:0006468,GO:0006468,GO:0007049,GO:0007067,GO:0008283,GO:0009555,GO:0010389,GO:0016301,GO:0016301,GO:0016310,GO:0016310,GO:0016444,GO:0016568,GO:0016740,GO:0016740,GO:0016772,GO:0016772,GO:0018108,GO:0018108,GO:0018108,GO:0031047,GO:0042023,GO:0046872,GO:0046872,GO:0051225,GO:0051301,GO:0051567,GO:0051726	nucleotide binding,nucleotide binding,mitotic cell cycle,nuclear division,double-strand break repair via homologous recombination,cytokinesis by cell plate formation,protein kinase activity,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein tyrosine kinase activity,protein tyrosine kinase activity,non-membrane spanning protein tyrosine kinase activity,non-membrane spanning protein tyrosine kinase activity,ATP binding,ATP binding,ATP binding,nucleus,DNA replication,DNA-dependent DNA replication,DNA replication initiation,regulation of DNA replication,DNA methylation,protein phosphorylation,protein phosphorylation,cell cycle,mitotic nuclear division,cell proliferation,pollen development,regulation of G2/M transition of mitotic cell cycle,kinase activity,kinase activity,phosphorylation,phosphorylation,somatic cell DNA recombination,chromatin modification,transferase activity,transferase activity, transferring phosphorus-containing groups,transferase activity, transferring phosphorus-containing groups,peptidyl-tyrosine phosphorylation,peptidyl-tyrosine phosphorylation,peptidyl-tyrosine phosphorylation,gene silencing by RNA,DNA endoreduplication,metal ion binding,metal ion binding,spindle assembly,cell division,histone H3-K9 methylation,regulation of cell cycle
comp33648_c0_seq1.p1				
comp33649_c0_seq1.p1				
comp33650_c0_seq1.p1	sp|Q8LSN3|FYPP_PEA_Phytochrome-associated_serine/threonine-protein_phosphatase_OS=Pisum_sativum_GN=FYPP_PE=1_SV=1	1.00E-154	GO:0004721,GO:0004721,GO:0005737,GO:0005737,GO:0008152,GO:0008152,GO:0016311,GO:0016311,GO:0016787,GO:0016787,GO:0046872	phosphoprotein phosphatase activity,phosphoprotein phosphatase activity,cytoplasm,cytoplasm,metabolic process,metabolic process,dephosphorylation,dephosphorylation,hydrolase activity,hydrolase activity,metal ion binding
comp33651_c0_seq1.p1	sp|Q9C8J8|AB13G_ARATH_ABC_transporter_G_family_member_13_OS=Arabidopsis_thaliana_GN=ABCG13_PE=2_SV=1	2.00E-39	GO:0000166,GO:0005524,GO:0005524,GO:0006200,GO:0006810,GO:0009506,GO:0009651,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016887,GO:0080051,GO:0080172	nucleotide binding,ATP binding,ATP binding,ATP catabolic process,transport,plasmodesma,response to salt stress,membrane,membrane,membrane,integral component of membrane,ATPase activity,cutin transport,petal epidermis patterning
comp33652_c0_seq1.p1	sp|Q86V88|MGDP1_HUMAN_Magnesium-dependent_phosphatase_1_OS=Homo_sapiens_GN=MDP1_PE=1_SV=1	9.00E-12	GO:0004721,GO:0004725,GO:0008152,GO:0016311,GO:0016311,GO:0016787,GO:0016791,GO:0035335,GO:0046872,GO:0070062	phosphoprotein phosphatase activity,protein tyrosine phosphatase activity,metabolic process,dephosphorylation,dephosphorylation,hydrolase activity,phosphatase activity,peptidyl-tyrosine dephosphorylation,metal ion binding,extracellular vesicular exosome
comp33653_c0_seq1.p1				
comp33654_c0_seq1.p1	sp|Q9FF81|VPS36_ARATH_Vacuolar_protein_sorting-associated_protein_36_OS=Arabidopsis_thaliana_GN=VPS36_PE=1_SV=1	4.00E-56	GO:0000814,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005768,GO:0005768,GO:0006810,GO:0015031,GO:0032266,GO:0043130	ESCRT II complex,protein binding,protein binding,protein binding,protein binding,protein binding,endosome,endosome,transport,protein transport,phosphatidylinositol-3-phosphate binding,ubiquitin binding
comp33657_c0_seq1.p1	sp|Q9UKM7|MA1B1_HUMAN_Endoplasmic_reticulum_mannosyl-oligosaccharide_1,2-alpha-mannosidase_OS=Homo_sapiens_GN=MAN1B1_PE=1_SV=2	1.00E-135	GO:0004571,GO:0004571,GO:0004571,GO:0004571,GO:0004571,GO:0004571,GO:0005509,GO:0005509,GO:0005783,GO:0005783,GO:0005783,GO:0005789,GO:0006457,GO:0006486,GO:0006487,GO:0008152,GO:0009311,GO:0016020,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016787,GO:0016798,GO:0018279,GO:0030433,GO:0030433,GO:0031982,GO:0043687,GO:0044267,GO:0044322,GO:0044322,GO:0044322,GO:0044322	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity,mannosyl-oligosaccharide 1,2-alpha-mannosidase activity,mannosyl-oligosaccharide 1,2-alpha-mannosidase activity,mannosyl-oligosaccharide 1,2-alpha-mannosidase activity,mannosyl-oligosaccharide 1,2-alpha-mannosidase activity,mannosyl-oligosaccharide 1,2-alpha-mannosidase activity,calcium ion binding,calcium ion binding,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum,endoplasmic reticulum membrane,protein folding,protein glycosylation,protein N-linked glycosylation,metabolic process,oligosaccharide metabolic process,membrane,membrane,membrane,membrane,integral component of membrane,integral component of membrane,hydrolase activity,hydrolase activity, acting on glycosyl bonds,protein N-linked glycosylation via asparagine,ER-associated ubiquitin-dependent protein catabolic process,ER-associated ubiquitin-dependent protein catabolic process,vesicle,post-translational protein modification,cellular protein metabolic process,endoplasmic reticulum quality control compartment,endoplasmic reticulum quality control compartment,endoplasmic reticulum quality control compartment,endoplasmic reticulum quality control compartment
comp33658_c0_seq1.p1				
comp33660_c0_seq1.p1	sp|Q8H0U5|TIC62_ARATH_Protein_TIC_62,_chloroplastic_OS=Arabidopsis_thaliana_GN=TIC62_PE=1_SV=1	5.00E-14	GO:0006810,GO:0009507,GO:0009507,GO:0009507,GO:0009528,GO:0009534,GO:0009534,GO:0009535,GO:0009536,GO:0009570,GO:0009579,GO:0009706,GO:0009941,GO:0009941,GO:0010103,GO:0015031,GO:0016020,GO:0016556,GO:0019684	transport,chloroplast,chloroplast,chloroplast,plastid inner membrane,chloroplast thylakoid,chloroplast thylakoid,chloroplast thylakoid membrane,plastid,chloroplast stroma,thylakoid,chloroplast inner membrane,chloroplast envelope,chloroplast envelope,stomatal complex morphogenesis,protein transport,membrane,mRNA modification,photosynthesis, light reaction
comp33662_c0_seq1.p1				
comp33665_c0_seq1.p1				
comp33666_c0_seq1.p1				
comp33666_c0_seq1.p5				
comp33669_c0_seq1.p1				
comp33671_c0_seq1.p1				
comp33673_c0_seq1.p1	sp|P26640|SYVC_HUMAN_Valine--tRNA_ligase_OS=Homo_sapiens_GN=VARS_PE=1_SV=4	0	GO:0000166,GO:0000166,GO:0002161,GO:0004812,GO:0004812,GO:0004832,GO:0004832,GO:0004832,GO:0005524,GO:0005524,GO:0005739,GO:0005829,GO:0006412,GO:0006418,GO:0006418,GO:0006418,GO:0006438,GO:0006438,GO:0006450,GO:0010467,GO:0016874,GO:0005829	nucleotide binding,nucleotide binding,aminoacyl-tRNA editing activity,aminoacyl-tRNA ligase activity,aminoacyl-tRNA ligase activity,valine-tRNA ligase activity,valine-tRNA ligase activity,valine-tRNA ligase activity,ATP binding,ATP binding,mitochondrion,cytosol,translation,tRNA aminoacylation for protein translation,tRNA aminoacylation for protein translation,tRNA aminoacylation for protein translation,valyl-tRNA aminoacylation,valyl-tRNA aminoacylation,regulation of translational fidelity,gene expression,ligase activity,cytosol
comp33677_c0_seq1.p1				
comp33678_c0_seq1.p1	sp|P15690|NDUS1_BOVIN_NADH-ubiquinone_oxidoreductase_75_kDa_subunit,_mitochondrial_OS=Bos_taurus_GN=NDUFS1_PE=1_SV=1	2.00E-104	GO:0003954,GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005747,GO:0005747,GO:0005747,GO:0005758,GO:0005758,GO:0008137,GO:0008137,GO:0008137,GO:0008637,GO:0008637,GO:0009055,GO:0016020,GO:0016020,GO:0016491,GO:0016491,GO:0016651,GO:0042773,GO:0045333,GO:0045333,GO:0045333,GO:0046034,GO:0046034,GO:0046872,GO:0051536,GO:0051536,GO:0051537,GO:0051539,GO:0051881,GO:0051881,GO:0055114,GO:0055114,GO:0055114,GO:0070469,GO:0072593,GO:0072593,GO:0008137	NADH dehydrogenase activity,mitochondrion,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial respiratory chain complex I,mitochondrial respiratory chain complex I,mitochondrial respiratory chain complex I,mitochondrial intermembrane space,mitochondrial intermembrane space,NADH dehydrogenase (ubiquinone) activity,NADH dehydrogenase (ubiquinone) activity,NADH dehydrogenase (ubiquinone) activity,apoptotic mitochondrial changes,apoptotic mitochondrial changes,electron carrier activity,membrane,membrane,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on NAD(P)H,ATP synthesis coupled electron transport,cellular respiration,cellular respiration,cellular respiration,ATP metabolic process,ATP metabolic process,metal ion binding,iron-sulfur cluster binding,iron-sulfur cluster binding,2 iron, 2 sulfur cluster binding,4 iron, 4 sulfur cluster binding,regulation of mitochondrial membrane potential,regulation of mitochondrial membrane potential,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,respiratory chain,reactive oxygen species metabolic process,reactive oxygen species metabolic process,NADH dehydrogenase (ubiquinone) activity
comp33680_c0_seq1.p1	sp|Q6I5Y0|CDKC1_ORYSJ_Cyclin-dependent_kinase_C-1_OS=Oryza_sativa_subsp._japonica_GN=CDKC-1_PE=2_SV=1	3.00E-98	GO:0000166,GO:0004672,GO:0004674,GO:0004674,GO:0004693,GO:0005524,GO:0005524,GO:0006468,GO:0008353,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0051726	[illegible]

comp33681_c0_seq1.p1				
comp33684_c0_seq1.p1	sp|Q90965|RAB2A_CHICK_Ras-related_protein_Rab-2A_OS=Gallus_gallus_GN=RAB2A_PE=2_SV=1	8.00E-109	GO:0000139,GO:0000166,GO:0005525,GO:0005525,GO:0005765,GO:0005783,GO:0005789,GO:0005794,GO:0005794,GO:0006810,GO:0007264,GO:0015031,GO:0015031,GO:0016020,GO:0016192,GO:0019003,GO:0033116,GO:0070062	[illegible]
comp33688_c0_seq1.p1	sp|Q8SSN5|NAA20_DICDI_N-alpha-acetyltransferase_20_OS=Dictyostelium_discoideum_GN=nat5_PE=3_SV=2	3.00E-81	GO:0004596,GO:0004596,GO:0005737,GO:0008080,GO:0016740,GO:0016746,GO:0017196,GO:0017196,GO:0031416,GO:0044351	[illegible]
comp33691_c0_seq1.p1	sp|Q5EA26|DJC18_BOVIN_DnaJ_homolog_subfamily_C_member_18_OS=Bos_taurus_GN=DNAJC18_PE=2_SV=1	4.00E-22	GO:0016020,GO:0016020,GO:0016021	membrane,membrane,integral component of membrane
comp33695_c0_seq1.p1				
comp33697_c0_seq1.p1	sp|Q5R5S4|PSMD1_PONAB_26S_proteasome_non-ATPase_regulatory_subunit_1_OS=Pongo_abelii_GN=PSMD1_PE=2_SV=1	0	GO:0000502,GO:0000502,GO:0016020,GO:0022624,GO:0030234,GO:0042176,GO:0050790,GO:0070062	[illegible]
comp33700_c0_seq1.p1				
comp33701_c0_seq1.p1	sp|Q9D6Z1|NOP56_MOUSE_Nucleolar_protein_56_OS=Mus_musculus_GN=Nop56_PE=1_SV=2	2.00E-167	GO:0000154,GO:0005634,GO:0005654,GO:0005730,GO:0005730,GO:0005732,GO:0005737,GO:0005737,GO:0008150,GO:0016020,GO:0030515,GO:0030529,GO:0031428,GO:0042254,GO:0044822,GO:0070761	[illegible]
comp33704_c0_seq1.p1				
comp33705_c0_seq1.p1	sp|Q54T05|RIO2_DICDI_Serine/threonine-protein_kinase_rio2_OS=Dictyostelium_discoideum_GN=rio2_PE=3_SV=1	4.00E-114	GO:0000166,GO:0003824,GO:0004672,GO:0004674,GO:0004674,GO:0005524,GO:0005524,GO:0005524,GO:0005575,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006468,GO:0006468,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0042254	[illegible]
comp33708_c0_seq1.p1	sp|Q9MA15|Y1960_ARATH_Uncharacterized_aarF_domain-containing_protein_kinase_At1g79600,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g79600_PE=1_SV=1	2.00E-151	GO:0000166,GO:0004672,GO:0004672,GO:0005524,GO:0005524,GO:0006468,GO:0009507,GO:0009507,GO:0009536,GO:0010287,GO:0010287,GO:0010287,GO:0010287,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0050821,GO:1902171	[illegible]
comp33709_c0_seq1.p1	sp|Q5XFW8|SEC13_RAT_Protein_SEC13_homolog_OS=Rattus_norvegicus_GN=Sec13_PE=1_SV=1	2.00E-99	GO:0005634,GO:0005643,GO:0005643,GO:0005783,GO:0005789,GO:0006810,GO:0006810,GO:0006888,GO:0012507,GO:0015031,GO:0016020,GO:0016192,GO:0031080,GO:0031410,GO:0051028	[illegible]
comp33709_c0_seq1.p2	sp|Q9VTJ8|TIM14_DROME_Mitochondrial_import_inner_membrane_translocase_subunit_TIM14_OS=Drosophila_melanogaster_GN=Tim14_PE=3_SV=2	3.00E-22	GO:0001405,GO:0001671,GO:0005739,GO:0005743,GO:0005743,GO:0005744,GO:0006810,GO:0006810,GO:0015031,GO:0016020,GO:0016021,GO:0022008,GO:0030150,GO:0032781	[illegible]
comp33712_c0_seq1.p1	sp|B1XNQ1|PGK_SYNP2_Phosphoglycerate_kinase_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=pgk_PE=3_SV=1	0	GO:0000166,GO:0004618,GO:0004618,GO:0004618,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0006096,GO:0006096,GO:0006096,GO:0006096,GO:0016301,GO:0016310,GO:0016740	[illegible]
comp33714_c0_seq1.p3	sp|P62856|RS26_RAT_40S_ribosomal_protein_S26_OS=Rattus_norvegicus_GN=Rps26_PE=3_SV=3	5.00E-31	GO:0003674,GO:0003729,GO:0003735,GO:0005622,GO:0005730,GO:0005737,GO:0005840,GO:0005840,GO:0006412,GO:0008150,GO:0015935,GO:0016020,GO:0022627,GO:0022627,GO:0022627,GO:0030529,GO:0033119,GO:0044822,GO:0070062	[illegible]
comp33715_c0_seq1.p2				
comp33718_c0_seq1.p1	sp|O82314|U082_ARATH_Probable_transcriptional_regulatory_protein_At2g25830_OS=Arabidopsis_thaliana_GN=At2g25830_PE=2_SV=2	4.00E-39	GO:0009073,GO:0009507,GO:0016226,GO:0042819	[illegible]
comp33719_c0_seq1.p1				
comp33720_c0_seq1.p1	sp|Q5ZME8|SMU1_CHICK_WD40_repeat-containing_protein_SMU1_OS=Gallus_gallus_GN=SMU1_PE=2_SV=1	0	GO:0005634,GO:0005634,GO:0005737,GO:0005737	nucleus,nucleus,cytoplasm,cytoplasm
comp33721_c0_seq1.p1	sp|Q8VHE0|SEC63_MOUSE_Translocation_protein_SEC63_homolog_OS=Mus_musculus_GN=Sec63_PE=1_SV=4	7.00E-55	GO:0001889,GO:0001889,GO:0005783,GO:0005789,GO:0006614,GO:0006614,GO:0006614,GO:0006620,GO:0006620,GO:0006620,GO:0006807,GO:0006810,GO:0008565,GO:0010259,GO:0015031,GO:0016020,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0031204,GO:0044822,GO:0072001	[illegible]
comp33723_c0_seq1.p2	sp|O64644|SAP18_ARATH_Histone_deacetylase_complex_subunit_SAP18_OS=Arabidopsis_thaliana_GN=At2g45640_PE=1_SV=1	7.00E-34	GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005730,GO:0006351,GO:0006355,GO:0009062,GO:0009651,GO:0009737	[illegible]
comp33724_c0_seq1.p1	sp|Q1XDM1|ODPB_PORYE_Pyruvate_dehydrogenase_E1_component_subunit_beta_OS=Porphyra_yezoensis_GN=pdhB_PE=3_SV=1	2.00E-63	GO:0003824,GO:0004739,GO:0006096,GO:0008152,GO:0009507,GO:0009507,GO:0009536,GO:0016491,GO:0055114	[illegible]
comp33726_c0_seq1.p1	sp|Q9LD28|H2A6_ARATH_Histone_H2A.6_OS=Arabidopsis_thaliana_GN=RAT5_PE=1_SV=1	5.00E-33	GO:0000786,GO:0000786,GO:0003677,GO:0003677,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0005730,GO:0009294,GO:0009294,GO:0009611,GO:0009617,GO:0046982	[illegible]
comp33727_c0_seq1.p1				
comp33728_c0_seq1.p1	sp|Q2JWJ1|CLPP1_SYNJA_ATP-dependent_Clp_protease_proteolytic_subunit_1_OS=Synechococcus_sp._(strain_JA-3-3Ab)_GN=clpP1_PE=3_SV=1	2.00E-50	GO:0004252,GO:0004252,GO:0005737,GO:0005737,GO:0005737,GO:0006508,GO:0006508,GO:0006508,GO:0008233,GO:0008236,GO:0016787	[illegible]
comp33729_c0_seq1.p1				
comp33730_c0_seq1.p1	sp|Q8W593|LGUC_ARATH_Probable_lactoylglutathione_lyase,_chloroplast_OS=Arabidopsis_thaliana_GN=At1g67280_PE=2_SV=1	3.00E-79	[illegible]	[illegible]
comp33733_c0_seq1.p1				
comp33734_c0_seq1.p1				
comp33735_c0_seq1.p1				
comp33736_c0_seq1.p2				
comp33737_c0_seq1.p2				
comp33739_c0_seq1.p1				
comp3374_c0_seq1.p2	sp|O43014|MPI_SCHPO_Mannose-6-phosphate_isomerase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=pmi40_PE=2_SV=1	1.00E-38	[illegible]	[illegible]
comp33743_c0_seq1.p1	sp|Q58556|Y1156_METJA_Cell_division_cycle_protein_48_homolog_MJ1156_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ1156_PE=3_SV=1	2.00E-55	[illegible]	[illegible]
comp33745_c0_seq1.p1				
comp33748_c0_seq1.p1	sp|Q9SL67|PRS4B_ARATH_26S_proteasome_regulatory_subunit_4_homolog_B_OS=Arabidopsis_thaliana_GN=RPT2B_PE=2_SV=1	0	[illegible]	[illegible]
comp33750_c0_seq1.p1				
comp33751_c0_seq1.p1				
comp33752_c0_seq1.p1	sp|Q58455|Y1055_METJA_Uncharacterized_protein_MJ1055_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ1055_PE=3_SV=1	2.00E-71	[illegible]	[illegible]
comp33755_c0_seq1.p1				
comp33756_c0_seq1.p1	sp|P35567|CDK1A_XENLA_Cyclin-dependent_kinase_1-A_OS=Xenopus_laevis_GN=cdk1-a_PE=1_SV=1	4.00E-124	[illegible]	[illegible]
comp33756_c0_seq1.p4				
comp33760_c0_seq1.p1				
comp33761_c0_seq1.p1	sp|P78417|GSTO1_HUMAN_Glutathione_S-transferase_omega-1_OS=Homo_sapiens_GN=GSTO1_PE=1_SV=2	3.00E-11	[illegible]	[illegible]
comp33763_c0_seq1.p1				
comp33764_c0_seq1.p1	sp|Q6ICZ8|NACA3_ARATH_Nascent_polypeptide-associated_complex_subunit_alpha-like_protein_3_OS=Arabidopsis_thaliana_GN=At5g13850_PE=1_SV=1	8.00E-47	[illegible]	[illegible]
comp33765_c0_seq1.p1	sp|Q640T2|WIPI3_XENTR_WD_repeat_domain_phosphoinositide-interacting_protein_3_OS=Xenopus_tropicalis_GN=wdr45l_PE=2_SV=1	9.00E-11	[illegible]	[illegible]
comp33766_c0_seq1.p1				
comp33767_c0_seq1.p1	sp|Q6NY52|THOC5_DANRE_THO_complex_subunit_5_homolog_OS=Danio_rerio_GN=thoc5_PE=2_SV=1	1.00E-15	[illegible]	[illegible]
comp33771_c0_seq1.p1	sp|Q0VC06|LTV1_BOVIN_Protein_LTV1_homolog_OS=Bos_taurus_GN=LTV1_PE=2_SV=1	8.00E-24		
comp33772_c0_seq1.p1				
comp33774_c0_seq1.p1				
comp33775_c0_seq1.p1	sp|B6JH69|RRF_OLICO_Ribosome-recycling_factor_OS=Oligotropha_carboxidovorans_(strain_ATCC_49405_/_DSM_1227_/_OM5)_GN=frr_PE=3_SV=1	8.00E-29	[illegible]	[illegible]
comp33776_c0_seq1.p1	sp|O43181|NDUS4_HUMAN_NADH_dehydrogenase_[ubiquinone]_iron-sulfur_protein_4,_mitochondrial_OS=Homo_sapiens_GN=NDUFS4_PE=1_SV=1	3.00E-18	[illegible]	[illegible]
comp33777_c0_seq1.p1	sp|P73574|FABG1_SYNY3_3-oxoacyl-[acyl-carrier-protein]_reductase_1_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=fabG1_PE=3_SV=1	8.00E-96	[illegible]	[illegible]
comp33778_c0_seq1.p1	sp|Q9SYM5|RHM1_ARATH_Probable_rhamnose_biosynthetic_enzyme_1_OS=Arabidopsis_thaliana_GN=RHM1_PE=1_SV=1	2.00E-113	[illegible]	[illegible]
comp33779_c0_seq1.p1	sp|P42742|PSB1_ARATH_Proteasome_subunit_beta_type-1_OS=Arabidopsis_thaliana_GN=PBF1_PE=1_SV=2	1.00E-82	[illegible]	[illegible]
comp33783_c0_seq1.p1	sp|B7K8R0|RL28_CYAP7_50S_ribosomal_protein_L28_OS=Cyanothece_sp._(strain_PCC_7424)_GN=rpmB_PE=3_SV=1	3.00E-21	[illegible]	[illegible]
comp33786_c0_seq1.p1	sp|P55180|GALE_BACSU_UDP-glucose_4-epimerase_OS=Bacillus_subtilis_GN=galE_PE=3_SV=1	3.00E-147	[illegible]	[illegible]
comp33787_c0_seq1.p1	sp|O77622|TCPZ_RABIT_T-complex_protein_1_subunit_zeta_OS=Oryctolagus_cuniculus_GN=CCT6_PE=2_SV=3	0	[illegible]	[illegible]
comp33790_c0_seq1.p1	sp|Q8K203|NEIL3_MOUSE_Endonuclease_8-like_3_OS=Mus_musculus_GN=Neil3_PE=1_SV=1	3.00E-13	[illegible]	[illegible]
comp33791_c0_seq1.p4	sp|Q5XGC9|SRFB1_XENTR_Serum_response_factor-binding_protein_1_OS=Xenopus_tropicalis_GN=srfbp1_PE=2_SV=1	1.00E-11	[illegible]	[illegible]
comp33791_c0_seq2.p4				
comp33793_c0_seq1.p1	sp|Q9P2C4|TM181_HUMAN_Transmembrane_protein_181_OS=Homo_sapiens_GN=TMEM181_PE=1_SV=2	2.00E-15	[illegible]	[illegible]
comp33795_c0_seq1.p1				
comp33797_c0_seq1.p1	sp|Q01852|TIM44_YEAST_Mitochondrial_import_inner_membrane_translocase_subunit_TIM44_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TIM44_PE=1_SV=1	7.00E-20	[illegible]	[illegible]
comp33800_c0_seq1.p1				
comp33803_c0_seq1.p1	sp|P62282|RS11_RAT_40S_ribosomal_protein_S11_OS=Rattus_norvegicus_GN=Rps11_PE=1_SV=3	8.00E-67	[illegible]	[illegible]
comp33805_c0_seq1.p1				
comp33807_c0_seq1.p2				
comp33808_c0_seq1.p1	sp|Q498U3|S2540_RAT_Solute_carrier_family_25_member_40_OS=Rattus_norvegicus_GN=Slc25a40_PE=2_SV=2	1.00E-48	[illegible]	[illegible]
comp33810_c0_seq1.p1				
comp33811_c0_seq1.p1				
comp33812_c0_seq1.p1				
comp33813_c0_seq1.p1	sp|O97508|THIO_HORSE_Thioredoxin_OS=Equus_caballus_GN=TXN_PE=3_SV=3	3.00E-19	[illegible]	[illegible]
comp33815_c0_seq1.p1				
comp33816_c0_seq1.p1				
comp33817_c0_seq1.p1	sp|Q5ZLA5|EIF3E_CHICK_Eukaryotic_translation_initiation_factor_3_subunit_E_OS=Gallus_gallus_GN=EIF3E_PE=2_SV=1	4.00E-122	[illegible]	[illegible]
comp33818_c0_seq1.p1				
comp33821_c0_seq1.p1				
comp33822_c0_seq1.p2	sp|Q642A5|DPOE3_RAT_DNA_polymerase_epsilon_subunit_3_OS=Rattus_norvegicus_GN=Pole3_PE=2_SV=1	8.00E-25	[illegible]	[illegible]
comp33824_c0_seq1.p1				
comp33825_c0_seq1.p1	sp|Q91YQ5|RPN1_MOUSE_Dolichyl-diphosphooligosaccharide--protein_glycosyltransferase_subunit_1_OS=Mus_musculus_GN=Rpn1_PE=2_SV=1	1.00E-85	[illegible]	[illegible]
comp33826_c0_seq1.p1				
comp33829_c0_seq1.p1				
comp33832_c0_seq1.p1				
comp33833_c0_seq1.p1				
comp33834_c0_seq1.p1	sp|Q9ZT29|SC5D_TOBAC_Delta(7)-sterol-C5(6)-desaturase_OS=Nicotiana_tabacum_PE=2_SV=1	1.00E-60	[illegible]	[illegible]
comp33835_c0_seq1.p1	sp|A6T4E6|Y006_KLEP7_UPF0246_protein_KPN78578_00060_OS=Klebsiella_pneumoniae_subsp._pneumoniae_(strain_ATCC_700721_/_MGH_78578)_GN=KPN78578_00060_PE=3_SV=1	4.00E-55		
comp33836_c0_seq1.p1	sp|Q8VE80|THOC3_MOUSE_THO_complex_subunit_3_OS=Mus_musculus_GN=Thoc3_PE=2_SV=1	1.00E-46	[illegible]	[illegible]
comp33837_c0_seq1.p1				
comp33838_c0_seq1.p1	sp|Q14181|DPOA2_HUMAN_DNA_polymerase_alpha_subunit_B_OS=Homo_sapiens_GN=POLA2_PE=1_SV=2	2.00E-81	[illegible]	[illegible]
comp33839_c0_seq1.p1				
comp33842_c0_seq1.p1				
comp33843_c0_seq1.p1				
comp33844_c0_seq1.p2				
comp33846_c0_seq1.p1				
comp33847_c0_seq1.p1	sp|Q9XT11|FKBP5_AOTNA_Peptidyl-prolyl_cis-trans_isomerase_FKBP5_OS=Aotus_nancymaae_GN=FKBP5_PE=2_SV=2	3.00E-15	[illegible]	[illegible]
comp33849_c0_seq1.p1	sp|F4JMJ1|HSP7R_ARATH_Heat_shock_70_kDa_protein_17_OS=Arabidopsis_thaliana_GN=HSP70-17_PE=2_SV=1	1.00E-72	[illegible]	[illegible]
comp33850_c0_seq1.p1				
comp33852_c0_seq1.p1				
comp33854_c0_seq1.p1	sp|O05394|MCCB_BACSU_Cystathionine_gamma-lyase_OS=Bacillus_subtilis_GN=mccB_PE=1_SV=1	2.00E-94	[illegible]	[illegible]
comp33856_c0_seq1.p1				
comp33857_c0_seq1.p1				
comp33861_c0_seq1.p1	sp|P83291|NCB5R_ARATH_NADH-cytochrome_b5_reductase-like_protein_OS=Arabidopsis_thaliana_GN=At5g20080_PE=1_SV=2	2.00E-84	[illegible]	[illegible]
comp33863_c0_seq1.p1	sp|Q9SDM1|CB121_HORVU_Chlorophyll_a-b_binding_protein_1B-21,_chloroplastic_OS=Hordeum_vulgare_GN=LHC_Ib-21_PE=1_SV=1	2.00E-13	[illegible]	[illegible]
comp33864_c0_seq1.p1	sp|B2J384|SYK_NOSP7_Lysine--tRNA_ligase_OS=Nostoc_punctiforme_(strain_ATCC_29133_/_PCC_73102)_GN=lysS_PE=3_SV=1	0	[illegible]	[illegible]
comp33865_c0_seq1.p1	sp|Q9Y7K1|YGL4_SCHPO_Uncharacterized_protein_C216.04c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC216.04c_PE=2_SV=1	1.00E-43	[illegible]	[illegible]
comp33866_c0_seq1.p1				
comp33868_c0_seq1.p1	sp|Q8IUF1|CBWD2_HUMAN_COBW_domain-containing_protein_2_OS=Homo_sapiens_GN=CBWD2_PE=1_SV=1	2.00E-30	[illegible]	[illegible]
comp33869_c0_seq1.p1	sp|Q53PC7|COPB1_ORYSJ_Coatomer_subunit_beta-1_OS=Oryza_sativa_subsp._japonica_GN=Os11g0174000_PE=2_SV=1	0	[illegible]	[illegible]
comp33871_c0_seq1.p1	sp|Q12731|TBP_EMENI_TATA-box-binding_protein_OS=Emericella_nidulans_(strain_FGSC_A4_/_ATCC_38163_/_CBS_112.46_/_NRRL_194_/_M139)_GN=tbpA_PE=2_SV=1	2.00E-59	[illegible]	[illegible]
comp33872_c0_seq1.p1				
comp33873_c0_seq1.p1	sp|Q62651|ECH1_RAT_Delta(3,5)-Delta(2,4)-dienoyl-CoA_isomerase,_mitochondrial_OS=Rattus_norvegicus_GN=Ech1_PE=1_SV=2	3.00E-85	[illegible]	[illegible]
comp33874_c0_seq1.p1				
comp33876_c0_seq1.p1				
comp33877_c0_seq1.p1				
comp33878_c0_seq1.p1	sp|Q2H5Z7|DENR_CHAGB_Translation_machinery-associated_protein_22_OS=Chaetomium_globosum_(strain_ATCC_6205_/_CBS_148.51_/_DSM_1962_/_NBRC_6347_/_NRRL_1970)_GN=TMA22_PE=3_SV=1	3.00E-17	[illegible]	[illegible]
comp33879_c0_seq1.p1				
comp33881_c0_seq1.p1				
comp33882_c0_seq1.p1	sp|P50580|PA2G4_MOUSE_Proliferation-associated_protein_2G4_OS=Mus_musculus_GN=Pa2g4_PE=1_SV=3	4.00E-80	[illegible]	[illegible]
comp33883_c0_seq1.p1				
comp33884_c0_seq1.p3				
comp33886_c0_seq1.p1	sp|Q84QU8|PPT2_ORYSJ_Phosphoenolpyruvate/phosphate_translocator_2,_chloroplastic_OS=Oryza_sativa_subsp._japonica_GN=PPT2_PE=2_SV=1	1.00E-42	[illegible]	[illegible]
comp33888_c0_seq1.p1				
comp33890_c0_seq1.p1	sp|Q653T6|SPS1_ORYSJ_Solanesyl-diphosphate_synthase_1,_mitochondrial_OS=Oryza_sativa_subsp._japonica_GN=SPS1_PE=1_SV=1	5.00E-78	[illegible]	[illegible]
comp33891_c0_seq1.p1				
comp33894_c0_seq1.p1				
comp33895_c0_seq1.p1				
comp33896_c0_seq1.p1	sp|P42784|CTPA_SYNP2_Carboxyl-terminal-processing_protease_OS=Synechococcus_sp._(strain_ATCC_27264_/_PCC_7002_/_PR-6)_GN=ctpA_PE=3_SV=2	3.00E-61	[illegible]	[illegible]
comp33898_c0_seq1.p1				
comp33900_c0_seq1.p1	sp|Q15061|WDR43_HUMAN_WD_repeat-containing_protein_43_OS=Homo_sapiens_GN=WDR43_PE=1_SV=3	1.00E-24	[illegible]	[illegible]
comp33901_c0_seq1.p1	sp|P0CR02|DBP8_CRYNJ_ATP-dependent_RNA_helicase_DBP8_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=DBP8_PE=3_SV=1	5.00E-11	[illegible]	[illegible]
comp33902_c0_seq1.p1	sp|O34614|YTQB_BACSU_Putative_rRNA_methylase_ytqB_OS=Bacillus_subtilis_GN=ytqB_PE=3_SV=1	7.00E-32	[illegible]	[illegible]
comp33904_c0_seq1.p1	sp|Q9SA78|COPE1_ARATH_Coatomer_subunit_epsilon-1_OS=Arabidopsis_thaliana_GN=At1g30630_PE=2_SV=1	2.00E-86	[illegible]	[illegible]
comp33905_c0_seq1.p1				
comp33907_c0_seq1.p1	sp|Q54CU7|TPC2L_DICDI_Trafficking_protein_particle_complex_subunit_2-like_protein_OS=Dictyostelium_discoideum_GN=trappc2l_PE=3_SV=1	7.00E-27	[illegible]	[illegible]
comp33909_c0_seq1.p1	sp|Q24134|NELFD_DROME_Negative_elongation_factor_D_OS=Drosophila_melanogaster_GN=TH1_PE=1_SV=2	7.00E-14	[illegible]	[illegible]
comp33911_c0_seq1.p2	sp|Q9NQP4|PFD4_HUMAN_Prefoldin_subunit_4_OS=Homo_sapiens_GN=PFDN4_PE=1_SV=1	2.00E-14	[illegible]	[illegible]
comp33912_c0_seq1.p2				
comp33917_c0_seq1.p1				
comp33918_c0_seq1.p1	sp|Q8K2P7|S38A1_MOUSE_Sodium-coupled_neutral_amino_acid_transporter_1_OS=Mus_musculus_GN=Slc38a1_PE=1_SV=1	8.00E-14	[illegible]	[illegible]
comp33919_c0_seq1.p1				
comp33920_c0_seq1.p1				
comp33921_c0_seq1.p1	sp|Q5VJS5|DYXC1_RAT_Dyslexia_susceptibility_1_candidate_gene_1_protein_homolog_OS=Rattus_norvegicus_GN=Dyx1c1_PE=1_SV=1	7.00E-21	[illegible]	[illegible]
comp33921_c0_seq1.p3				
comp33922_c0_seq1.p1	sp|Q0DHL4|FTSH8_ORYSJ_ATP-dependent_zinc_metalloprotease_FTSH_8,_mitochondrial_OS=Oryza_sativa_subsp._japonica_GN=FTSH8_PE=3_SV=1	0	[illegible]	[illegible]
comp33923_c0_seq1.p3				
comp33924_c0_seq1.p1	sp|O74783|POF2_SCHPO_SCF_E3_ubiquitin_ligase_complex_F-box_protein_pof2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=pof2_PE=1_SV=1	7.00E-14	[illegible]	[illegible]
comp33925_c0_seq1.p1	sp|Q9Z0N2|IF2H_MOUSE_Eukaryotic_translation_initiation_factor_2_subunit_3,_Y-linked_OS=Mus_musculus_GN=Eif2s3y_PE=2_SV=2	0	[illegible]	[illegible]
comp33928_c0_seq1.p1	sp|A5UQV0|UPP_ROSS1_Uracil_phosphoribosyltransferase_OS=Roseiflexus_sp._(strain_RS-1)_GN=upp_PE=3_SV=1	6.00E-56	[illegible]	[illegible]
comp33929_c0_seq1.p1				
comp33931_c0_seq1.p1				
comp33933_c0_seq1.p1	sp|P0CI65|NPHP3_DANRE_Nephrocystin-3_OS=Danio_rerio_GN=nphp3_PE=3_SV=1	9.00E-19	[illegible]	[illegible]
comp33934_c0_seq1.p1	sp|Q54E29|THG1_DICDI_Probable_tRNA(His)_guanylyltransferase_OS=Dictyostelium_discoideum_GN=thg1_PE=3_SV=1	4.00E-70	[illegible]	[illegible]
comp33937_c0_seq1.p1	sp|Q91785|KI15A_XENLA_Kinesin-like_protein_KIF15-A_OS=Xenopus_laevis_GN=kif15-a_PE=1_SV=1	2.00E-109	[illegible]	[illegible]
comp33938_c0_seq1.p1				
comp33939_c0_seq1.p1				
comp33940_c0_seq1.p1	sp|Q54JC2|Y2881_DICDI_Uncharacterized_protein_DDB_G0288155_OS=Dictyostelium_discoideum_GN=DDB_G0288155_PE=1_SV=1	2.00E-37	[illegible]	[illegible]
comp33941_c0_seq1.p1				
comp33943_c0_seq1.p1	sp|Q3A9V2|RS9_CARHZ_30S_ribosomal_protein_S9_OS=Carboxydothermus_hydrogenoformans_(strain_Z-2901_/_DSM_6008)_GN=rpsI_PE=3_SV=1	1.00E-22	[illegible]	[illegible]
comp33944_c0_seq1.p1	sp|Q8BG58|P4HTM_MOUSE_Transmembrane_prolyl_4-hydroxylase_OS=Mus_musculus_GN=P4htm_PE=2_SV=1	4.00E-14	[illegible]	[illegible]
comp33946_c0_seq1.p1	sp|Q05580|YD266_YEAST_LIM_domain_and_RING_finger_protein_YDR266C_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YDR266C_PE=1_SV=1	1.00E-18	[illegible]	[illegible]
comp33952_c0_seq1.p1	sp|Q94B74|NUDT2_ARATH_Nudix_hydrolase_2_OS=Arabidopsis_thaliana_GN=NUDT2_PE=1_SV=1	6.00E-62	[illegible]	[illegible]
comp33954_c0_seq1.p1				
comp33955_c0_seq1.p2				
comp33956_c0_seq1.p1	sp|Q8VY89|APC7_ARATH_Anaphase-promoting_complex_subunit_7_OS=Arabidopsis_thaliana_GN=APC7_PE=2_SV=1	2.00E-75	[illegible]	[illegible]
comp33959_c0_seq1.p1				
comp33959_c0_seq1.p2	sp|P34120|PSA7_DICDI_Proteasome_subunit_alpha_type-7_OS=Dictyostelium_discoideum_GN=psmA7_PE=3_SV=1	1.00E-90	[illegible]	[illegible]
comp3396_c1_seq1.p2				
comp33960_c0_seq1.p1	sp|Q6MD85|ISPG_PARUW_4-hydroxy-3-methylbut-2-en-1-yl_diphosphate_synthase_OS=Protochlamydia_amoebophila_(strain_UWE25)_GN=ispG_PE=3_SV=1	3.00E-178	[illegible]	[illegible]
comp33961_c0_seq1.p2				
comp33963_c0_seq1.p1	sp|Q5RBU2|RM46_PONAB_39S_ribosomal_protein_L46,_mitochondrial_OS=Pongo_abelii_GN=MRPL46_PE=2_SV=1	2.00E-20	[illegible]	[illegible]
comp33967_c0_seq1.p2				
comp33969_c0_seq1.p1				
comp33970_c0_seq1.p1				
comp33972_c0_seq1.p1	sp|Q15067|ACOX1_HUMAN_Peroxisomal_acyl-coenzyme_A_oxidase_1_OS=Homo_sapiens_GN=ACOX1_PE=1_SV=3	2.00E-131	[illegible]	[illegible]
comp33973_c0_seq1.p1	sp|Q9SM43|VDE_SPIOL_Violaxanthin_de-epoxidase,_chloroplastic_OS=Spinacia_oleracea_GN=VDE1_PE=1_SV=2	3.00E-90	[illegible]	[illegible]
comp33974_c0_seq1.p1				
comp33977_c0_seq1.p1				
comp33979_c0_seq1.p1				
comp33981_c0_seq1.p1				
comp33982_c0_seq1.p1	sp|Q8T137|GSHR_DICDI_Glutathione_reductase_OS=Dictyostelium_discoideum_GN=gsr_PE=3_SV=2	3.00E-159	[illegible]	[illegible]
comp33983_c0_seq1.p1	sp|P54967|BIOB_ARATH_Biotin_synthase_OS=Arabidopsis_thaliana_GN=BIO2_PE=2_SV=1	2.00E-145	[illegible]	[illegible]
comp33984_c0_seq1.p1				
comp33985_c0_seq1.p1				
comp33986_c0_seq1.p1	sp|Q9LEV3|CBSX3_ARATH_CBS_domain-containing_protein_CBSX3,_mitochondrial_OS=Arabidopsis_thaliana_GN=CBSX3_PE=1_SV=1	9.00E-17	[illegible]	[illegible]
comp33987_c0_seq1.p1	sp|P36580|ALF_SCHPO_Fructose-bisphosphate_aldolase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=fba1_PE=1_SV=2	3.00E-156	[illegible]	[illegible]
comp33989_c0_seq1.p1	sp|Q2W367|DXS_MAGSA_1-deoxy-D-xylulose-5-phosphate_synthase_OS=Magnetospirillum_magneticum_(strain_AMB-1_/_ATCC_700264)_GN=dxs_PE=3_SV=1	0	[illegible]	[illegible]
comp33990_c0_seq1.p1				
comp33993_c0_seq1.p1	sp|Q8T2T5|C560_DICDI_Succinate_dehydrogenase_cytochrome_b560_subunit,_mitochondrial_OS=Dictyostelium_discoideum_GN=sdhC_PE=3_SV=1	2.00E-14	[illegible]	[illegible]
comp33994_c0_seq1.p1	sp|O49954|GCSP_SOLTU_Glycine_dehydrogenase_[decarboxylating],_mitochondrial_OS=Solanum_tuberosum_GN=GDCSP_PE=2_SV=1	0	[illegible]	[illegible]
comp33996_c0_seq1.p1				
comp33998_c0_seq1.p1				
comp33999_c0_seq1.p1				
comp34000_c0_seq1.p1	sp|Q93XM7|MCAT_ARATH_Mitochondrial_carnitine/acylcarnitine_carrier-like_protein_OS=Arabidopsis_thaliana_GN=BOU_PE=1_SV=1	9.00E-42	[illegible]	[illegible]
comp34001_c0_seq1.p1	sp|Q317Y6|CLPP4_PROM9_ATP-dependent_Clp_protease_proteolytic_subunit_4_OS=Prochlorococcus_marinus_(strain_MIT_9312)_GN=clpP4_PE=3_SV=1	5.00E-81	[illegible]	[illegible]
comp34002_c0_seq1.p1	sp|P51570|GALK1_HUMAN_Galactokinase_OS=Homo_sapiens_GN=GALK1_PE=1_SV=1	2.00E-91	[illegible]	[illegible]
comp34004_c0_seq1.p1				
comp34007_c0_seq1.p1	sp|Q3ZC22|HSBP1_BOVIN_Heat_shock_factor-binding_protein_1_OS=Bos_taurus_GN=HSBP1_PE=3_SV=1	1.00E-17	[illegible]	[illegible]
comp34010_c0_seq1.p1	sp|B8EMS0|RL7_METSB_50S_ribosomal_protein_L7/L12_OS=Methylocella_silvestris_(strain_BL2_/_DSM_15510_/_NCIMB_13906)_GN=rplL_PE=3_SV=1	6.00E-23	[illegible]	[illegible]
comp34011_c0_seq1.p1	sp|Q0DA50|C3H45_ORYSJ_Zinc_finger_CCCH_domain-containing_protein_45_OS=Oryza_sativa_subsp._japonica_GN=Os06g0677700_PE=2_SV=1	3.00E-23	[illegible]	[illegible]
comp34012_c0_seq1.p1				
comp34013_c0_seq1.p1				
comp34014_c0_seq1.p1				
comp34016_c0_seq1.p1				
comp34017_c0_seq1.p1	sp|Q5XGY9|MND1_XENLA_Meiotic_nuclear_division_protein_1_homolog_OS=Xenopus_laevis_GN=mnd1_PE=2_SV=1	1.00E-37	[illegible]	[illegible]
comp34018_c0_seq1.p1	sp|P29197|CH60A_ARATH_Chaperonin_CPN60,_mitochondrial_OS=Arabidopsis_thaliana_GN=CPN60_PE=1_SV=2	0	[illegible]	[illegible]
comp34019_c0_seq1.p1	sp|Q9WUM5|SUCA_MOUSE_Succinyl-CoA_ligase_[ADP/GDP-forming]_subunit_alpha,_mitochondrial_OS=Mus_musculus_GN=Suclg1_PE=1_SV=4	3.00E-144	[illegible]	[illegible]
comp34024_c0_seq1.p1	sp|Q9EQ15|GNB1L_MOUSE_Guanine_nucleotide-binding_protein_subunit_beta-like_protein_1_OS=Mus_musculus_GN=Gnb1l_PE=2_SV=2	4.00E-28	[illegible]	[illegible]
comp34025_c0_seq1.p1				
comp34027_c0_seq1.p1				
comp34028_c0_seq1.p1	sp|Q54J73|PAP_DICDI_Poly(A)_polymerase_OS=Dictyostelium_discoideum_GN=papA_PE=3_SV=1	1.00E-89	[illegible]	[illegible]
comp34030_c0_seq1.p1				
comp34032_c0_seq1.p1	sp|Q86JP3|RAB5A_DICDI_Ras-related_protein_Rab-5A_OS=Dictyostelium_discoideum_GN=rab5A_PE=3_SV=1	2.00E-36	[illegible]	[illegible]
comp34037_c0_seq1.p1	sp|Q5VVQ6|OTU1_HUMAN_Ubiquitin_thioesterase_OTU1_OS=Homo_sapiens_GN=YOD1_PE=1_SV=1	1.00E-44	[illegible]	[illegible]
comp34038_c0_seq1.p1	sp|Q8H7Y6|HFA2D_ORYSJ_Heat_stress_transcription_factor_A-2d_OS=Oryza_sativa_subsp._japonica_GN=HSFA2D_PE=2_SV=2	2.00E-18	[illegible]	[illegible]
comp34042_c0_seq1.p1	sp|Q4N655|RL5_THEPA_60S_ribosomal_protein_L5_OS=Theileria_parva_GN=RPL5_PE=3_SV=1	8.00E-54	[illegible]	[illegible]
comp34043_c0_seq1.p1				
comp34044_c0_seq1.p1	sp|Q9M354|AGD6_ARATH_Probable_ADP-ribosylation_factor_GTPase-activating_protein_AGD6_OS=Arabidopsis_thaliana_GN=AGD6_PE=1_SV=1	6.00E-34	[illegible]	[illegible]
comp34045_c0_seq1.p1				
comp34049_c0_seq1.p1	sp|Q5PPK9|TSSC1_RAT_Protein_TSSC1_OS=Rattus_norvegicus_GN=Tssc1_PE=2_SV=1	9.00E-59		
comp34050_c0_seq1.p1				
comp34051_c0_seq1.p1	sp|Q9GLM4|TENS1_BOVIN_Tensin-1_OS=Bos_taurus_GN=TNS1_PE=2_SV=1	4.00E-32	[illegible]	[illegible]
comp34053_c0_seq1.p1	sp|O59790|ARK1_SCHPO_Serine/threonine-protein_kinase_ark1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ark1_PE=1_SV=2	1.00E-28	[illegible]	[illegible]
comp34054_c0_seq1.p1	sp|O13775|SYEC_SCHPO_Probable_glutamate--tRNA_ligase,_cytoplasmic_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC17A5.15c_PE=1_SV=1	1.00E-179	[illegible]	[illegible]
comp34055_c0_seq1.p1	sp|Q6CAB8|GPI10_YARLI_GPI_mannosyltransferase_3_OS=Yarrowia_lipolytica_(strain_CLIB_122_/_E_150)_GN=GPI10_PE=3_SV=1	5.00E-41	[illegible]	[illegible]
comp34056_c0_seq1.p1				
comp34057_c0_seq1.p1	sp|B6TNK6|MOC31_MAIZE_Adenylyltransferase_and_sulfurtransferase_MOCS3_1_OS=Zea_mays_GN=MOCS3-1_PE=2_SV=1	1.00E-106	[illegible]	[illegible]
comp34060_c0_seq1.p1				
comp34062_c0_seq1.p1	sp|Q52KN9|CWC22_XENLA_Pre-mRNA-splicing_factor_CWC22_homolog_OS=Xenopus_laevis_GN=cwc22_PE=2_SV=1	9.00E-176	[illegible]	[illegible]
comp34064_c0_seq1.p1	sp|Q8GXR9|DHNA_ARATH_NADH_dehydrogenase_C1,_chloroplastic/mitochondrial_OS=Arabidopsis_thaliana_GN=NDC1_PE=1_SV=2	4.00E-47	[illegible]	[illegible]
comp34065_c0_seq1.p2				
comp34066_c0_seq1.p1	sp|Q8VBV4|FBXW7_MOUSE_F-box/WD_repeat-containing_protein_7_OS=Mus_musculus_GN=Fbxw7_PE=1_SV=1	6.00E-30	[illegible]	[illegible]
comp34067_c0_seq1.p1	sp|Q2HJJ0|KLC4_BOVIN_Kinesin_light_chain_4_OS=Bos_taurus_GN=KLC4_PE=2_SV=2	5.00E-18	[illegible]	[illegible]
comp34069_c0_seq1.p1				
comp34070_c0_seq1.p1	sp|Q9SDM1|CB121_HORVU_Chlorophyll_a-b_binding_protein_1B-21,_chloroplastic_OS=Hordeum_vulgare_GN=LHC_Ib-21_PE=1_SV=1	4.00E-18	[illegible]	[illegible]
comp34071_c0_seq1.p1				
comp34072_c0_seq1.p1	sp|Q08480|KAD2_ORYSJ_Adenylate_kinase_B_OS=Oryza_sativa_subsp._japonica_GN=ADK-B_PE=2_SV=1	3.00E-103	[illegible]	[illegible]
comp34073_c0_seq1.p1				
comp34074_c0_seq1.p1	sp|Q7KF90|RL31_SPOFR_60S_ribosomal_protein_L31_OS=Spodoptera_frugiperda_GN=RpL31_PE=2_SV=1	6.00E-46	[illegible]	[illegible]
comp34075_c0_seq1.p1	sp|Q9QY36|NAA10_MOUSE_N-alpha-acetyltransferase_10_OS=Mus_musculus_GN=Naa10_PE=1_SV=1	3.00E-64	[illegible]	[illegible]
comp34077_c0_seq1.p1				
comp34078_c0_seq1.p1				
comp34079_c0_seq1.p1				
comp3408_c0_seq1.p1	sp|P14407|FUMB_ECOLI_Fumarate_hydratase_class_I,_anaerobic_OS=Escherichia_coli_(strain_K12)_GN=fumB_PE=1_SV=2	2.00E-84	[illegible]	[illegible]
comp34080_c0_seq1.p1	sp|Q96JB2|COG3_HUMAN_Conserved_oligomeric_Golgi_complex_subunit_3_OS=Homo_sapiens_GN=COG3_PE=1_SV=3	9.00E-63	[illegible]	[illegible]
comp34081_c0_seq1.p1	sp|Q9KJ21|SDMT_ECTHL_Sarcosine/dimethylglycine_N-methyltransferase_OS=Ectothiorhodospira_halochloris_PE=1_SV=1	3.00E-23	[illegible]	[illegible]
comp34082_c0_seq1.p1	sp|O14435|GBB_CRYPA_Guanine_nucleotide-binding_protein_subunit_beta_OS=Cryphonectria_parasitica_GN=GB-1_PE=3_SV=1	2.00E-142	[illegible]	[illegible]
comp34084_c0_seq1.p1	sp|Q5XPI3|RN123_MOUSE_E3_ubiquitin-protein_ligase_RNF123_OS=Mus_musculus_GN=Rnf123_PE=2_SV=1	2.00E-14	[illegible]	[illegible]
comp34085_c0_seq1.p1				
comp34086_c0_seq1.p1				
comp34087_c0_seq1.p1				
comp34088_c0_seq1.p1				
comp34089_c0_seq1.p1	sp|Q9UQ35|SRRM2_HUMAN_Serine/arginine_repetitive_matrix_protein_2_OS=Homo_sapiens_GN=SRRM2_PE=1_SV=2	8.00E-17	[illegible]	[illegible]
comp34090_c0_seq1.p1	sp|Q54MP8|Y5837_DICDI_Bromodomain_and_WD_repeat-containing_DDB_G0285837_OS=Dictyostelium_discoideum_GN=DDB_G0285837_PE=4_SV=1	4.00E-22	[illegible]	[illegible]
comp34091_c0_seq1.p1	sp|P46228|RS1_SYNP6_30S_ribosomal_protein_S1_OS=Synechococcus_sp._(strain_ATCC_27144_/_PCC_6301_/_SAUG_1402/1)_GN=rpsA_PE=1_SV=4	1.00E-90	[illegible]	[illegible]
comp34093_c0_seq1.p1	sp|P42824|DNJH2_ALLPO_DnaJ_protein_homolog_2_OS=Allium_porrum_GN=LDJ2_PE=2_SV=1	1.00E-126	[illegible]	[illegible]
comp34096_c0_seq1.p1	sp|Q54BQ5|NSF1C_DICDI_NSFL1_cofactor_p47_homolog_OS=Dictyostelium_discoideum_GN=nsfl1c_PE=3_SV=1	1.00E-33	[illegible]	[illegible]
comp34097_c0_seq1.p1	sp|Q9Y388|RBMX2_HUMAN_RNA-binding_motif_protein,_X-linked_2_OS=Homo_sapiens_GN=RBMX2_PE=1_SV=2	4.00E-47	[illegible]	[illegible]
comp34098_c0_seq1.p1	sp|Q9FVR6|Y1222_ARATH_Uncharacterized_protein_At1g32220,_chloroplastic_OS=Arabidopsis_thaliana_GN=At1g32220_PE=1_SV=1	8.00E-17	[illegible]	[illegible]
comp34098_c0_seq1.p2	sp|Q9VFR1|F206_DROME_FAM206_family_protein_CG9288_OS=Drosophila_melanogaster_GN=CG9288_PE=1_SV=1	4.00E-17	[illegible]	[illegible]
comp34099_c0_seq1.p1	sp|O80507|CSK2E_ARATH_Putative_casein_kinase_II_subunit_beta-4_OS=Arabidopsis_thaliana_GN=At2g44680_PE=2_SV=1	5.00E-64	[illegible]	[illegible]
comp34102_c0_seq1.p1	sp|Q9V730|EXT1_DROME_Exostosin-1_OS=Drosophila_melanogaster_GN=ttv_PE=1_SV=1	3.00E-24	[illegible]	[illegible]
comp34104_c0_seq1.p1				
comp34105_c0_seq1.p1				
comp34106_c0_seq1.p1	sp|Q9LYR5|FKB19_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP19,_chloroplastic_OS=Arabidopsis_thaliana_GN=FKBP19_PE=1_SV=1	6.00E-51	[illegible]	[illegible]
comp34107_c0_seq1.p1	sp|Q9LZW3|PUB16_ARATH_U-box_domain-containing_protein_16_OS=Arabidopsis_thaliana_GN=PUB16_PE=2_SV=1	8.00E-14	[illegible]	[illegible]
comp34109_c0_seq1.p1				
comp34111_c0_seq1.p1	sp|Q06827|CATR_SCHDU_Caltractin_OS=Scherffelia_dubia_PE=1_SV=1	1.00E-96	[illegible]	[illegible]
comp34113_c0_seq1.p1	sp|Q502K3|ANR52_DANRE_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_C_OS=Danio_rerio_GN=ankrd52_PE=2_SV=1	5.00E-17	[illegible]	[illegible]
comp34114_c0_seq1.p1				
comp34115_c0_seq1.p1				
comp34115_c0_seq2.p1				
comp34116_c0_seq1.p1	sp|Q3ZBR5|TTC1_BOVIN_Tetratricopeptide_repeat_protein_1_OS=Bos_taurus_GN=TTC1_PE=2_SV=1	2.00E-42	[illegible]	[illegible]
comp34118_c0_seq1.p1	sp|Q8T1C6|GNT1_DICDI_[Skp1-protein]-hydroxyproline_N-acetylglucosaminyltransferase_OS=Dictyostelium_discoideum_GN=gnt1_PE=1_SV=2	2.00E-21	[illegible]	[illegible]
comp34119_c0_seq1.p1	sp|P50408|VATF_RAT_V-type_proton_ATPase_subunit_F_OS=Rattus_norvegicus_GN=Atp6v1f_PE=1_SV=1	5.00E-35	[illegible]	[illegible]
comp34120_c0_seq1.p1				
comp34122_c0_seq1.p1	sp|Q9WV60|GSK3B_MOUSE_Glycogen_synthase_kinase-3_beta_OS=Mus_musculus_GN=Gsk3b_PE=1_SV=2	9.00E-158	[illegible]	[illegible]
comp34123_c0_seq1.p2				
comp34126_c0_seq1.p1				
comp34128_c0_seq1.p1	sp|Q9S9P8|FNRR2_ARATH_Ferredoxin--NADP_reductase,_root_isozyme_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=RFNR2_PE=1_SV=1	4.00E-136	[illegible]	[illegible]
comp34130_c0_seq1.p1	sp|P54752|ARGD_NOSS1_Acetylornithine_aminotransferase_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=argD_PE=3_SV=1	4.00E-180	[illegible]	[illegible]

<table>
<tr><td>comp34132_c0_seq1.p1</td><td>sp|Q8CI15|SPHK1_MOUSE_Sphingosine_kinase_1_OS=Mus_musculus_GN=Sphk1_PE=1_SV=1</td><td>2.00E-41</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34133_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34136_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34137_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34139_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34140_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34142_c0_seq1.p1</td><td>sp|Q9CQI7|RU2B_MOUSE_U2_small_nuclear_ribonucleoprotein_B''_OS=Mus_musculus_GN=Snrpb2_PE=2_SV=1</td><td>1.00E-56</td><td>GO:0000166,GO:0000398,GO:0003676,GO:0003723,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005681,GO:0005681,GO:0005730,GO:0006397,GO:0008380,GO:0017069,GO:0030529,GO:0071013</td><td>[illegible]</td></tr>
<tr><td>comp34143_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34144_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34150_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34151_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34152_c0_seq1.p1</td><td>sp|Q54ED4|GRWD1_DICDI_Glutamate-rich_WD_repeat-containing_protein_1_OS=Dictyostelium_discoideum_GN=grwd1_PE=3_SV=1</td><td>2.00E-129</td><td>GO:0003674,GO:0005634,GO:0005730</td><td>molecular_function,nucleus,nucleolus</td></tr>
<tr><td>comp34152_c0_seq1.p2</td><td>sp|Q4R828|RCCD1_MACFA_RCC1_domain-containing_protein_1_OS=Macaca_fascicularis_GN=RCCD1_PE=2_SV=1</td><td>5.00E-18</td><td></td><td></td></tr>
<tr><td>comp34153_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34154_c0_seq1.p1</td><td>sp|Q80ZG5|SLU7_RAT_Pre-mRNA-splicing_factor_SLU7_OS=Rattus_norvegicus_GN=Slu7_PE=2_SV=2</td><td>8.00E-91</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34155_c0_seq1.p1</td><td>sp|P62321|RUXF_XENLA_Small_nuclear_ribonucleoprotein_F_OS=Xenopus_laevis_GN=snrpf_PE=3_SV=1</td><td>6.00E-35</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34156_c0_seq1.p1</td><td>sp|Q05974|RAB1A_LYMST_Ras-related_protein_Rab-1A_OS=Lymnaea_stagnalis_GN=RAB1A_PE=2_SV=1</td><td>1.00E-85</td><td>GO:0000166,GO:0005525,GO:0005525,GO:0005783,GO:0005783,GO:0005794,GO:0005794,GO:0006810,GO:0007264,GO:0015031,GO:0015031,GO:0016192</td><td>[illegible]</td></tr>
<tr><td>comp34156_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34159_c0_seq1.p1</td><td>sp|Q99805|TM9S2_HUMAN_Transmembrane_9_superfamily_member_2_OS=Homo_sapiens_GN=TM9SF2_PE=1_SV=1</td><td>2.00E-170</td><td>GO:0005768,GO:0005768,GO:0005887,GO:0006810,GO:0010008,GO:0016020,GO:0016021,GO:0016021,GO:0070062</td><td>[illegible]</td></tr>
<tr><td>comp34161_c0_seq1.p1</td><td>sp|P55862|MCM5A_XENLA_DNA_replication_licensing_factor_mcm5-A_OS=Xenopus_laevis_GN=mcm5-a_PE=1_SV=2</td><td>0</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34163_c0_seq1.p1</td><td>sp|P35681|TCTP_ORYSJ_Translationally-controlled_tumor_protein_homolog_OS=Oryza_sativa_subsp._japonica_GN=TCTP_PE=1_SV=1</td><td>6.00E-32</td><td>GO:0005737,GO:0005737</td><td>cytoplasm,cytoplasm</td></tr>
<tr><td>comp34164_c0_seq1.p1</td><td>sp|Q5RA77|COPD_PONAB_Coatomer_subunit_delta_OS=Pongo_abelii_GN=ARCN1_PE=2_SV=1</td><td>2.00E-106</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34166_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34167_c0_seq1.p1</td><td>sp|Q9CQ79|TXND9_MOUSE_Thioredoxin_domain-containing_protein_9_OS=Mus_musculus_GN=Txndc9_PE=1_SV=1</td><td>6.00E-48</td><td>GO:0003674,GO:0005634,GO:0005737,GO:0005813,GO:0008150,GO:0030496,GO:0045454</td><td>[illegible]</td></tr>
<tr><td>comp34168_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34171_c0_seq1.p1</td><td>sp|Q8HXY4|ODBA_MACFA_2-oxoisovalerate_dehydrogenase_subunit_alpha,_mitochondrial_OS=Macaca_fascicularis_GN=BCKDHA_PE=2_SV=1</td><td>2.00E-146</td><td>GO:0003863,GO:0005739,GO:0005759,GO:0008152,GO:0016491,GO:0016624,GO:0046872,GO:0055114</td><td>[illegible]</td></tr>
<tr><td>comp34172_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34175_c0_seq1.p1</td><td>sp|Q19749|ODP2_CAEEL_Dihydrolipoyllysine-residue_acetyltransferase_component_of_pyruvate_dehydrogenase_complex,_mitochondrial_OS=Caenorhabditis_elegans_GN=F23B12.5_PE=1_SV=1</td><td>5.00E-12</td><td>GO:0004742,GO:0004742,GO:0005739,GO:0005759,GO:0006090,GO:0006096,GO:0008152,GO:0016740,GO:0016746,GO:0016746,GO:0045254</td><td>[illegible]</td></tr>
<tr><td>comp34176_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34178_c0_seq1.p1</td><td>sp|A3DH43|SYC_CLOTH_Cysteine--tRNA_ligase_OS=Clostridium_thermocellum_(strain_ATCC_27405_/_DSM_1237)_GN=cysS_PE=3_SV=1</td><td>7.00E-108</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34179_c0_seq1.p1</td><td>sp|Q9NDJ2|DOM_DROME_Helicase_domino_OS=Drosophila_melanogaster_GN=dom_PE=1_SV=2</td><td>3.00E-23</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34181_c0_seq1.p1</td><td>sp|Q6R0H1|LHY_ARATH_Protein_LHY_OS=Arabidopsis_thaliana_GN=LHY_PE=1_SV=2</td><td>2.00E-11</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34182_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34183_c0_seq1.p1</td><td>sp|O76512|RENT1_CAEEL_Regulator_of_nonsense_transcripts_1_OS=Caenorhabditis_elegans_GN=smg-2_PE=1_SV=1</td><td>1.00E-25</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34184_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34186_c0_seq1.p1</td><td>sp|Q54CL2|TCPD_DICDI_T-complex_protein_1_subunit_delta_OS=Dictyostelium_discoideum_GN=cct4_PE=3_SV=1</td><td>0</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34189_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34190_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34192_c0_seq1.p1</td><td>sp|Q9S9K4|ASPL2_ARATH_Aspartic_proteinase-like_protein_2_OS=Arabidopsis_thaliana_GN=At1g65240_PE=1_SV=2</td><td>3.00E-23</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34196_c0_seq1.p1</td><td>sp|Q55CA0|VPS26_DICDI_Vacuolar_protein_sorting-associated_protein_26_OS=Dictyostelium_discoideum_GN=vps26_PE=2_SV=1</td><td>7.00E-112</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34198_c0_seq1.p1</td><td>sp|Q9H773|DCTP1_HUMAN_dCTP_pyrophosphatase_1_OS=Homo_sapiens_GN=DCTPP1_PE=1_SV=1</td><td>8.00E-20</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34199_c0_seq1.p1</td><td>sp|Q7VEJ7|GRPE_PROMA_Protein_grpE_OS=Prochlorococcus_marinus_(strain_SARG_/_CCMP1375_/_SS120)_GN=grpE_PE=3_SV=1</td><td>9.00E-12</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34200_c0_seq1.p1</td><td>sp|Q8VEH6|CBWD1_MOUSE_COBW_domain-containing_protein_1_OS=Mus_musculus_GN=Cbwd1_PE=2_SV=1</td><td>2.00E-60</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34201_c0_seq1.p1</td><td>sp|A2VD82|TTC38_XENLA_Tetratricopeptide_repeat_protein_38_OS=Xenopus_laevis_GN=ttc38_PE=2_SV=1</td><td>6.00E-40</td><td></td><td></td></tr>
<tr><td>comp34205_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34206_c0_seq1.p1</td><td>sp|Q9CAX6|RS142_ARATH_40S_ribosomal_protein_S14-2_OS=Arabidopsis_thaliana_GN=RPS14B_PE=1_SV=1</td><td>2.00E-67</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34212_c0_seq1.p1</td><td>sp|Q95276|RL5_PIG_60S_ribosomal_protein_L5_(Fragment)_OS=Sus_scrofa_GN=RPL5_PE=2_SV=3</td><td>1.00E-55</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34213_c0_seq1.p1</td><td>sp|P29758|OAT_MOUSE_Ornithine_aminotransferase,_mitochondrial_OS=Mus_musculus_GN=Oat_PE=1_SV=1</td><td>0</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34214_c0_seq1.p1</td><td>sp|Q80VQ1|LRRC1_MOUSE_Leucine-rich_repeat-containing_protein_1_OS=Mus_musculus_GN=Lrrc1_PE=2_SV=2</td><td>2.00E-27</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34215_c0_seq1.p1</td><td>sp|Q5ZIM5|AMPM1_CHICK_Methionine_aminopeptidase_1_OS=Gallus_gallus_GN=METAP1_PE=2_SV=1</td><td>9.00E-110</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34216_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34220_c0_seq1.p1</td><td>sp|Q9HRP0|DGGGP_HALSA_Digeranylgeranylglyceryl_phosphate_synthase_OS=Halobacterium_salinarium_(strain_ATCC_700922_/_JCM_11081_/_NRC-1)_GN=VNG_0610G_PE=3_SV=2</td><td>2.00E-19</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34221_c0_seq1.p1</td><td>sp|Q96DI7|SNR40_HUMAN_U5_small_nuclear_ribonucleoprotein_40_kDa_protein_OS=Homo_sapiens_GN=SNRNP40_PE=1_SV=1</td><td>2.00E-14</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34222_c0_seq1.p1</td><td>sp|P49637|R27A3_ARATH_60S_ribosomal_protein_L27a-3_OS=Arabidopsis_thaliana_GN=RPL27AC_PE=2_SV=2</td><td>6.00E-73</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34224_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34225_c0_seq1.p1</td><td>sp|Q7K0F0|CC130_DROME_Coiled-coil_domain-containing_protein_130_homolog_OS=Drosophila_melanogaster_GN=CG15084_PE=2_SV=1</td><td>2.00E-34</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34227_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34231_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34232_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34233_c0_seq1.p1</td><td>sp|P32233|DRG1_MOUSE_Developmentally-regulated_GTP-binding_protein_1_OS=Mus_musculus_GN=Drg1_PE=1_SV=1</td><td>5.00E-155</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34236_c0_seq1.p1</td><td>sp|Q8ISP0|RS18_BRABE_40S_ribosomal_protein_S18_OS=Branchiostoma_belcheri_GN=RPS18_PE=2_SV=1</td><td>9.00E-77</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34239_c0_seq1.p1</td><td>sp|Q9XGM1|VATD_ARATH_V-type_proton_ATPase_subunit_D_OS=Arabidopsis_thaliana_GN=VHA-D_PE=1_SV=2</td><td>1.00E-57</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34240_c0_seq1.p1</td><td>sp|Q4V8A1|PCT2B_RAT_Lysophosphatidylcholine_acyltransferase_2B_OS=Rattus_norvegicus_GN=Lpcat2b_PE=2_SV=1</td><td>7.00E-17</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34244_c0_seq1.p1</td><td>sp|Q0IH40|DNLZ_XENLA_DNL-type_zinc_finger_protein_OS=Xenopus_laevis_GN=dnlz_PE=2_SV=1</td><td>2.00E-16</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34245_c0_seq1.p1</td><td>sp|Q54QR2|PSB7_DICDI_Proteasome_subunit_beta_type-7_OS=Dictyostelium_discoideum_GN=psmB7_PE=3_SV=1</td><td>1.00E-97</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34246_c0_seq1.p1</td><td>sp|Q14AI0|DCC1_MOUSE_Sister_chromatid_cohesion_protein_DCC1_OS=Mus_musculus_GN=DSCC1_PE=2_SV=1</td><td>3.00E-27</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34247_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34248_c0_seq1.p1</td><td>sp|Q9Y4C4|MFHA1_HUMAN_Malignant_fibrous_histiocytoma-amplified_sequence_1_OS=Homo_sapiens_GN=MFHAS1_PE=1_SV=2</td><td>3.00E-14</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34251_c0_seq1.p1</td><td>sp|Q9JIM3|RAD26_MOUSE_Putative_DNA_repair_and_recombination_protein_RAD26-like_OS=Mus_musculus_GN=Rad26l_PE=2_SV=2</td><td>5.00E-49</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34253_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34255_c0_seq1.p1</td><td>sp|A7RP64|PNO1_NEMVE_RNA-binding_protein_pno1_OS=Nematostella_vectensis_GN=pno1_PE=3_SV=1</td><td>9.00E-87</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34257_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34258_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34261_c0_seq1.p1</td><td>sp|Q4QRC6|ISCA1_DANRE_Iron-sulfur_cluster_assembly_1_homolog,_mitochondrial_OS=Danio_rerio_GN=isca1_PE=2_SV=1</td><td>3.00E-24</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34262_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34266_c0_seq1.p1</td><td>sp|Q9NYZ1|F18B1_HUMAN_Protein_FAM18B1_OS=Homo_sapiens_GN=FAM18B1_PE=2_SV=2</td><td>2.00E-41</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34267_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34268_c0_seq1.p1</td><td>sp|Q7ZWE9|KCY_DANRE_UMP-CMP_kinase_OS=Danio_rerio_GN=cmpk1_PE=2_SV=2</td><td>2.00E-57</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34271_c0_seq1.p1</td><td>sp|Q9XEA8|CYSK2_ORYSJ_Cysteine_synthase_OS=Oryza_sativa_subsp._japonica_GN=RCS3_PE=2_SV=1</td><td>1.00E-130</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34276_c0_seq1.p1</td><td>sp|P36086|YKH1_YEAST_Uncharacterized_oxidoreductase_YKL071W_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YKL071W_PE=1_SV=1</td><td>1.00E-13</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34279_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34281_c0_seq1.p1</td><td>sp|Q7MBB4|CH602_GLOVI_60_kDa_chaperonin_2_OS=Gloeobacter_violaceus_(strain_PCC_7421)_GN=groL2_PE=3_SV=1</td><td>0</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34282_c0_seq1.p1</td><td>sp|Q05120|UBIL_NPVOP_Ubiquitin-like_protein_OS=Orgyia_pseudotsugata_multicapsid_polyhedrosis_virus_GN=V-UBI_PE=3_SV=1</td><td>1.00E-21</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34284_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34286_c0_seq1.p1</td><td>sp|Q9SCY2|FKB13_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP13,_chloroplastic_OS=Arabidopsis_thaliana_GN=FKBP13_PE=1_SV=2</td><td>2.00E-14</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34288_c0_seq1.p1</td><td>sp|Q8WWF8|CAPSL_HUMAN_Calcyphosin-like_protein_OS=Homo_sapiens_GN=CAPSL_PE=2_SV=4</td><td>1.00E-32</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34289_c0_seq1.p1</td><td>sp|Q8BFV2|PCID2_MOUSE_PCI_domain-containing_protein_2_OS=Mus_musculus_GN=Pcid2_PE=2_SV=1</td><td>8.00E-46</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34292_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34293_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34294_c0_seq1.p1</td><td>sp|Q9N0T5|IF4E_BOVIN_Eukaryotic_translation_initiation_factor_4E_OS=Bos_taurus_GN=EIF4E_PE=2_SV=2</td><td>2.00E-44</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34296_c0_seq1.p1</td><td>sp|O75937|DNJC8_HUMAN_DnaJ_homolog_subfamily_C_member_8_OS=Homo_sapiens_GN=DNAJC8_PE=1_SV=2</td><td>2.00E-27</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34300_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34303_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34304_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34307_c0_seq1.p1</td><td>sp|P54904|P5CR1_ARATH_Pyrroline-5-carboxylate_reductase_OS=Arabidopsis_thaliana_GN=PROC1_PE=2_SV=1</td><td>8.00E-70</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34312_c0_seq1.p1</td><td>sp|Q3SYZ4|SYDC_BOVIN_Aspartate--tRNA_ligase,_cytoplasmic_OS=Bos_taurus_GN=DARS_PE=2_SV=1</td><td>5.00E-160</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34314_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34316_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34319_c0_seq1.p1</td><td>sp|O49668|PAM68_ARATH_Protein_PAM68,_chloroplastic_OS=Arabidopsis_thaliana_GN=PAM68_PE=1_SV=1</td><td>4.00E-13</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34320_c0_seq1.p1</td><td>sp|Q8DJZ9|CLPP2_THEEB_ATP-dependent_Clp_protease_proteolytic_subunit_2_OS=Thermosynechococcus_elongatus_(strain_BP-1)_GN=clpP2_PE=3_SV=1</td><td>2.00E-91</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34321_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34326_c0_seq1.p1</td><td>sp|Q54QF9|GRPE_DICDI_GrpE_protein_homolog,_mitochondrial_OS=Dictyostelium_discoideum_GN=grpE_PE=3_SV=1</td><td>4.00E-29</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34327_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34327_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34329_c0_seq1.p1</td><td>sp|P0CO86|EAF3_CRYNJ_Chromatin_modification-related_protein_EAF3_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=EAF3_PE=3_SV=1</td><td>1.00E-37</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34330_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34331_c0_seq1.p1</td><td>sp|O96102|CALM_PHYPO_Calmodulin_OS=Physarum_polycephalum_PE=2_SV=3</td><td>1.00E-50</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34333_c0_seq1.p1</td><td>sp|P54672|AP2M_DICDI_AP-2_complex_subunit_mu_OS=Dictyostelium_discoideum_GN=apm2_PE=2_SV=2</td><td>5.00E-162</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34334_c0_seq1.p1</td><td>sp|Q8YPK4|RL17_NOSS1_50S_ribosomal_protein_L17_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=rplQ_PE=3_SV=1</td><td>9.00E-54</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34336_c0_seq1.p1</td><td>sp|Q96BR5|SELR1_HUMAN_Sel1_repeat-containing_protein_1_OS=Homo_sapiens_GN=SELRC1_PE=1_SV=2</td><td>3.00E-23</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34339_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34344_c0_seq1.p1</td><td>sp|P32897|TIM23_YEAST_Mitochondrial_import_inner_membrane_translocase_subunit_TIM23_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=TIM23_PE=1_SV=1</td><td>6.00E-14</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34346_c0_seq1.p1</td><td>sp|Q39709|FCP_ISOGA_Fucoxanthin-chlorophyll_a-c_binding_protein,_chloroplastic_OS=Isochrysis_galbana_GN=FCP_PE=1_SV=1</td><td>6.00E-22</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34348_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34349_c0_seq1.p1</td><td>sp|P49914|MTHFS_HUMAN_5-formyltetrahydrofolate_cyclo-ligase_OS=Homo_sapiens_GN=MTHFS_PE=1_SV=2</td><td>1.00E-24</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34351_c0_seq1.p1</td><td>sp|Q13247|SRSF6_HUMAN_Serine/arginine-rich_splicing_factor_6_OS=Homo_sapiens_GN=SRSF6_PE=1_SV=2</td><td>4.00E-26</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34351_c0_seq1.p4</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34352_c0_seq1.p1</td><td>sp|Q94465|GCH1_DICDI_GTP_cyclohydrolase_1_OS=Dictyostelium_discoideum_GN=gchA_PE=1_SV=2</td><td>1.00E-80</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34355_c0_seq1.p1</td><td>sp|Q969G6|RIFK_HUMAN_Riboflavin_kinase_OS=Homo_sapiens_GN=RFK_PE=1_SV=2</td><td>5.00E-37</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34357_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34357_c0_seq1.p2</td><td>sp|A4IIB8|TTC26_XENTR_Tetratricopeptide_repeat_protein_26_OS=Xenopus_tropicalis_GN=ttc26_PE=2_SV=1</td><td>1.00E-56</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34358_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34360_c0_seq1.p3</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34361_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34363_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34367_c0_seq1.p2</td><td>sp|Q9SIK2|RS252_ARATH_40S_ribosomal_protein_S25-2_OS=Arabidopsis_thaliana_GN=RPS25B_PE=2_SV=1</td><td>1.00E-23</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34369_c0_seq1.p1</td><td>sp|P26642|EF1GA_XENLA_Elongation_factor_1-gamma-A_OS=Xenopus_laevis_GN=eef1g-a_PE=1_SV=1</td><td>3.00E-54</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34370_c0_seq1.p1</td><td>sp|P73068|RUBR_SYNY3_Rubredoxin_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=rub_PE=3_SV=1</td><td>9.00E-14</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34371_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34373_c0_seq1.p1</td><td>sp|Q503V9|ENDUB_DANRE_Poly(U)-specific_endoribonuclease-B_OS=Danio_rerio_GN=endoub_PE=2_SV=1</td><td>2.00E-59</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34374_c0_seq1.p1</td><td>sp|P54985|PPIA_BLAGE_Peptidyl-prolyl_cis-trans_isomerase_OS=Blattella_germanica_GN=CYPA_PE=2_SV=1</td><td>1.00E-77</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34377_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34378_c0_seq1.p1</td><td>sp|Q54F05|DHX8_DICDI_ATP-dependent_RNA_helicase_dhx8_OS=Dictyostelium_discoideum_GN=dhx8_PE=3_SV=1</td><td>0</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34379_c0_seq1.p1</td><td>sp|Q9DC48|PRP17_MOUSE_Pre-mRNA-processing_factor_17_OS=Mus_musculus_GN=Cdc40_PE=1_SV=1</td><td>3.00E-132</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34380_c0_seq1.p1</td><td>sp|Q3ABS1|TRPC_CARHZ_Indole-3-glycerol_phosphate_synthase_OS=Carboxydothermus_hydrogenoformans_(strain_Z-2901_/_DSM_6008)_GN=trpC_PE=3_SV=1</td><td>1.00E-12</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34381_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34382_c0_seq1.p1</td><td>sp|Q9BXS5|AP1M1_HUMAN_AP-1_complex_subunit_mu-1_OS=Homo_sapiens_GN=AP1M1_PE=1_SV=3</td><td>0</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34383_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34383_c0_seq1.p4</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34384_c0_seq1.p1</td><td>sp|Q2K2Y1|RL21_RHIEC_50S_ribosomal_protein_L21_OS=Rhizobium_etli_(strain_CFN_42_/_ATCC_51251)_GN=rplU_PE=3_SV=1</td><td>1.00E-22</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34385_c0_seq1.p1</td><td>sp|Q2S535|RSMH_SALRD_Ribosomal_RNA_small_subunit_methyltransferase_H_OS=Salinibacter_ruber_(strain_DSM_13855_/_M31)_GN=rsmH_PE=3_SV=1</td><td>5.00E-56</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34390_c0_seq1.p1</td><td>sp|P53978|EF3B_YEAST_Elongation_factor_3B_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=HEF3_PE=1_SV=2</td><td>0</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34392_c0_seq1.p1</td><td>sp|O82204|RL281_ARATH_60S_ribosomal_protein_L28-1_OS=Arabidopsis_thaliana_GN=RPL28A_PE=1_SV=1</td><td>1.00E-17</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34393_c0_seq1.p1</td><td>sp|Q38799|ODPB_ARATH_Pyruvate_dehydrogenase_E1_component_subunit_beta,_mitochondrial_OS=Arabidopsis_thaliana_GN=PDH2_PE=1_SV=2</td><td>7.00E-162</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34395_c0_seq1.p1</td><td>sp|Q04HQ3|RL9_OENOB_50S_ribosomal_protein_L9_OS=Oenococcus_oeni_(strain_ATCC_BAA-331_/_PSU-1)_GN=rplI_PE=3_SV=1</td><td>3.00E-11</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34396_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34397_c0_seq1.p1</td><td>sp|P41150|CAYP1_RABIT_Calcyphosin_OS=Oryctolagus_cuniculus_GN=CAPS_PE=1_SV=1</td><td>4.00E-11</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34401_c0_seq1.p1</td><td>sp|Q54XF2|KGUA_DICDI_Guanylate_kinase_OS=Dictyostelium_discoideum_GN=guk1_PE=3_SV=1</td><td>6.00E-63</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34404_c0_seq1.p1</td><td>sp|Q5R419|SERC1_PONAB_Serine_incorporator_1_OS=Pongo_abelii_GN=SERINC1_PE=2_SV=1</td><td>7.00E-35</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34406_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34408_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34410_c0_seq1.p1</td><td>sp|Q8BGC0|HTSF1_MOUSE_HIV_Tat-specific_factor_1_homolog_OS=Mus_musculus_GN=Htatsf1_PE=1_SV=1</td><td>8.00E-35</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34411_c0_seq1.p1</td><td>sp|Q9UUB1|RIB4_SCHPO_6,7-dimethyl-8-ribityllumazine_synthase_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rib4_PE=1_SV=1</td><td>7.00E-32</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34413_c0_seq1.p1</td><td>sp|A1R1C7|UREF_ARTAT_Urease_accessory_protein_UreF_OS=Arthrobacter_aurescens_(strain_TC1)_GN=ureF_PE=3_SV=1</td><td>4.00E-14</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34419_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34420_c0_seq1.p1</td><td>sp|P42327|ADH2_GEOSE_Alcohol_dehydrogenase_OS=Geobacillus_stearothermophilus_GN=adh_PE=1_SV=1</td><td>6.00E-44</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34422_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34423_c0_seq1.p1</td><td>sp|Q7SC15|DPH3_NEUCR_Diphthamide_biosynthesis_protein_3_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=dph-3_PE=3_SV=1</td><td>6.00E-21</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34424_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34425_c0_seq1.p1</td><td>sp|Q32L10|TM205_BOVIN_Transmembrane_protein_205_OS=Bos_taurus_GN=TMEM205_PE=2_SV=1</td><td>1.00E-13</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34428_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34428_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34430_c0_seq1.p1</td><td>sp|O02691|HCD2_BOVIN_3-hydroxyacyl-CoA_dehydrogenase_type-2_OS=Bos_taurus_GN=HSD17B10_PE=1_SV=3</td><td>7.00E-86</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34431_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34431_c0_seq1.p3</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34434_c0_seq1.p1</td><td>sp|Q54EY2|EI2BB_DICDI_Translation_initiation_factor_eIF-2B_subunit_beta_OS=Dictyostelium_discoideum_GN=eif2b2_PE=3_SV=1</td><td>2.00E-91</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34435_c0_seq1.p1</td><td>sp|O01666|ATPG_DROME_ATP_synthase_subunit_gamma,_mitochondrial_OS=Drosophila_melanogaster_GN=ATPsyn-gamma_PE=2_SV=2</td><td>6.00E-56</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34437_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34439_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34444_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34446_c0_seq1.p2</td><td>sp|P20435|RPAB2_YEAST_DNA-directed_RNA_polymerases_I,_II,_and_III_subunit_RPABC2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=RPO26_PE=1_SV=1</td><td>3.00E-37</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34447_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34451_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34457_c0_seq1.p1</td><td>sp|P52233|THIO_THIFE_Thioredoxin_OS=Thiobacillus_ferrooxidans_GN=trxA_PE=3_SV=1</td><td>3.00E-17</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34458_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34459_c0_seq1.p2</td><td>sp|Q9UK45|LSM7_HUMAN_U6_snRNA-associated_Sm-like_protein_LSm7_OS=Homo_sapiens_GN=LSM7_PE=1_SV=1</td><td>1.00E-43</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34460_c0_seq1.p1</td><td>sp|P70563|NUDT6_RAT_Nucleoside_diphosphate-linked_moiety_X_motif_6_OS=Rattus_norvegicus_GN=Nudt6_PE=1_SV=1</td><td>8.00E-43</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34462_c0_seq1.p1</td><td>sp|Q9P7S2|RPN6_SCHPO_Probable_26S_proteasome_regulatory_subunit_rpn6_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpn6_PE=2_SV=1</td><td>3.00E-108</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34467_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34468_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34470_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34474_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34476_c0_seq1.p1</td><td>sp|Q869R1|CTLHB_DICDI_CTL-like_protein_DDB_G0274487_OS=Dictyostelium_discoideum_GN=DDB_G0274487_PE=3_SV=1</td><td>2.00E-15</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34481_c0_seq1.p1</td><td>sp|Q9NPF5|DMAP1_HUMAN_DNA_methyltransferase_1-associated_protein_1_OS=Homo_sapiens_GN=DMAP1_PE=1_SV=1</td><td>8.00E-35</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34482_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34483_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34484_c0_seq1.p1</td><td>sp|O43396|TXNL1_HUMAN_Thioredoxin-like_protein_1_OS=Homo_sapiens_GN=TXNL1_PE=1_SV=3</td><td>2.00E-30</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34485_c0_seq1.p1</td><td>sp|Q8R2Y8|PTH2_MOUSE_Peptidyl-tRNA_hydrolase_2,_mitochondrial_OS=Mus_musculus_GN=Ptrh2_PE=2_SV=1</td><td>1.00E-32</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34486_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34487_c0_seq1.p1</td><td>sp|P23193|TCEA1_HUMAN_Transcription_elongation_factor_A_protein_1_OS=Homo_sapiens_GN=TCEA1_PE=1_SV=2</td><td>9.00E-27</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34490_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34491_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34493_c0_seq1.p1</td><td>sp|P70187|HIAT1_MOUSE_Hippocampus_abundant_transcript_1_protein_OS=Mus_musculus_GN=Hiat1_PE=2_SV=3</td><td>1.00E-45</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34494_c0_seq1.p1</td><td>sp|P41976|SODM_BOVIN_Superoxide_dismutase_[Mn],_mitochondrial_OS=Bos_taurus_GN=SOD2_PE=2_SV=1</td><td>6.00E-82</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34495_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34496_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34498_c0_seq1.p1</td><td>sp|Q148L6|DHDH_BOVIN_Trans-1,2-dihydrobenzene-1,2-diol_dehydrogenase_OS=Bos_taurus_GN=DHDH_PE=2_SV=1</td><td>3.00E-58</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34499_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34500_c0_seq1.p1</td><td>sp|Q43468|STIP_SOYBN_Heat_shock_protein_STI_OS=Glycine_max_GN=STI_PE=2_SV=1</td><td>2.00E-11</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34503_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34504_c0_seq1.p1</td><td>sp|Q5U2P3|ZFN2A_RAT_AN1-type_zinc_finger_protein_2A_OS=Rattus_norvegicus_GN=Zfand2a_PE=2_SV=1</td><td>2.00E-33</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34505_c0_seq1.p1</td><td>sp|Q4N4N8|TXND_THEPA_Thioredoxin_domain-containing_protein_OS=Theileria_parva_GN=TP02_0602_PE=1_SV=1</td><td>1.00E-42</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34508_c0_seq1.p1</td><td>sp|D3DFG8|PSPA_HYDTT_Phosphoserine_phosphatase_1_OS=Hydrogenobacter_thermophilus_(strain_DSM_6534_/_IAM_12695_/_TK-6)_GN=pspA_PE=1_SV=1</td><td>2.00E-12</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34509_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34512_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34516_c0_seq1.p2</td><td>sp|Q6NRI0|P6R3A_XENLA_Serine/threonine-protein_phosphatase_6_regulatory_subunit_3-A_OS=Xenopus_laevis_GN=ppp6r3-a_PE=2_SV=1</td><td>2.00E-19</td><td></td><td></td></tr>
<tr><td>comp34517_c0_seq1.p1</td><td>sp|Q8H124|Y2446_ARATH_Uncharacterized_protein_At2g34460,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g34460_PE=1_SV=1</td><td>3.00E-16</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34518_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34520_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34522_c0_seq1.p1</td><td>sp|Q9GSB0|CRTP1_DICDI_Crt_homolog_1_OS=Dictyostelium_discoideum_GN=crtp1_PE=2_SV=1</td><td>1.00E-31</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34523_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34525_c0_seq1.p1</td><td>sp|Q5SPB1|S38A2_DANRE_Sodium-coupled_neutral_amino_acid_transporter_2_OS=Danio_rerio_GN=slc38a2_PE=2_SV=1</td><td>1.00E-25</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34526_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34527_c0_seq1.p1</td><td>sp|Q94CG2|BET12_ARATH_Bet1-like_SNARE_1-2_OS=Arabidopsis_thaliana_GN=BET12_PE=2_SV=4</td><td>2.00E-13</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34530_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34531_c0_seq1.p1</td><td>sp|Q9HC07|TM165_HUMAN_Transmembrane_protein_165_OS=Homo_sapiens_GN=TMEM165_PE=1_SV=1</td><td>3.00E-39</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34532_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34533_c0_seq1.p1</td><td>sp|Q95266|KCC2D_PIG_Calcium/calmodulin-dependent_protein_kinase_type_II_subunit_delta_OS=Sus_scrofa_GN=CAMK2D_PE=2_SV=1</td><td>2.00E-70</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34534_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34535_c0_seq1.p1</td><td>sp|P58674|ISPH_NOSS1_4-hydroxy-3-methylbut-2-enyl_diphosphate_reductase_OS=Nostoc_sp._(strain_PCC_7120_/_UTEX_2576)_GN=ispH_PE=3_SV=1</td><td>6.00E-132</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34536_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34541_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34542_c0_seq1.p1</td><td>sp|Q9FIX3|PP407_ARATH_Pentatricopeptide_repeat-containing_protein_At5g39710_OS=Arabidopsis_thaliana_GN=EMB2745_PE=2_SV=1</td><td>1.00E-54</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34543_c0_seq1.p1</td><td>sp|Q9WUU7|CATZ_MOUSE_Cathepsin_Z_OS=Mus_musculus_GN=Ctsz_PE=2_SV=1</td><td>2.00E-70</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34549_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp3455_c0_seq2.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34552_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34553_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34555_c0_seq1.p1</td><td>sp|O96622|ARPC1_DICDI_Actin-related_protein_2/3_complex_subunit_1_OS=Dictyostelium_discoideum_GN=arcA_PE=1_SV=1</td><td>4.00E-87</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34556_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34557_c0_seq1.p1</td><td>sp|Q55499|SSB_SYNY3_Single-stranded_DNA-binding_protein_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=ssb_PE=3_SV=1</td><td>3.00E-16</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34559_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34560_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34561_c0_seq1.p1</td><td>sp|Q2KII6|NGDN_BOVIN_Neuroguidin_OS=Bos_taurus_GN=NGDN_PE=2_SV=1</td><td>6.00E-26</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34562_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34566_c0_seq1.p1</td><td>sp|Q4R8Y8|RU2A_MACFA_U2_small_nuclear_ribonucleoprotein_A'_OS=Macaca_fascicularis_GN=SNRPA1_PE=2_SV=1</td><td>8.00E-62</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34571_c0_seq1.p1</td><td>sp|Q8H0W1|PLSP1_ARATH_Chloroplast_processing_peptidase_OS=Arabidopsis_thaliana_GN=PLSP1_PE=2_SV=2</td><td>1.00E-22</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34574_c0_seq1.p1</td><td>sp|Q1LXS2|PSMG2_DANRE_Proteasome_assembly_chaperone_2_OS=Danio_rerio_GN=psmg2_PE=2_SV=1</td><td>2.00E-14</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34575_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34578_c0_seq1.p1</td><td>sp|Q06652|GPX4_CITSI_Probable_phospholipid_hydroperoxide_glutathione_peroxidase_OS=Citrus_sinensis_GN=CSA_PE=1_SV=1</td><td>7.00E-40</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34580_c0_seq1.p1</td><td>sp|Q54BM8|U652_DICDI_UPF0652_protein_OS=Dictyostelium_discoideum_GN=DDB_G0293552_PE=3_SV=1</td><td>7.00E-159</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34582_c0_seq1.p1</td><td>sp|Q2RP11|ENGB_RHORT_Probable_GTP-binding_protein_EngB_OS=Rhodospirillum_rubrum_(strain_ATCC_11170_/_NCIB_8255)_GN=engB_PE=3_SV=1</td><td>3.00E-24</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34583_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34584_c0_seq1.p1</td><td>sp|Q68EH8|FAD1_DANRE_FAD_synthase_OS=Danio_rerio_GN=flad1_PE=2_SV=1</td><td>4.00E-32</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34590_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34591_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34592_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34595_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34597_c0_seq1.p1</td><td>sp|Q24740|CDC37_DROVI_Hsp90_co-chaperone_Cdc37_OS=Drosophila_virilis_GN=Cdc37_PE=3_SV=1</td><td>2.00E-48</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34599_c0_seq1.p1</td><td>sp|Q9Y253|POLH_HUMAN_DNA_polymerase_eta_OS=Homo_sapiens_GN=POLH_PE=1_SV=1</td><td>9.00E-27</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34601_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34605_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34606_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34607_c0_seq1.p1</td><td>sp|P62246|RS15A_RAT_40S_ribosomal_protein_S15a_OS=Rattus_norvegicus_GN=Rps15a_PE=1_SV=2</td><td>4.00E-73</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34611_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34612_c0_seq1.p1</td><td>sp|Q54PV7|EIF2A_DICDI_Eukaryotic_translation_initiation_factor_2A_OS=Dictyostelium_discoideum_GN=eif2a_PE=3_SV=1</td><td>1.00E-75</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34620_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34621_c0_seq1.p1</td><td>sp|Q06683|IRC3_YEAST_Putative_ATP-dependent_helicase_IRC3_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=IRC3_PE=1_SV=1</td><td>1.00E-41</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34622_c0_seq1.p1</td><td>sp|Q5R7R9|SNW1_PONAB_SNW_domain-containing_protein_1_OS=Pongo_abelii_GN=SNW1_PE=2_SV=1</td><td>5.00E-83</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34624_c0_seq1.p1</td><td>sp|P04636|MDHM_RAT_Malate_dehydrogenase,_mitochondrial_OS=Rattus_norvegicus_GN=Mdh2_PE=1_SV=2</td><td>5.00E-118</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34632_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34633_c0_seq1.p1</td><td>sp|B5EC42|DNAK_GEOBB_Chaperone_protein_DnaK_OS=Geobacter_bemidjiensis_(strain_Bem_/_ATCC_BAA-1014_/_DSM_16622)_GN=dnaK_PE=3_SV=1</td><td>5.00E-54</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34635_c0_seq1.p1</td><td>sp|Q12271|INP53_YEAST_Polyphosphatidylinositol_phosphatase_INP53_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=INP53_PE=1_SV=1</td><td>6.00E-20</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34638_c0_seq1.p1</td><td>sp|P35627|CYPX_USEUD_Peptidyl-prolyl_cis-trans_isomerase_OS=Unspecified_eudicot_DB-1992_PE=2_SV=1</td><td>3.00E-34</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34639_c0_seq1.p1</td><td>sp|Q8BGB8|COQ4_MOUSE_Ubiquinone_biosynthesis_protein_COQ4_homolog,_mitochondrial_OS=Mus_musculus_GN=Coq4_PE=2_SV=1</td><td>8.00E-69</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34641_c1_seq1.p1</td><td>sp|Q38942|RAE1L_ARATH_Rae1-like_protein_At1g80670_OS=Arabidopsis_thaliana_GN=At1g80670_PE=2_SV=2</td><td>8.00E-96</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34642_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34643_c0_seq1.p1</td><td>sp|O61231|RL10_DROME_60S_ribosomal_protein_L10_OS=Drosophila_melanogaster_GN=RpL10_PE=2_SV=1</td><td>2.00E-102</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34644_c0_seq1.p1</td><td>sp|Q9H7B2|RPF2_HUMAN_Ribosome_production_factor_2_homolog_OS=Homo_sapiens_GN=RPF2_PE=1_SV=2</td><td>1.00E-82</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34646_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34652_c0_seq1.p1</td><td>sp|B6K180|RSSA1_SCHJY_40S_ribosomal_protein_S0-A_OS=Schizosaccharomyces_japonicus_(strain_yFS275_/_FY16936)_GN=rps0a_PE=3_SV=1</td><td>1.00E-98</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34653_c0_seq1.p1</td><td>sp|P13021|CAPZB_DICDI_F-actin-capping_protein_subunit_beta_OS=Dictyostelium_discoideum_GN=acpA_PE=1_SV=1</td><td>8.00E-70</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34654_c0_seq1.p2</td><td>sp|Q9CQ90|CI085_MOUSE_Uncharacterized_protein_C9orf85_homolog_OS=Mus_musculus_PE=2_SV=1</td><td>8.00E-23</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34657_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34664_c0_seq1.p1</td><td>sp|Q55909|Y305_SYNY3_TVP38/TMEM64_family_membrane_protein_slr0305_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr0305_PE=3_SV=1</td><td>4.00E-11</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34665_c0_seq1.p1</td><td>sp|Q54TC5|MAFL2_DICDI_Maf-like_protein_DDB_G0281937_OS=Dictyostelium_discoideum_GN=DDB_G0281937_PE=3_SV=1</td><td>1.00E-28</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34667_c0_seq1.p1</td><td>sp|Q2S591|Y495_SALRD_UPF0301_protein_SRU_0495_OS=Salinibacter_ruber_(strain_DSM_13855_/_M31)_GN=SRU_0495_PE=3_SV=1</td><td>5.00E-16</td><td></td><td></td></tr>
<tr><td>comp34670_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34672_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34678_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34680_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34681_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34688_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34691_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34692_c0_seq1.p2</td><td>sp|Q9STX1|ACBP3_ARATH_Acyl-CoA-binding_domain-containing_protein_3_OS=Arabidopsis_thaliana_GN=ACBP3_PE=1_SV=1</td><td>2.00E-12</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34699_c0_seq1.p1</td><td>sp|Q9R1P4|PSA1_MOUSE_Proteasome_subunit_alpha_type-1_OS=Mus_musculus_GN=Psma1_PE=1_SV=1</td><td>1.00E-91</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34705_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34707_c0_seq1.p1</td><td>sp|P60901|PSA6_RAT_Proteasome_subunit_alpha_type-6_OS=Rattus_norvegicus_GN=Psma6_PE=1_SV=1</td><td>1.00E-41</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34709_c0_seq1.p1</td><td>sp|Q75GM1|TRXH5_ORYSJ_Thioredoxin_H5_OS=Oryza_sativa_subsp._japonica_GN=Os05g0480200_PE=2_SV=1</td><td>1.00E-18</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34712_c0_seq1.p1</td><td>sp|Q58549|ADPP_METJA_ADP-ribose_pyrophosphatase_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=nudF_PE=1_SV=1</td><td>1.00E-19</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34714_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34719_c0_seq1.p2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34721_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34723_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34724_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34726_c0_seq1.p1</td><td>sp|Q8C8R3|ANK2_MOUSE_Ankyrin-2_OS=Mus_musculus_GN=Ank2_PE=1_SV=2</td><td>1.00E-29</td><td>[illegible]</td><td>[illegible]</td></tr>
<tr><td>comp34727_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34728_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34731_c0_seq1.p1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>comp34732_c0_seq1.p1</td><td>sp|Q8LGF7|PEX4_ARATH_Protein_PEROXIN-4_OS=Arabidopsis_thaliana_GN=PEX4_PE=1_SV=1</td><td>1.00E-56</td><td>[illegible]</td><td>[illegible]</td></tr>
</table>

comp34737_c0_seq1.p1	sp|P78898|TGCE2_SCHPO_Probable_lipase_C16A3.12c_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC16A3.12c_PE=2_SV=2	2.00E-69	[illegible]	[illegible]
comp3474_c0_seq1.p1	sp|P54678|ATC1_DICDI_Calcium-transporting_ATPase_PAT1_OS=Dictyostelium_discoideum_GN=patA_PE=2_SV=2	5.00E-33	[illegible]	[illegible]
comp3474_c1_seq1.p2	sp|Q37145|ACA1_ARATH_Calcium-transporting_ATPase_1,_chloroplastic_OS=Arabidopsis_thaliana_GN=ACA1_PE=1_SV=3	2.00E-27	[illegible]	[illegible]
comp34740_c0_seq1.p1	sp|Q03965|L181_CHLMO_Chlorophyll_a-b_binding_protein_L1818,_chloroplastic_OS=Chlamydomonas_moewusii_GN=L1818_PE=2_SV=1	3.00E-12	[illegible]	[illegible]
comp34746_c0_seq1.p1				
comp34747_c0_seq1.p1				
comp34748_c0_seq1.p1				
comp34750_c0_seq1.p1				
comp34751_c0_seq1.p1	sp|Q921I9|EXOS4_MOUSE_Exosome_complex_component_RRP41_OS=Mus_musculus_GN=Exosc4_PE=2_SV=3	1.00E-64	[illegible]	[illegible]
comp34752_c0_seq1.p1				
comp34753_c0_seq1.p1				
comp34754_c0_seq1.p1				
comp34761_c0_seq1.p1				
comp34762_c0_seq1.p2	sp|Q9FG71|U172_ARATH_UPF0172_protein_At5g55940_OS=Arabidopsis_thaliana_GN=EMB2731_PE=2_SV=1	2.00E-18	GO:0003674,GO:0005783,GO:0005783	[illegible]
comp34763_c0_seq1.p1				
comp34763_c0_seq1.p2				
comp34766_c0_seq1.p2	sp|Q869V1|NRAM1_DICDI_Metal_transporter_nramp1_homolog_OS=Dictyostelium_discoideum_GN=nramp1_PE=2_SV=1	5.00E-18	[illegible]	[illegible]
comp34772_c0_seq1.p1				
comp34773_c0_seq1.p1	sp|Q0BU77|ENGB_GRABC_Probable_GTP-binding_protein_EngB_OS=Granulibacter_bethesdensis_(strain_ATCC_BAA-1260_/_CGDNIH1)_GN=engB_PE=3_SV=1	2.00E-32	[illegible]	[illegible]
comp34779_c0_seq1.p1	sp|Q8VZ67|Y4919_ARATH_Uncharacterized_zinc_finger_CCHC_domain-containing_protein_At4g19190_OS=Arabidopsis_thaliana_GN=At4g19190_PE=2_SV=1	3.00E-15	GO:0003676,GO:0008150,GO:0008270,GO:0046872	[illegible]
comp34781_c0_seq1.p1	sp|Q6AXT8|SF3A2_RAT_Splicing_factor_3A_subunit_2_OS=Rattus_norvegicus_GN=Sf3a2_PE=2_SV=1	1.00E-99	[illegible]	[illegible]
comp34784_c0_seq1.p1				
comp34788_c0_seq1.p1	sp|P35143|G3P_COLGL_Glyceraldehyde-3-phosphate_dehydrogenase_OS=Colletotrichum_gloeosporioides_GN=GPDA_PE=2_SV=1	4.00E-149	[illegible]	[illegible]
comp34789_c0_seq1.p1				
comp34800_c0_seq1.p1				
comp34803_c0_seq1.p1	sp|Q86V88|MGDP1_HUMAN_Magnesium-dependent_phosphatase_1_OS=Homo_sapiens_GN=MDP1_PE=1_SV=1	3.00E-24	[illegible]	[illegible]
comp34804_c0_seq1.p1				
comp34805_c0_seq1.p1	sp|Q9FVT2|EF1G2_ARATH_Probable_elongation_factor_1-gamma_2_OS=Arabidopsis_thaliana_GN=At1g57720_PE=2_SV=1	4.00E-33	[illegible]	[illegible]
comp34807_c0_seq1.p1				
comp34815_c0_seq1.p1	sp|Q5RFL8|YTHD3_PONAB_YTH_domain_family_protein_3_OS=Pongo_abelii_GN=YTHDF3_PE=2_SV=1	6.00E-11	GO:0003723,GO:1990247	[illegible]
comp34816_c0_seq1.p1				
comp34820_c0_seq1.p2				
comp34821_c0_seq1.p1	sp|O82782|HIS4_ARATH_1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]_imidazole-4-carboxamide_isomerase,_chloroplastic_OS=Arabidopsis_thaliana_GN=HIS6_PE=2_SV=1	4.00E-97	[illegible]	[illegible]
comp34828_c0_seq1.p1				
comp34834_c0_seq1.p1	sp|Q9M2E2|SDR1_ARATH_(+)-neomenthol_dehydrogenase_OS=Arabidopsis_thaliana_GN=SDR1_PE=1_SV=1	3.00E-22	[illegible]	[illegible]
comp34835_c0_seq1.p1	sp|Q39211|RPB3A_ARATH_DNA-directed_RNA_polymerase_II_subunit_RPB3-A_OS=Arabidopsis_thaliana_GN=RPB36A_PE=2_SV=1	1.00E-66	[illegible]	[illegible]
comp34836_c0_seq1.p1	sp|P19881|PNPP_YEAST_4-nitrophenylphosphatase_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PHO13_PE=1_SV=2	4.00E-49	[illegible]	[illegible]
comp34837_c0_seq1.p1	sp|Q6DID3|SCAF8_MOUSE_Protein_SCAF8_OS=Mus_musculus_GN=Scaf8_PE=1_SV=1	1.00E-17	[illegible]	[illegible]
comp34845_c0_seq1.p1	sp|Q13432|U119A_HUMAN_Protein_unc-119_homolog_A_OS=Homo_sapiens_GN=UNC119_PE=1_SV=1	2.00E-57	[illegible]	[illegible]
comp34849_c0_seq1.p2	sp|P17078|RL35_RAT_60S_ribosomal_protein_L35_OS=Rattus_norvegicus_GN=Rpl35_PE=1_SV=3	8.00E-40	[illegible]	[illegible]
comp34852_c0_seq1.p1				
comp34853_c0_seq1.p2				
comp34855_c0_seq1.p2				
comp34855_c0_seq1.p4				
comp34859_c0_seq1.p1	sp|P56286|IF2A_SCHPO_Eukaryotic_translation_initiation_factor_2_subunit_alpha_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=tif211_PE=1_SV=1	2.00E-107	[illegible]	[illegible]
comp34868_c0_seq1.p1	sp|P43394|K502_ACTDE_Fruit_protein_pKIWI502_OS=Actinidia_deliciosa_GN=pKIWI502_PE=2_SV=1	5.00E-23	GO:0016491,GO:0055114	[illegible]
comp34869_c0_seq1.p1				
comp34874_c0_seq1.p1				
comp34876_c0_seq1.p1	sp|P63164|RSMN_RAT_Small_nuclear_ribonucleoprotein-associated_protein_N_OS=Rattus_norvegicus_GN=Snrpn_PE=2_SV=1	4.00E-38	[illegible]	[illegible]
comp34877_c0_seq1.p1	sp|P73056|YC64L_SYNY3_Uncharacterized_monothiol_glutaredoxin_ycf64-like_OS=Synechocystis_sp._(strain_PCC_6803_/_Kazusa)_GN=slr1846_PE=3_SV=1	7.00E-42	[illegible]	[illegible]
comp34880_c0_seq1.p1	sp|Q83CJ2|CBPA_COXBU_Curved_DNA-binding_protein_OS=Coxiella_burnetii_(strain_RSA_493_/_Nine_Mile_phase_I)_GN=cbpA_PE=3_SV=1	5.00E-43	[illegible]	[illegible]
comp34884_c0_seq1.p1	sp|A9TND9|CYNS_PHYPA_Cyanate_hydratase_OS=Physcomitrella_patens_subsp._patens_GN=CYN_PE=3_SV=1	9.00E-57	[illegible]	[illegible]
comp34887_c0_seq1.p2				
comp34889_c0_seq1.p1				
comp34904_c0_seq1.p1				
comp34906_c0_seq1.p2				
comp34907_c0_seq1.p1	sp|Q32L10|TM205_BOVIN_Transmembrane_protein_205_OS=Bos_taurus_GN=TMEM205_PE=2_SV=1	4.00E-18	[illegible]	[illegible]
comp34910_c0_seq1.p1				
comp34912_c0_seq1.p1				
comp34915_c0_seq1.p1				
comp34920_c0_seq1.p1	sp|Q8K2U2|ALKB6_MOUSE_Probable_alpha-ketoglutarate-dependent_dioxygenase_ABH6_OS=Mus_musculus_GN=Alkbh6_PE=2_SV=2	4.00E-15	[illegible]	[illegible]
comp34931_c0_seq1.p3				
comp34935_c0_seq1.p1				
comp34941_c0_seq1.p1				
comp34966_c0_seq1.p1				
comp34977_c0_seq1.p1				
comp34978_c0_seq1.p2	sp|Q99N89|RM43_MOUSE_39S_ribosomal_protein_L43,_mitochondrial_OS=Mus_musculus_GN=Mrpl43_PE=2_SV=1	3.00E-15	[illegible]	[illegible]
comp34985_c0_seq1.p1	sp|Q46845|YGHU_ECOLI_Uncharacterized_GST-like_protein_yghU_OS=Escherichia_coli_(strain_K12)_GN=yghU_PE=1_SV=2	3.00E-73	[illegible]	[illegible]
comp34986_c0_seq1.p1	sp|Q24439|ATPO_DROME_ATP_synthase_subunit_O,_mitochondrial_OS=Drosophila_melanogaster_GN=Oscp_PE=2_SV=2	1.00E-35	[illegible]	[illegible]
comp34987_c0_seq1.p1				
comp34988_c0_seq1.p1				
comp34994_c0_seq1.p2				
comp34995_c0_seq1.p1				
comp35000_c0_seq1.p1	sp|A6H7B5|CSN3_BOVIN_COP9_signalosome_complex_subunit_3_OS=Bos_taurus_GN=COPS3_PE=2_SV=1	1.00E-61	[illegible]	[illegible]
comp35003_c0_seq1.p1				
comp35007_c0_seq1.p1	sp|P0AG10|RPE_SHIFL_Ribulose-phosphate_3-epimerase_OS=Shigella_flexneri_GN=rpe_PE=3_SV=1	1.00E-115	[illegible]	[illegible]
comp35012_c0_seq1.p1	sp|P50607|TUB_HUMAN_Tubby_protein_homolog_OS=Homo_sapiens_GN=TUB_PE=1_SV=1	4.00E-19	[illegible]	[illegible]
comp35013_c0_seq1.p1	sp|Q92372|RFA1_SCHPO_Replication_factor_A_protein_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=ssb1_PE=1_SV=1	3.00E-15	[illegible]	[illegible]
comp35015_c0_seq1.p1				
comp35017_c0_seq1.p1				
comp35022_c0_seq1.p1	sp|P42791|RL182_ARATH_60S_ribosomal_protein_L18-2_OS=Arabidopsis_thaliana_GN=RPL18B_PE=1_SV=2	1.00E-69	[illegible]	[illegible]
comp35023_c0_seq1.p1				
comp35025_c0_seq1.p2	sp|Q9VU02|SMD1_DROME_Probable_small_nuclear_ribonucleoprotein_Sm_D1_OS=Drosophila_melanogaster_GN=SmD1_PE=1_SV=1	2.00E-29	[illegible]	[illegible]
comp35026_c0_seq1.p1	sp|Q9SVV6|KCO6_ARATH_Probable_calcium-activated_outward-rectifying_potassium_channel_6_OS=Arabidopsis_thaliana_GN=KCO6_PE=2_SV=1	2.00E-29	[illegible]	[illegible]
comp35029_c0_seq1.p1				
comp35036_c0_seq1.p1				
comp35038_c0_seq1.p1	sp|Q945U1|RS15_ELAOL_40S_ribosomal_protein_S15_OS=Elaeis_oleifera_GN=RPS15_PE=2_SV=1	6.00E-66	[illegible]	[illegible]
comp35046_c0_seq1.p3				
comp35046_c0_seq1.p4				
comp35050_c0_seq1.p1				
comp35051_c0_seq1.p2	sp|Q03685|BIP5_TOBAC_Luminal-binding_protein_5_OS=Nicotiana_tabacum_GN=BIP5_PE=2_SV=1	4.00E-71	[illegible]	[illegible]
comp35058_c0_seq1.p1				
comp35060_c0_seq1.p1				
comp35061_c0_seq1.p1	sp|P81760|TL17_ARATH_Thylakoid_lumenal_17.4_kDa_protein,_chloroplastic_OS=Arabidopsis_thaliana_GN=At5g53490_PE=1_SV=2	1.00E-28	[illegible]	[illegible]
comp35065_c0_seq1.p1				
comp35069_c0_seq1.p1				
comp35071_c0_seq1.p1				
comp35073_c0_seq1.p1	sp|Q5XQC7|BON3_ARATH_Protein_BONZAI_3_OS=Arabidopsis_thaliana_GN=BON3_PE=1_SV=1	2.00E-20	[illegible]	[illegible]
comp35075_c0_seq1.p3				
comp35089_c0_seq1.p1				
comp35092_c0_seq1.p1				
comp35093_c0_seq1.p2	sp|Q1ZXG8|D1060_DICDI_Probable_tyrosine-protein_phosphatase_DG1060_OS=Dictyostelium_discoideum_GN=DG1060_PE=3_SV=1	4.00E-24	[illegible]	[illegible]
comp35102_c0_seq1.p1				
comp35104_c0_seq1.p2				
comp35110_c0_seq1.p1	sp|P25851|F16P1_ARATH_Fructose-1,6-bisphosphatase,_chloroplastic_OS=Arabidopsis_thaliana_GN=FBP_PE=1_SV=2	1.00E-63	[illegible]	[illegible]
comp35115_c0_seq1.p1	sp|P22232|FBRL_XENLA_rRNA_2'-O-methyltransferase_fibrillarin_OS=Xenopus_laevis_GN=fbl_PE=2_SV=1	5.00E-129	[illegible]	[illegible]
comp35125_c0_seq1.p1				
comp35131_c0_seq1.p1	sp|Q567Z6|CRIPT_DANRE_Cysteine-rich_PDZ-binding_protein_OS=Danio_rerio_GN=cript_PE=3_SV=1	3.00E-31	[illegible]	[illegible]
comp35133_c0_seq1.p1				
comp35137_c0_seq1.p2				
comp35144_c0_seq1.p2				
comp35145_c0_seq1.p1	sp|Q54MV7|NDUAC_DICDI_NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_12_OS=Dictyostelium_discoideum_GN=ndufa12_PE=2_SV=2	4.00E-20	[illegible]	[illegible]
comp35148_c0_seq1.p1	sp|Q8H124|Y2446_ARATH_Uncharacterized_protein_At2g34460,_chloroplastic_OS=Arabidopsis_thaliana_GN=At2g34460_PE=1_SV=1	7.00E-12	[illegible]	[illegible]
comp35152_c0_seq1.p1				
comp35153_c0_seq1.p1				
comp35154_c0_seq1.p1				
comp35158_c0_seq1.p1				
comp35163_c0_seq1.p1				
comp35176_c0_seq1.p1	sp|O04375|2A5A_ARATH_Serine/threonine_protein_phosphatase_2A_57_kDa_regulatory_subunit_B'_alpha_isoform_OS=Arabidopsis_thaliana_GN=B'ALPHA_PE=1_SV=1	3.00E-47	[illegible]	[illegible]
comp35185_c0_seq1.p1				
comp35191_c0_seq1.p1	sp|Q9SS17|RS241_ARATH_40S_ribosomal_protein_S24-1_OS=Arabidopsis_thaliana_GN=RPS24A_PE=2_SV=1	2.00E-38	[illegible]	[illegible]
comp35204_c0_seq1.p1				
comp35208_c0_seq1.p1				
comp35209_c0_seq1.p2	sp|B4NIN8|ARMET_DROWI_Mesencephalic_astrocyte-derived_neurotrophic_factor_homolog_OS=Drosophila_willistoni_GN=Manf_PE=3_SV=1	5.00E-29	[illegible]	[illegible]
comp3521_c0_seq1.p2	sp|Q9SF40|RL4A_ARATH_60S_ribosomal_protein_L4-1_OS=Arabidopsis_thaliana_GN=RPL4A_PE=2_SV=1	2.00E-45	[illegible]	[illegible]
comp35213_c0_seq1.p1				
comp35217_c0_seq1.p1				
comp35219_c0_seq1.p1				
comp35229_c0_seq1.p1				
comp35230_c0_seq1.p1				
comp35245_c0_seq1.p2				
comp35250_c0_seq1.p1				
comp35270_c0_seq1.p1	sp|O43447|PPIH_HUMAN_Peptidyl-prolyl_cis-trans_isomerase_H_OS=Homo_sapiens_GN=PPIH_PE=1_SV=1	2.00E-88	[illegible]	[illegible]
comp35275_c0_seq1.p2				
comp35279_c0_seq1.p1				
comp35290_c0_seq1.p1				
comp35294_c0_seq1.p1	sp|Q9LVV5|TL15B_ARATH_Thylakoid_lumenal_15.0_kDa_protein_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=At5g52970_PE=1_SV=2	2.00E-44	[illegible]	[illegible]
comp35302_c0_seq1.p1				
comp35303_c0_seq1.p1				
comp35305_c0_seq1.p1				
comp35306_c0_seq1.p1				
comp35323_c0_seq1.p1	sp|Q13347|EIF3I_HUMAN_Eukaryotic_translation_initiation_factor_3_subunit_I_OS=Homo_sapiens_GN=EIF3I_PE=1_SV=1	3.00E-102	[illegible]	[illegible]
comp35337_c0_seq1.p1				
comp35355_c0_seq1.p1				
comp35357_c0_seq1.p1				
comp35363_c0_seq1.p1	sp|Q9LSU1|PSA5_ORYSJ_Proteasome_subunit_alpha_type-5_OS=Oryza_sativa_subsp._japonica_GN=PAE1_PE=2_SV=1	7.00E-115	[illegible]	[illegible]
comp35364_c0_seq1.p1				
comp35365_c0_seq1.p2				
comp35367_c0_seq1.p1				
comp35373_c0_seq1.p1	sp|Q6PH85|DCNL2_HUMAN_DCN1-like_protein_2_OS=Homo_sapiens_GN=DCUN1D2_PE=2_SV=1	1.00E-30		
comp35375_c0_seq1.p1				
comp3539_c0_seq1.p1	sp|P26458|APPB_ECOLI_Cytochrome_bd-II_oxidase_subunit_2_OS=Escherichia_coli_(strain_K12)_GN=appB_PE=1_SV=2	4.00E-109	[illegible]	[illegible]
comp35391_c0_seq1.p1				
comp35399_c0_seq1.p1				
comp35400_c0_seq1.p1				
comp35401_c0_seq1.p2				
comp35401_c0_seq1.p3				
comp35410_c0_seq1.p1				
comp35415_c0_seq1.p1				
comp35429_c0_seq1.p1				
comp35438_c0_seq1.p1	sp|Q9FLU1|BIN4_ARATH_DNA-binding_protein_BIN4_OS=Arabidopsis_thaliana_GN=BIN4_PE=1_SV=2	2.00E-15	[illegible]	[illegible]
comp35439_c0_seq1.p1				
comp35446_c0_seq1.p1				
comp35448_c0_seq1.p1				
comp35462_c0_seq1.p2				
comp35464_c0_seq1.p1				
comp35466_c0_seq1.p1				
comp35468_c0_seq1.p1				
comp35474_c0_seq1.p2				
comp35485_c0_seq1.p1				
comp35506_c0_seq1.p1				
comp3551_c0_seq1.p1	sp|Q3YUR7|ACTP_SHISS_Cation/acetate_symporter_ActP_OS=Shigella_sonnei_(strain_Ss046)_GN=actP_PE=3_SV=1	5.00E-175	[illegible]	[illegible]
comp35511_c0_seq1.p2				
comp35520_c0_seq1.p1	sp|P49154|RS2_URECA_40S_ribosomal_protein_S2_OS=Urechis_caupo_GN=RPS2_PE=2_SV=1	1.00E-119	[illegible]	[illegible]
comp35535_c0_seq1.p1				
comp35538_c0_seq1.p2				
comp35559_c0_seq1.p1				
comp35571_c0_seq1.p3				
comp35573_c0_seq1.p1				
comp35585_c0_seq1.p1				
comp35587_c0_seq1.p1	sp|Q96JK4|HIPL1_HUMAN_HHIP-like_protein_1_OS=Homo_sapiens_GN=HHIPL1_PE=2_SV=2	7.00E-11	[illegible]	[illegible]
comp35604_c0_seq1.p1				
comp35625_c0_seq1.p1				
comp35638_c0_seq1.p3				
comp35646_c0_seq1.p1				
comp35648_c0_seq1.p1				
comp35650_c0_seq1.p1				
comp35653_c0_seq1.p1				
comp35666_c0_seq1.p1				
comp35679_c0_seq1.p1				
comp35682_c0_seq1.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	2.00E-14	[illegible]	[illegible]
comp35686_c0_seq1.p1	sp|Q5BLD8|MT21A_DANRE_Methyltransferase-like_protein_21A_OS=Danio_rerio_GN=mettl21a_PE=2_SV=1	5.00E-20	[illegible]	[illegible]
comp35702_c0_seq1.p1				
comp35716_c0_seq1.p1				
comp35742_c0_seq1.p1	sp|P62083|RS7_RAT_40S_ribosomal_protein_S7_OS=Rattus_norvegicus_GN=Rps7_PE=1_SV=1	2.00E-73	[illegible]	[illegible]
comp35754_c0_seq1.p1				
comp35765_c0_seq1.p1				
comp35768_c0_seq1.p1				
comp35780_c0_seq1.p1	sp|P74838|FKBM_STRTA_31-O-demethyl-FK506_methyltransferase_FkbM_OS=Streptomyces_tacrolimicus_GN=fkbM_PE=1_SV=1	5.00E-30	[illegible]	[illegible]
comp35802_c0_seq1.p1				
comp35804_c0_seq1.p1				
comp35873_c0_seq1.p1				
comp35877_c0_seq1.p1				
comp35883_c0_seq1.p1				
comp35885_c0_seq1.p1				
comp35888_c0_seq1.p2	sp|Q945U1|RS15_ELAOL_40S_ribosomal_protein_S15_OS=Elaeis_oleifera_GN=RPS15_PE=2_SV=1	4.00E-47	[illegible]	[illegible]
comp35898_c0_seq1.p1				
comp35905_c0_seq1.p2				
comp35965_c0_seq1.p1				
comp35972_c0_seq1.p2				
comp35981_c0_seq1.p1				
comp36005_c0_seq1.p1	sp|A8CEP3|CALM_SACJA_Calmodulin_OS=Saccharina_japonica_GN=cam_PE=2_SV=1	5.00E-28	GO:0005509,GO:0046872	[illegible]
comp36017_c0_seq1.p1				
comp3602_c0_seq1.p1	sp|Q26481|RL5_STYCL_60S_ribosomal_protein_L5_OS=Styela_clava_GN=RPL5_PE=3_SV=3	1.00E-89	[illegible]	[illegible]
comp36092_c0_seq1.p2				
comp36121_c0_seq1.p1				
comp36122_c0_seq1.p1				
comp36129_c0_seq1.p1	sp|O35604|NPC1_MOUSE_Niemann-Pick_C1_protein_OS=Mus_musculus_GN=Npc1_PE=1_SV=1	5.00E-40	[illegible]	[illegible]
comp36155_c0_seq1.p1				
comp36161_c0_seq1.p1				
comp36170_c0_seq1.p2				
comp36180_c0_seq1.p1	sp|Q556Y9|MD2L1_DICDI_Mitotic_spindle_assembly_checkpoint_protein_MAD2A_OS=Dictyostelium_discoideum_GN=mad2l1-1_PE=3_SV=1	7.00E-68	[illegible]	[illegible]
comp36236_c0_seq1.p1				
comp36278_c0_seq1.p1				
comp36282_c0_seq1.p1				
comp36292_c0_seq1.p3	sp|Q0ITS8|RL101_ORYSJ_60S_ribosomal_protein_L10-1_OS=Oryza_sativa_subsp._japonica_GN=SC34_PE=2_SV=1	2.00E-91	[illegible]	[illegible]
comp36463_c0_seq1.p1				
comp36499_c0_seq1.p1	sp|A7RK30|QORL2_NEMVE_Quinone_oxidoreductase-like_protein_2_homolog_OS=Nematostella_vectensis_GN=v1g238856_PE=3_SV=1	8.00E-32	[illegible]	[illegible]
comp36508_c0_seq1.p1				
comp36537_c0_seq1.p1				
comp36562_c0_seq1.p1				
comp36594_c0_seq1.p1				
comp36607_c0_seq1.p1	sp|P78055|FSAA_ECOLI_Fructose-6-phosphate_aldolase_1_OS=Escherichia_coli_(strain_K12)_GN=fsaA_PE=1_SV=2	2.00E-136	[illegible]	[illegible]
comp36607_c0_seq1.p2	sp|P75794|PFLE_ECOLI_Putative_pyruvate_formate-lyase_3-activating_enzyme_OS=Escherichia_coli_(strain_K12)_GN=ybiY_PE=3_SV=2	3.00E-99	[illegible]	[illegible]
comp36620_c0_seq1.p1				
comp36688_c0_seq1.p1				
comp36711_c0_seq1.p1				
comp36808_c0_seq1.p1				
comp36860_c0_seq1.p2				
comp36875_c0_seq1.p1				
comp36888_c0_seq1.p1				
comp36890_c0_seq1.p2	sp|P0DJ25|RL40_TETTS_Ubiquitin-60S_ribosomal_protein_L40_OS=Tetrahymena_thermophila_(strain_SB210)_GN=RPL40_PE=1_SV=1	8.00E-21	[illegible]	[illegible]
comp36894_c0_seq1.p1				
comp36896_c0_seq1.p1				
comp36899_c0_seq1.p1				
comp37054_c0_seq1.p1	sp|Q5RFQ0|FCF1_PONAB_rRNA-processing_protein_FCF1_homolog_OS=Pongo_abelii_GN=FCF1_PE=2_SV=1	3.00E-86	[illegible]	[illegible]
comp37152_c0_seq1.p1				
comp37155_c0_seq1.p1				
comp37174_c0_seq1.p1				
comp37182_c0_seq1.p1	sp|Q71UH5|CALM_PYTSP_Calmodulin_OS=Pythium_splendens_PE=2_SV=1	2.00E-67	GO:0005509,GO:0046872	[illegible]
comp37193_c0_seq1.p1				
comp37231_c0_seq1.p2				
comp37238_c0_seq1.p1				
comp37283_c0_seq1.p1	sp|Q54MJ7|ALAM_DICDI_Probable_alanine_aminotransferase,_mitochondrial_OS=Dictyostelium_discoideum_GN=gpt_PE=3_SV=1	1.00E-27	[illegible]	[illegible]
comp3729_c0_seq1.p1				
comp3731_c0_seq1.p1	sp|P0ADC3|LOLC_ECOLI_Lipoprotein-releasing_system_transmembrane_protein_lolC_OS=Escherichia_coli_(strain_K12)_GN=lolC_PE=1_SV=1	8.00E-118	[illegible]	[illegible]
comp37314_c0_seq1.p1				
comp37325_c0_seq1.p1	sp|Q9FR53|TOR_ARATH_Serine/threonine-protein_kinase_TOR_OS=Arabidopsis_thaliana_GN=TOR_PE=1_SV=1	7.00E-28	[illegible]	[illegible]
comp37337_c0_seq1.p1				
comp37447_c0_seq1.p2	sp|P41041|CALM_PNECA_Calmodulin_OS=Pneumocystis_carinii_PE=3_SV=1	3.00E-32	GO:0005509,GO:0046872	[illegible]
comp3745_c0_seq1.p1	sp|P17994|YFAA_ECOLI_Uncharacterized_protein_yfaA_OS=Escherichia_coli_(strain_K12)_GN=yfaA_PE=4_SV=3	4.00E-60		
comp37465_c0_seq1.p2				
comp37473_c0_seq1.p1	sp|Q32BN8|RLMG_SHIDS_Ribosomal_RNA_large_subunit_methyltransferase_G_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=rlmG_PE=3_SV=2	5.00E-67	[illegible]	[illegible]
comp37506_c0_seq1.p2				
comp37510_c0_seq1.p1	sp|P84239|H3_URECA_Histone_H3_OS=Urechis_caupo_PE=1_SV=2	5.00E-79	[illegible]	[illegible]
comp37513_c0_seq1.p1				
comp37562_c0_seq1.p1				
comp37583_c0_seq1.p1				
comp37591_c0_seq1.p1				
comp37598_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	9.00E-22		
comp37618_c0_seq1.p1	sp|O13828|DCP2_SCHPO_mRNA_decapping_complex_subunit_2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=dcp2_PE=1_SV=1	4.00E-22	[illegible]	[illegible]
comp3762_c0_seq1.p1				
comp37667_c0_seq1.p1				
comp3770_c0_seq1.p1				
comp3771_c0_seq1.p1	sp|P32703|YJCE_ECOLI_Uncharacterized_Na(+)/H(+)_exchanger_yjcE_OS=Escherichia_coli_(strain_K12)_GN=yjcE_PE=3_SV=1	2.00E-50	[illegible]	[illegible]
comp37731_c0_seq1.p1	sp|P57681|PCYOX_ARATH_Farnesylcysteine_lyase_OS=Arabidopsis_thaliana_GN=FLCY_PE=1_SV=1	5.00E-29	[illegible]	[illegible]
comp37744_c0_seq1.p2				
comp37753_c0_seq1.p1				
comp3776_c0_seq1.p1				
comp37767_c0_seq1.p1				
comp37786_c0_seq1.p1				
comp37836_c0_seq1.p2				
comp37837_c0_seq1.p1				
comp37959_c0_seq1.p1				
comp3807_c0_seq1.p1	sp|P0ADU1|YGIM_SHIFL_Uncharacterized_protein_ygiM_OS=Shigella_flexneri_GN=ygiM_PE=4_SV=1	2.00E-79	[illegible]	[illegible]
comp38090_c0_seq1.p2				
comp38092_c0_seq1.p1				
comp3814_c0_seq1.p1				
comp38141_c0_seq1.p1				
comp38167_c0_seq1.p1	sp|Q8CBH5|MFSD6_MOUSE_Major_facilitator_superfamily_domain-containing_protein_6_OS=Mus_musculus_GN=Mfsd6_PE=1_SV=1	7.00E-19	[illegible]	[illegible]
comp38275_c0_seq1.p1				
comp3829_c0_seq1.p1	sp|Q4V890|FEM1A_RAT_Protein_fem-1_homolog_A_OS=Rattus_norvegicus_GN=Fem1a_PE=2_SV=1	6.00E-16	[illegible]	[illegible]
comp38300_c0_seq1.p2				
comp38317_c0_seq1.p1				
comp38318_c0_seq1.p1				
comp38421_c0_seq1.p2				
comp38440_c0_seq1.p1				
comp3846_c0_seq1.p1				
comp38498_c0_seq1.p1				
comp38514_c0_seq1.p1				
comp38526_c0_seq1.p1	sp|Q9FX83|NDS8B_ARATH_NADH_dehydrogenase_[ubiquinone]_iron-sulfur_protein_8-B,_mitochondrial_OS=Arabidopsis_thaliana_GN=At1g16700_PE=1_SV=1	1.00E-35	[illegible]	[illegible]
comp38530_c0_seq1.p1	sp|Q54S90|RS11_DICDI_40S_ribosomal_protein_S11_OS=Dictyostelium_discoideum_GN=rps11_PE=1_SV=1	1.00E-62	[illegible]	[illegible]
comp38546_c0_seq1.p1				
comp38657_c0_seq1.p1				
comp38725_c0_seq1.p3				
comp38773_c0_seq1.p2				
comp38778_c0_seq1.p1	sp|Q9U7D0|H4_MASBA_Histone_H4_OS=Mastigamoeba_balamuthi_PE=3_SV=3	1.00E-51	[illegible]	[illegible]
comp3878_c0_seq1.p2				
comp38842_c0_seq1.p1	sp|Q9FJX2|RL262_ARATH_60S_ribosomal_protein_L26-2_OS=Arabidopsis_thaliana_GN=RPL26B_PE=2_SV=1	3.00E-40	[illegible]	[illegible]
comp38899_c0_seq1.p1				
comp38906_c0_seq1.p1				
comp3891_c0_seq1.p1				
comp38916_c0_seq1.p1	sp|Q5ZI74|DHX30_CHICK_Putative_ATP-dependent_RNA_helicase_DHX30_OS=Gallus_gallus_GN=DHX30_PE=2_SV=1	3.00E-57	[illegible]	[illegible]
comp38968_c0_seq1.p1				
comp38981_c0_seq1.p1				
comp39026_c0_seq1.p1				
comp39028_c0_seq1.p1				
comp39044_c0_seq1.p2	sp|Q9AY76|ADF2_ORYSJ_Actin-depolymerizing_factor_2_OS=Oryza_sativa_subsp._japonica_GN=ADF2_PE=2_SV=1	7.00E-30	[illegible]	[illegible]
comp39061_c0_seq1.p1	sp|Q54RA4|Y3291_DICDI_Probable_iron/ascorbate_oxidoreductase_DDB_G0283291_OS=Dictyostelium_discoideum_GN=DDB_G0283291_PE=3_SV=1	8.00E-26	[illegible]	[illegible]
comp39071_c0_seq1.p1				
comp3908_c0_seq1.p1	sp|P49216|RS26_ORYSJ_40S_ribosomal_protein_S26_OS=Oryza_sativa_subsp._japonica_GN=RPS26_PE=2_SV=2	3.00E-38	[illegible]	[illegible]
comp3909_c0_seq1.p1	sp|P08550|CVPA_ECOLI_Colicin_V_production_protein_OS=Escherichia_coli_(strain_K12)_GN=cvpA_PE=1_SV=1	4.00E-76	[illegible]	[illegible]
comp39110_c0_seq1.p1				
comp39131_c0_seq1.p1				
comp39156_c0_seq1.p2	sp|P63502|CBL_MYCTU_Putative_cystathionine_beta-lyase_OS=Mycobacterium_tuberculosis_GN=Rv2294_PE=3_SV=1	3.00E-15		
comp39182_c0_seq1.p1				
comp39185_c0_seq1.p1				
comp39208_c0_seq1.p1	sp|Q6FJH3|RS6_CANGA_40S_ribosomal_protein_S6_OS=Candida_glabrata_(strain_ATCC_2001_/_CBS_138_/_JCM_3761_/_NBRC_0622_/_NRRL_Y-65)_GN=RPS6A_PE=3_SV=1	5.00E-57	[illegible]	[illegible]
comp39253_c0_seq1.p1				
comp39272_c0_seq1.p1				
comp39297_c0_seq1.p1				
comp39318_c0_seq1.p1				
comp39318_c0_seq1.p2				
comp39433_c0_seq1.p1	sp|A8HS48|RS3A_CHLRE_40S_ribosomal_protein_S3a_OS=Chlamydomonas_reinhardtii_GN=CHLREDRAFT_168484_PE=3_SV=1	2.00E-97	[illegible]	[illegible]
comp3946_c0_seq1.p1				
comp39581_c0_seq1.p1				
comp39634_c0_seq1.p1				
comp39657_c0_seq1.p1				
comp39670_c0_seq1.p1				
comp39687_c0_seq1.p1	sp|C0LGQ5|GSO1_ARATH_LRR_receptor-like_serine/threonine-protein_kinase_GSO1_OS=Arabidopsis_thaliana_GN=GSO1_PE=2_SV=1	5.00E-44	[illegible]	[illegible]
comp39729_c0_seq1.p1				
comp39732_c0_seq1.p1	sp|P0ACD9|MBHL_SHIFL_Hydrogenase-1_large_chain_OS=Shigella_flexneri_GN=hyaB_PE=3_SV=1	2.00E-92	[illegible]	[illegible]
comp39744_c0_seq1.p1				
comp39779_c0_seq1.p1				
comp39822_c0_seq1.p1				
comp39861_c0_seq1.p1				
comp3988_c0_seq1.p1				
comp39898_c0_seq1.p1				
comp39910_c0_seq1.p1				
comp39910_c0_seq1.p2				
comp39929_c0_seq1.p1				
comp3996_c0_seq1.p3	sp|Q86AD7|MYLKB_DICDI_Probable_myosin_light_chain_kinase_DDB_G0271550_OS=Dictyostelium_discoideum_GN=DDB_G0271550_PE=3_SV=1	3.00E-14	[illegible]	[illegible]
comp39977_c0_seq1.p2	sp|Q9SMI3|RS12_CYAPA_40S_ribosomal_protein_S12_OS=Cyanophora_paradoxa_GN=RPS12_PE=2_SV=1	4.00E-37	[illegible]	[illegible]
comp39983_c0_seq1.p1				
comp4003_c0_seq1.p1				
comp40050_c0_seq1.p1				
comp40132_c0_seq1.p1	sp|P35684|RL3_ORYSJ_60S_ribosomal_protein_L3_OS=Oryza_sativa_subsp._japonica_GN=RPL3_PE=2_SV=2	6.00E-159	[illegible]	[illegible]
comp40151_c0_seq1.p1				
comp40159_c0_seq1.p1				
comp4016_c0_seq1.p1	sp|Q09564|PHLPP_CAEEL_Protein_phosphatase_PHLPP-like_protein_OS=Caenorhabditis_elegans_GN=F43C1.1_PE=2_SV=2	7.00E-11	[illegible]	[illegible]
comp40181_c0_seq1.p1	sp|Q57251|Y1218_HAEIN_Putative_L-lactate_permease_OS=Haemophilus_influenzae_(strain_ATCC_51907_/_DSM_11121_/_KW20_/_Rd)_GN=HI_1218_PE=3_SV=1	1.00E-84	[illegible]	[illegible]
comp40219_c0_seq1.p1				
comp40234_c0_seq1.p1				
comp40235_c0_seq1.p1	sp|Q7TNH6|NPHP3_MOUSE_Nephrocystin-3_OS=Mus_musculus_GN=Nphp3_PE=1_SV=2	3.00E-36	[illegible]	[illegible]
comp40257_c0_seq1.p1				
comp40276_c0_seq1.p1				
comp40279_c0_seq1.p1	sp|P10351|XDH_DROME_Xanthine_dehydrogenase_OS=Drosophila_melanogaster_GN=ry_PE=2_SV=2	8.00E-22	[illegible]	[illegible]
comp40295_c0_seq1.p1				
comp4031_c0_seq1.p1	sp|Q3YZF6|FCTA_SHISS_Formyl-coenzyme_A_transferase_OS=Shigella_sonnei_(strain_Ss046)_GN=frc_PE=3_SV=1	6.00E-56	[illegible]	[illegible]

comp40326_c0_seq1.p1				
comp40354_c0_seq1.p1				
comp40358_c0_seq1.p1	sp|Q8ZRJ7|FADE_SALTY_Acyl-coenzyme_A_dehydrogenase_OS=Salmonella_typhimurium_GN=fadE_PE=2_SV=1	5.00E-103	GO:0003995,GO:0006629,GO:0006631,GO:0006635,GO:0008152,GO:0016491,GO:0016627,GO:0033539,GO:0050660,GO:0055114,GO:0055114	acyl-CoA dehydrogenase activity,lipid metabolic process,fatty acid metabolic process,fatty acid beta-oxidation,metabolic process,oxidoreductase activity,oxidoreductase activity, acting on the CH-CH group of donors,fatty acid beta-oxidation using acyl-CoA dehydrogenase,flavin adenine dinucleotide binding,oxidation-reduction process,oxidation-reduction process
comp40417_c0_seq1.p1	sp|Q9HFU4|MPI_CRYNJ_Mannose-6-phosphate_isomerase_OS=Cryptococcus_neoformans_var._neoformans_serotype_D_(strain_JEC21_/_ATCC_MYA-565)_GN=MAN1_PE=3_SV=2	6.00E-19	GO:0004476,GO:0004476,GO:0005737,GO:0005737,GO:0005975,GO:0008270,GO:0009298,GO:0009298,GO:0016853,GO:0046872	mannose-6-phosphate isomerase activity,mannose-6-phosphate isomerase activity,cytoplasm,cytoplasm,carbohydrate metabolic process,zinc ion binding,GDP-mannose biosynthetic process,GDP-mannose biosynthetic process,isomerase activity,metal ion binding
comp40430_c0_seq1.p1	sp|P80639|IF5A_MAIZE_Eukaryotic_translation_initiation_factor_5A_OS=Zea_mays_GN=TIF5A_PE=1_SV=2	1.00E-39	GO:0003723,GO:0003743,GO:0003746,GO:0006412,GO:0006413,GO:0006452,GO:0008612,GO:0043022,GO:0045901,GO:0045905	RNA binding,translation initiation factor activity,translation elongation factor activity,translation,translational initiation,translational frameshifting,peptidyl-lysine modification to peptidyl-hypusine,ribosome binding,positive regulation of translational elongation,positive regulation of translational termination
comp40433_c0_seq1.p1				
comp40456_c0_seq1.p1				
comp40513_c0_seq1.p1				
comp40520_c0_seq1.p1				
comp40524_c0_seq1.p2	sp|P36241|RL19_DROME_60S_ribosomal_protein_L19_OS=Drosophila_melanogaster_GN=RpL19_PE=1_SV=2	7.00E-38	GO:0000022,GO:0003735,GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0005840,GO:0006412,GO:0030529,GO:0051298	mitotic spindle elongation,structural constituent of ribosome,structural constituent of ribosome,intracellular,ribosome,ribosome,ribosome,translation,ribonucleoprotein complex,centrosome duplication
comp40539_c0_seq1.p1				
comp40596_c0_seq1.p1				
comp40620_c0_seq1.p1				
comp40693_c0_seq1.p2				
comp40698_c0_seq1.p2				
comp40751_c0_seq1.p1	sp|Q90W04|NGB_TETNG_Neuroglobin_OS=Tetraodon_nigroviridis_GN=ngb_PE=2_SV=1	4.00E-13	GO:0001666,GO:0005344,GO:0005506,GO:0005737,GO:0005737,GO:0006810,GO:0015671,GO:0015671,GO:0019825,GO:0020037,GO:0043204,GO:0046872	response to hypoxia,oxygen transporter activity,iron ion binding,cytoplasm,cytoplasm,transport,oxygen transport,oxygen transport,oxygen binding,heme binding,perikaryon,metal ion binding
comp40827_c0_seq1.p1				
comp40844_c0_seq1.p1				
comp40862_c0_seq1.p1				
comp40873_c0_seq1.p1				
comp40888_c0_seq1.p3				
comp40901_c0_seq1.p1				
comp40946_c0_seq1.p1				
comp40950_c0_seq1.p2	sp|Q64433|CH10_MOUSE_10_kDa_heat_shock_protein,_mitochondrial_OS=Mus_musculus_GN=Hspe1_PE=1_SV=2	5.00E-25	GO:0001649,GO:0005524,GO:0005737,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005759,GO:0005759,GO:0006457,GO:0016020,GO:0044822,GO:0051087,GO:0070062	osteoblast differentiation,ATP binding,cytoplasm,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrial matrix,mitochondrial matrix,protein folding,membrane,poly(A) RNA binding,chaperone binding,extracellular vesicular exosome
comp40961_c0_seq1.p1				
comp40974_c0_seq1.p1				
comp40977_c0_seq1.p1				
comp41009_c0_seq1.p1	sp|P59828|ALGG_PSEFL_Poly(beta-D-mannuronate)_C5_epimerase_OS=Pseudomonas_fluorescens_GN=algG_PE=1_SV=1	8.00E-11	GO:0016853,GO:0042121,GO:0042121,GO:0042597,GO:0042597	isomerase activity,alginic acid biosynthetic process,alginic acid biosynthetic process,periplasmic space,periplasmic space
comp4102_c0_seq1.p1				
comp41045_c0_seq1.p1				
comp41061_c0_seq1.p1	sp|Q39584|DYL3_CHLRE_Dynein_18_kDa_light_chain,_flagellar_outer_arm_OS=Chlamydomonas_reinhardtii_PE=1_SV=1	2.00E-25	GO:0003774,GO:0005509,GO:0005874,GO:0005929,GO:0008152,GO:0030286,GO:0031514,GO:0042995,GO:0046872	motor activity,calcium ion binding,microtubule,cilium,metabolic process,dynein complex,motile cilium,cell projection,metal ion binding
comp41062_c0_seq1.p1				
comp41073_c0_seq1.p1				
comp41111_c0_seq1.p1				
comp41155_c0_seq1.p1				
comp41197_c0_seq1.p1				
comp41205_c0_seq1.p1	sp|P0ADP5|YIGM_ECOLI_Uncharacterized_membrane_protein_yigM_OS=Escherichia_coli_(strain_K12)_GN=yigM_PE=4_SV=1	4.00E-142	GO:0005886,GO:0005886,GO:0016020,GO:0016020,GO:0016021,GO:0016021	plasma membrane,plasma membrane,membrane,membrane,integral component of membrane,integral component of membrane
comp4122_c0_seq1.p1				
comp41320_c0_seq1.p1				
comp41340_c0_seq1.p1	sp|Q38931|FKB62_ARATH_Peptidyl-prolyl_cis-trans_isomerase_FKBP62_OS=Arabidopsis_thaliana_GN=FKBP62_PE=1_SV=2	6.00E-34	GO:0000413,GO:0000413,GO:0003755,GO:0003755,GO:0005515,GO:0005515,GO:0005515,GO:0005516,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0006457,GO:0016853,GO:0070370	protein peptidyl-prolyl isomerization,protein peptidyl-prolyl isomerization,peptidyl-prolyl cis-trans isomerase activity,peptidyl-prolyl cis-trans isomerase activity,protein binding,protein binding,protein binding,calmodulin binding,nucleus,nucleus,cytoplasm,cytoplasm,protein folding,isomerase activity,cellular heat acclimation
comp41356_c0_seq1.p1	sp|Q6B9X6|VWKA_DICDI_Alpha-protein_kinase_vwkA_OS=Dictyostelium_discoideum_GN=vwkA_PE=1_SV=1	4.00E-12	GO:0000166,GO:0000281,GO:0000331,GO:0000331,GO:0004672,GO:0004674,GO:0004674,GO:0004674,GO:0005516,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005773,GO:0005829,GO:0006468,GO:0006468,GO:0006971,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0018107,GO:0018209,GO:0031038,GO:0031156,GO:0031164,GO:0031288,GO:0033298,GO:0048471,GO:0048471,GO:0070177,GO:0016905	nucleotide binding,mitotic cytokinesis,contractile vacuole,contractile vacuole,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,calmodulin binding,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,vacuole,cytosol,protein phosphorylation,protein phosphorylation,hypotonic response,membrane,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,peptidyl-threonine phosphorylation,peptidyl-serine modification,myosin II filament organization,regulation of sorocarp development,contractile vacuolar membrane,sorocarp morphogenesis,contractile vacuole organization,perinuclear region of cytoplasm,perinuclear region of cytoplasm,contractile vacuole discharge,myosin heavy chain kinase activity
comp41358_c0_seq1.p1				
comp41396_c0_seq1.p1				
comp41401_c0_seq1.p1				
comp4141_c0_seq1.p1				
comp41416_c0_seq1.p1				
comp41421_c0_seq1.p2	sp|Q08699|RS14_PODCA_40S_ribosomal_protein_S14_OS=Podocoryne_carnea_GN=RPS14_PE=2_SV=1	2.00E-70	GO:0003735,GO:0005840,GO:0005840,GO:0006412,GO:0030529	structural constituent of ribosome,ribosome,ribosome,translation,ribonucleoprotein complex
comp41430_c0_seq1.p1	sp|Q83MI1|STHA_SHIFL_Soluble_pyridine_nucleotide_transhydrogenase_OS=Shigella_flexneri_GN=sthA_PE=3_SV=1	3.00E-99	GO:0003957,GO:0003957,GO:0003957,GO:0005737,GO:0005737,GO:0005737,GO:0006739,GO:0016491,GO:0016491,GO:0045454,GO:0050660,GO:0055114,GO:0055114,GO:1902600,GO:1902600,GO:1902600	NAD(P)+ transhydrogenase (B-specific) activity,NAD(P)+ transhydrogenase (B-specific) activity,NAD(P)+ transhydrogenase (B-specific) activity,cytoplasm,cytoplasm,cytoplasm,NADP metabolic process,oxidoreductase activity,oxidoreductase activity,cell redox homeostasis,flavin adenine dinucleotide binding,oxidation-reduction process,oxidation-reduction process,hydrogen ion transmembrane transport,hydrogen ion transmembrane transport,hydrogen ion transmembrane transport
comp41446_c0_seq1.p1				
comp41448_c0_seq1.p1				
comp41504_c0_seq1.p1				
comp41509_c0_seq1.p1	sp|P51818|HS903_ARATH_Heat_shock_protein_90-3_OS=Arabidopsis_thaliana_GN=HSP90-3_PE=1_SV=2	1.00E-32	GO:0000166,GO:0005515,GO:0005524,GO:0005524,GO:0005730,GO:0005737,GO:0005737,GO:0005794,GO:0005829,GO:0005886,GO:0006457,GO:0006950,GO:0009408,GO:0016020,GO:0051082,GO:0051131,GO:0071277,GO:0009408	nucleotide binding,protein binding,ATP binding,ATP binding,nucleolus,cytoplasm,cytoplasm,Golgi apparatus,cytosol,plasma membrane,protein folding,response to stress,response to heat,membrane,unfolded protein binding,chaperone-mediated protein complex assembly,cellular response to calcium ion,response to heat
comp41530_c0_seq1.p1				
comp41534_c0_seq1.p1				
comp41554_c0_seq1.p1				
comp41557_c0_seq1.p1				
comp41614_c0_seq1.p1				
comp41625_c0_seq1.p1	sp|P08570|RLA1_DROME_60S_acidic_ribosomal_protein_P1_OS=Drosophila_melanogaster_GN=RpLP1_PE=1_SV=2	3.00E-18	GO:0003735,GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0005840,GO:0006414,GO:0030529	structural constituent of ribosome,structural constituent of ribosome,intracellular,ribosome,ribosome,ribosome,translational elongation,ribonucleoprotein complex
comp41642_c0_seq1.p1				
comp41669_c0_seq1.p1				
comp41671_c0_seq1.p1				
comp41678_c0_seq1.p1				
comp41753_c0_seq1.p1				
comp41768_c0_seq1.p1	sp|P0ACP0|CYTR_SHIFL_HTH-type_transcriptional_repressor_CytR_OS=Shigella_flexneri_GN=cytR_PE=3_SV=1	2.00E-67	GO:0003677,GO:0003677,GO:0003700,GO:0006351,GO:0006355,GO:0006355	DNA binding,DNA binding,sequence-specific DNA binding transcription factor activity,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated
comp41772_c0_seq1.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	1.00E-16	GO:0005576,GO:0005618,GO:0005618,GO:0009279,GO:0009279,GO:0016020,GO:0016021,GO:0019867	extracellular region,cell wall,cell wall,cell outer membrane,cell outer membrane,membrane,integral component of membrane,outer membrane
comp41794_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	4.00E-33		
comp41808_c0_seq1.p1				
comp41810_c0_seq1.p1				
comp41811_c0_seq1.p1				
comp41824_c0_seq1.p1				
comp41922_c0_seq1.p1				
comp41939_c0_seq1.p1	sp|Q5M9P8|ARL6_DANRE_ADP-ribosylation_factor-like_protein_6_OS=Danio_rerio_GN=arl6_PE=2_SV=1	7.00E-26	GO:0000166,GO:0005525,GO:0005525,GO:0005622,GO:0005737,GO:0005856,GO:0005886,GO:0005929,GO:0007264,GO:0007368,GO:0007368,GO:0007368,GO:0007368,GO:0007368,GO:0007369,GO:0007601,GO:0007601,GO:0008593,GO:0016020,GO:0030030,GO:0032402,GO:0032402,GO:0032402,GO:0032402,GO:0032402,GO:0032402,GO:0033339,GO:0042384,GO:0042995,GO:0046872,GO:0050896,GO:0060170,GO:0070121,GO:0070121,GO:0070121,GO:0070121,GO:0070121	nucleotide binding,GTP binding,GTP binding,intracellular,cytoplasm,cytoskeleton,plasma membrane,cilium,small GTPase mediated signal transduction,determination of left/right symmetry,determination of left/right symmetry,determination of left/right symmetry,determination of left/right symmetry,determination of left/right symmetry,gastrulation,visual perception,visual perception,regulation of Notch signaling pathway,membrane,cell projection organization,melanosome transport,melanosome transport,melanosome transport,melanosome transport,melanosome transport,melanosome transport,pectoral fin development,cilium assembly,cell projection,metal ion binding,response to stimulus,ciliary membrane,Kupffer's vesicle development,Kupffer's vesicle development,Kupffer's vesicle development,Kupffer's vesicle development,Kupffer's vesicle development
comp41941_c0_seq1.p1				
comp41981_c0_seq1.p1				
comp42059_c0_seq1.p1	sp|O15270|SPTC2_HUMAN_Serine_palmitoyltransferase_2_OS=Homo_sapiens_GN=SPTLC2_PE=1_SV=1	2.00E-36	GO:0003824,GO:0004758,GO:0004758,GO:0004758,GO:0004758,GO:0004758,GO:0005739,GO:0005783,GO:0005789,GO:0005789,GO:0006629,GO:0006665,GO:0006665,GO:0006665,GO:0006686,GO:0008152,GO:0009058,GO:0016020,GO:0016021,GO:0016740,GO:0016740,GO:0016746,GO:0017059,GO:0030148,GO:0030148,GO:0030170,GO:0044281,GO:0046511,GO:0046512,GO:0046513	catalytic activity,serine C-palmitoyltransferase activity,serine C-palmitoyltransferase activity,serine C-palmitoyltransferase activity,serine C-palmitoyltransferase activity,serine C-palmitoyltransferase activity,mitochondrion,endoplasmic reticulum,endoplasmic reticulum membrane,endoplasmic reticulum membrane,lipid metabolic process,sphingolipid metabolic process,sphingolipid metabolic process,sphingomyelin biosynthetic process,metabolic process,biosynthetic process,membrane,integral component of membrane,transferase activity,transferase activity,transferase activity, transferring acyl groups,serine C-palmitoyltransferase complex,sphingolipid biosynthetic process,sphingolipid biosynthetic process,pyridoxal phosphate binding,small molecule metabolic process,sphinganine biosynthetic process,sphingosine biosynthetic process,ceramide biosynthetic process
comp42089_c0_seq1.p1	sp|P19804|NDKB_RAT_Nucleoside_diphosphate_kinase_B_OS=Rattus_norvegicus_GN=Nme2_PE=1_SV=1	1.00E-66	GO:0000166,GO:0001726,GO:0001726,GO:0001726,GO:0002762,GO:0004550,GO:0004550,GO:0004550,GO:0004673,GO:0004674,GO:0005504,GO:0005524,GO:0005524,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005886,GO:0005886,GO:0006165,GO:0006183,GO:0006183,GO:0006228,GO:0006228,GO:0006241,GO:0006241,GO:0007229,GO:0007229,GO:0008144,GO:0009117,GO:0009142,GO:0010976,GO:0016020,GO:0016301,GO:0016310,GO:0016740,GO:0018106,GO:0019215,GO:0019215,GO:0019899,GO:0030027,GO:0030027,GO:0030027,GO:0030819,GO:0031966,GO:0034599,GO:0042995,GO:0043066,GO:0043066,GO:0045618,GO:0045618,GO:0045682,GO:0045682,GO:0045944,GO:0045944,GO:0046777,GO:0046872,GO:0048471,GO:0050679,GO:0050679,GO:0051259,GO:0060416,GO:0070062,GO:0071333,GO:0071398,GO:0071944,GO:0071944,GO:0005925,GO:0005882	nucleotide binding,ruffle,ruffle,ruffle,negative regulation of myeloid leukocyte differentiation,nucleoside diphosphate kinase activity,nucleoside diphosphate kinase activity,nucleoside diphosphate kinase activity,protein histidine kinase activity,protein serine/threonine kinase activity,fatty acid binding,ATP binding,ATP binding,nucleus,cytoplasm,cytoplasm,cytoplasm,cytoplasm,plasma membrane,plasma membrane,nucleoside diphosphate phosphorylation,nucleoside diphosphate phosphorylation,GTP biosynthetic process,GTP biosynthetic process,UTP biosynthetic process,UTP biosynthetic process,CTP biosynthetic process,CTP biosynthetic process,integrin-mediated signaling pathway,integrin-mediated signaling pathway,drug binding,nucleotide metabolic process,nucleoside triphosphate biosynthetic process,positive regulation of neuron projection development,membrane,kinase activity,phosphorylation,transferase activity,peptidyl-histidine phosphorylation,intermediate filament binding,intermediate filament binding,enzyme binding,lamellipodium,lamellipodium,lamellipodium,positive regulation of cAMP biosynthetic process,mitochondrial membrane,cellular response to oxidative stress,cell projection,negative regulation of apoptotic process,negative regulation of apoptotic process,positive regulation of keratinocyte differentiation,positive regulation of keratinocyte differentiation,regulation of epidermis development,regulation of epidermis development,positive regulation of transcription from RNA polymerase II promoter,positive regulation of transcription from RNA polymerase II promoter,protein autophosphorylation,metal ion binding,perinuclear region of cytoplasm,positive regulation of epithelial cell proliferation,positive regulation of epithelial cell proliferation,protein oligomerization,response to growth hormone,extracellular vesicular exosome,cellular response to glucose stimulus,cellular response to fatty acid,cell periphery,cell periphery,focal adhesion,intermediate filament
comp42091_c0_seq1.p1				
comp42097_c0_seq1.p1				
comp42117_c0_seq1.p1	sp|P77337|YDIS_ECOLI_Probable_electron_transfer_flavoprotein-quinone_oxidoreductase_ydiS_OS=Escherichia_coli_(strain_K12)_GN=ydiS_PE=3_SV=1	5.00E-113	GO:0008152,GO:0016491,GO:0016491,GO:0055114,GO:0055114	metabolic process,oxidoreductase activity,oxidoreductase activity,oxidation-reduction process,oxidation-reduction process
comp4212_c0_seq1.p1				
comp42136_c0_seq1.p2				
comp42194_c0_seq1.p2				
comp42194_c0_seq1.p5				
comp42196_c0_seq1.p1				
comp42211_c0_seq1.p1				
comp42212_c0_seq1.p1	sp|P39366|SGCX_ECOLI_Putative_aminopeptidase_sgcX_OS=Escherichia_coli_(strain_K12)_GN=sgcX_PE=3_SV=3	0	GO:0004177,GO:0006508,GO:0008233,GO:0008237,GO:0016787,GO:0046872	aminopeptidase activity,proteolysis,peptidase activity,metallopeptidase activity,hydrolase activity,metal ion binding
comp42218_c0_seq1.p2				
comp42237_c0_seq1.p1				
comp42275_c0_seq1.p1				
comp42316_c0_seq1.p2	sp|Q03686|BIP8_TOBAC_Luminal-binding_protein_8_(Fragment)_OS=Nicotiana_tabacum_GN=BIP8_PE=2_SV=1	1.00E-47	GO:0000166,GO:0005524,GO:0005783,GO:0005788	nucleotide binding,ATP binding,endoplasmic reticulum,endoplasmic reticulum lumen
comp42333_c0_seq1.p1				
comp42367_c0_seq1.p1				
comp4242_c0_seq1.p1				
comp42453_c0_seq1.p1				
comp42516_c0_seq1.p2	sp|Q6T3U4|NPCL1_MOUSE_Niemann-Pick_C1-like_protein_1_OS=Mus_musculus_GN=Npc1l1_PE=2_SV=1	3.00E-15	GO:0005886,GO:0005886,GO:0006629,GO:0007165,GO:0008158,GO:0008202,GO:0008203,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016324,GO:0030301,GO:0042632	plasma membrane,plasma membrane,lipid metabolic process,signal transduction,hedgehog receptor activity,steroid metabolic process,cholesterol metabolic process,membrane,membrane,integral component of membrane,integral component of membrane,apical plasma membrane,cholesterol transport,cholesterol homeostasis
comp42548_c0_seq1.p1				
comp42582_c0_seq1.p1	sp|P56525|ATPD_NEUCR_ATP_synthase_subunit_delta,_mitochondrial_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=atp-16_PE=3_SV=2	1.00E-21	GO:0005739,GO:0005739,GO:0005743,GO:0005743,GO:0005756,GO:0006200,GO:0006754,GO:0006810,GO:0006811,GO:0015986,GO:0015992,GO:0016020,GO:0016887,GO:0045261,GO:0045261,GO:0046933,GO:0046961	mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,mitochondrial proton-transporting ATP synthase, central stalk,ATP catabolic process,ATP biosynthetic process,transport,ion transport,ATP synthesis coupled proton transport,proton transport,membrane,ATPase activity,proton-transporting ATP synthase complex, catalytic core F(1),proton-transporting ATP synthase complex, catalytic core F(1),proton-transporting ATP synthase activity, rotational mechanism,proton-transporting ATPase activity, rotational mechanism
comp42632_c0_seq1.p1				
comp42647_c0_seq1.p1				
comp4268_c0_seq1.p1				
comp42726_c0_seq1.p2	sp|P69924|RIR2_ECOLI_Ribonucleoside-diphosphate_reductase_1_subunit_beta_OS=Escherichia_coli_(strain_K12)_GN=nrdB_PE=1_SV=2	6.00E-135	GO:0004748,GO:0005506,GO:0005737,GO:0005829,GO:0005829,GO:0005971,GO:0006260,GO:0006260,GO:0009186,GO:0009263,GO:0015949,GO:0016491,GO:0016491,GO:0042802,GO:0042802,GO:0046872,GO:0055114,GO:0055114,GO:0004748	ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor,iron ion binding,cytoplasm,cytosol,cytosol,ribonucleoside-diphosphate reductase complex,DNA replication,DNA replication,deoxyribonucleoside diphosphate metabolic process,deoxyribonucleotide biosynthetic process,nucleobase-containing small molecule interconversion,oxidoreductase activity,oxidoreductase activity,identical protein binding,identical protein binding,metal ion binding,oxidation-reduction process,oxidation-reduction process,ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor
comp42735_c0_seq1.p1				
comp42739_c0_seq1.p1				
comp42772_c0_seq1.p1				
comp42781_c0_seq1.p1	sp|P74876|DPO3X_SALTY_DNA_polymerase_III_subunit_tau_OS=Salmonella_typhimurium_GN=dnaX_PE=3_SV=2	2.00E-85	GO:0000166,GO:0003677,GO:0003887,GO:0003887,GO:0003887,GO:0005524,GO:0005524,GO:0006260,GO:0006260,GO:0009360,GO:0016740,GO:0016779,GO:0071897,GO:0071897,GO:0071897	nucleotide binding,DNA binding,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,DNA-directed DNA polymerase activity,ATP binding,ATP binding,DNA replication,DNA replication,DNA polymerase III complex,transferase activity,nucleotidyltransferase activity,DNA biosynthetic process,DNA biosynthetic process,DNA biosynthetic process
comp42805_c0_seq1.p1	sp|Q8FBM1|METE_ECOL6_5-methyltetrahydropteroyltriglutamate--homocysteine_methyltransferase_OS=Escherichia_coli_O6_GN=metE_PE=3_SV=3	0	GO:0003871,GO:0003871,GO:0003871,GO:0008168,GO:0008270,GO:0008652,GO:0008652,GO:0009086,GO:0009086,GO:0009086,GO:0016740,GO:0032259,GO:0046872	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity,5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity,5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity,methyltransferase activity,zinc ion binding,cellular amino acid biosynthetic process,cellular amino acid biosynthetic process,methionine biosynthetic process,methionine biosynthetic process,methionine biosynthetic process,transferase activity,methylation,metal ion binding
comp42821_c0_seq1.p1				
comp42845_c0_seq1.p1	sp|Q8C863|ITCH_MOUSE_E3_ubiquitin-protein_ligase_Itchy_OS=Mus_musculus_GN=Itch_PE=1_SV=2	2.00E-11	GO:0000151,GO:0000209,GO:0002376,GO:0002669,GO:0004842,GO:0004842,GO:0004842,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005829,GO:0005829,GO:0005886,GO:0005886,GO:0005886,GO:0005938,GO:0006511,GO:0006511,GO:0006511,GO:0006511,GO:0006915,GO:0016020,GO:0016020,GO:0016020,GO:0016567,GO:0016567,GO:0016567,GO:0016874,GO:0016874,GO:0031410,GO:0032088,GO:0035519,GO:0035519,GO:0042787,GO:0043021,GO:0043066,GO:0043066,GO:0045087,GO:0045236,GO:0045732,GO:0045732,GO:0046329,GO:0046642,GO:0050687,GO:0050687,GO:0051607,GO:0061630,GO:0061630,GO:0070534,GO:0070534,GO:0070936,GO:0070936,GO:0070936,GO:0090085	ubiquitin ligase complex,protein polyubiquitination,immune system process,positive regulation of T cell anergy,ubiquitin-protein transferase activity,ubiquitin-protein transferase activity,ubiquitin-protein transferase activity,protein binding,protein binding,protein binding,protein binding,nucleus,nucleus,nucleus,cytoplasm,cytoplasm,cytoplasm,cytoplasm,cytosol,cytosol,plasma membrane,plasma membrane,plasma membrane,cell cortex,ubiquitin-dependent protein catabolic process,ubiquitin-dependent protein catabolic process,ubiquitin-dependent protein catabolic process,ubiquitin-dependent protein catabolic process,apoptotic process,membrane,membrane,membrane,protein ubiquitination,protein ubiquitination,protein ubiquitination,ligase activity,ligase activity,cytoplasmic vesicle,negative regulation of NF-kappaB transcription factor activity,protein K29-linked ubiquitination,protein K29-linked ubiquitination,protein ubiquitination involved in ubiquitin-dependent protein catabolic process,ribonucleoprotein complex binding,negative regulation of apoptotic process,negative regulation of apoptotic process,innate immune response,CXCR chemokine receptor binding,positive regulation of protein catabolic process,positive regulation of protein catabolic process,negative regulation of JNK cascade,negative regulation of alpha-beta T cell proliferation,negative regulation of defense response to virus,negative regulation of defense response to virus,defense response to virus,ubiquitin protein ligase activity,ubiquitin protein ligase activity,protein K63-linked ubiquitination,protein K63-linked ubiquitination,protein K48-linked ubiquitination,protein K48-linked ubiquitination,protein K48-linked ubiquitination,regulation of protein deubiquitination
comp42869_c0_seq1.p2				
comp42872_c0_seq1.p2				
comp42877_c0_seq1.p1	sp|Q3YUZ4|THIG_SHISS_Thiazole_synthase_OS=Shigella_sonnei_(strain_Ss046)_GN=thiG_PE=3_SV=2	1.00E-61	GO:0003824,GO:0005737,GO:0005737,GO:0005737,GO:0009228,GO:0009228,GO:0009228,GO:0009229,GO:0016740,GO:0016783,GO:0036355	catalytic activity,cytoplasm,cytoplasm,cytoplasm,thiamine biosynthetic process,thiamine biosynthetic process,thiamine biosynthetic process,thiamine diphosphate biosynthetic process,transferase activity,sulfurtransferase activity,2-iminoacetate synthase activity
comp42900_c0_seq1.p1				
comp42910_c0_seq1.p2				
comp42917_c0_seq1.p1				
comp42919_c0_seq1.p1	sp|A8HS48|RS3A_CHLRE_40S_ribosomal_protein_S3a_OS=Chlamydomonas_reinhardtii_GN=CHLREDRAFT_168484_PE=3_SV=1	3.00E-39	GO:0003735,GO:0003735,GO:0005622,GO:0005737,GO:0005737,GO:0005840,GO:0005840,GO:0006412,GO:0006412,GO:0022627,GO:0030529	structural constituent of ribosome,structural constituent of ribosome,intracellular,cytoplasm,cytoplasm,ribosome,ribosome,translation,translation,cytosolic small ribosomal subunit,ribonucleoprotein complex
comp42952_c0_seq1.p1				
comp42955_c0_seq1.p1				
comp42959_c0_seq1.p1				
comp42969_c0_seq1.p1	sp|A2BMD5|RL6_HYPBU_50S_ribosomal_protein_L6P_OS=Hyperthermus_butylicus_(strain_DSM_5456_/_JCM_9403)_GN=rpl6p_PE=3_SV=1	2.00E-20	GO:0003723,GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0006412,GO:0019843,GO:0019843,GO:0019843,GO:0030529	RNA binding,structural constituent of ribosome,intracellular,ribosome,ribosome,translation,translation,rRNA binding,rRNA binding,rRNA binding,ribonucleoprotein complex
comp43027_c0_seq1.p1	sp|P42791|RL182_ARATH_60S_ribosomal_protein_L18-2_OS=Arabidopsis_thaliana_GN=RPL18B_PE=1_SV=1	3.00E-38	GO:0003735,GO:0005515,GO:0005622,GO:0005737,GO:0005737,GO:0005773,GO:0005774,GO:0005840,GO:0005840,GO:0005886,GO:0006412,GO:0009220,GO:0009507,GO:0009507,GO:0015934,GO:0022625,GO:0030529,GO:0005794	structural constituent of ribosome,protein binding,intracellular,cytoplasm,cytoplasm,vacuole,vacuolar membrane,ribosome,ribosome,plasma membrane,translation,pyrimidine ribonucleotide biosynthetic process,chloroplast,chloroplast,large ribosomal subunit,cytosolic large ribosomal subunit,ribonucleoprotein complex,Golgi apparatus
comp43029_c0_seq1.p1				
comp43030_c0_seq1.p2	sp|O22644|RL23A_FRIAG_60S_ribosomal_protein_L23A_OS=Fritillaria_agrestis_GN=RPL23A_PE=2_SV=1	1.00E-40	GO:0000166,GO:0003723,GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0019843,GO:0030529	nucleotide binding,RNA binding,structural constituent of ribosome,intracellular,ribosome,ribosome,translation,rRNA binding,ribonucleoprotein complex
comp43034_c0_seq1.p1				
comp43082_c0_seq1.p1	sp|P28304|QOR1_ECOLI_Quinone_oxidoreductase_1_OS=Escherichia_coli_(strain_K12)_GN=qorA_PE=1_SV=1	0	GO:0003960,GO:0005737,GO:0008270,GO:0016491,GO:0016491,GO:0055114,GO:0055114	NADPH:quinone reductase activity,cytoplasm,zinc ion binding,oxidoreductase activity,oxidoreductase activity,oxidation-reduction process,oxidation-reduction process
comp43087_c0_seq1.p1	sp|Q3A8C3|DNAJ_PELCD_Chaperone_protein_DnaJ_OS=Pelobacter_carbinolicus_(strain_DSM_2380_/_Gra_Bd_1)_GN=dnaJ_PE=3_SV=1	1.00E-22	GO:0005524,GO:0005737,GO:0005737,GO:0006260,GO:0006457,GO:0008270,GO:0009408,GO:0031072,GO:0046872,GO:0051082,GO:0051082	ATP binding,cytoplasm,cytoplasm,DNA replication,protein folding,zinc ion binding,response to heat,heat shock protein binding,metal ion binding,unfolded protein binding,unfolded protein binding
comp43094_c0_seq1.p1				
comp4310_c0_seq1.p1	sp|P76104|YDCP_ECOLI_Uncharacterized_protease_ydcP_OS=Escherichia_coli_(strain_K12)_GN=ydcP_PE=3_SV=2	2.00E-74	GO:0005515,GO:0005515,GO:0006508,GO:0006508,GO:0008233,GO:0008233,GO:0016787	protein binding,protein binding,proteolysis,proteolysis,peptidase activity,peptidase activity,hydrolase activity
comp43111_c0_seq1.p1	sp|P47834|RL36_CANAX_60S_ribosomal_protein_L36_OS=Candida_albicans_GN=RPL36_PE=3_SV=1	2.00E-27	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0030529	structural constituent of ribosome,intracellular,ribosome,ribosome,translation,ribonucleoprotein complex
comp43114_c0_seq1.p1	sp|P37013|NORR_ECOLI_Anaerobic_nitric_oxide_reductase_transcription_regulator_norR_OS=Escherichia_coli_(strain_K12)_GN=norR_PE=1_SV=1	5.00E-91	GO:0000156,GO:0000160,GO:0000160,GO:0000166,GO:0000166,GO:0000785,GO:0003677,GO:0003677,GO:0003700,GO:0003700,GO:0003700,GO:0005524,GO:0005524,GO:0005524,GO:0006351,GO:0006351,GO:0006351,GO:0006351,GO:0006351,GO:0006355,GO:0006355,GO:0006355,GO:0006355,GO:0006355,GO:0008134,GO:0043565,GO:0044212	phosphorelay response regulator activity,phosphorelay signal transduction system,phosphorelay signal transduction system,nucleotide binding,nucleotide binding,chromatin,DNA binding,DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,ATP binding,ATP binding,ATP binding,transcription, DNA-templated,transcription, DNA-templated,transcription, DNA-templated,transcription, DNA-templated,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,transcription factor binding,sequence-specific DNA binding,transcription regulatory region DNA binding
comp43122_c0_seq1.p1				
comp43126_c0_seq1.p1				
comp43163_c0_seq1.p1				
comp43169_c0_seq1.p1				
comp43199_c0_seq1.p1				
comp43201_c0_seq1.p1				
comp43211_c0_seq1.p1				
comp4322_c0_seq1.p1				
comp43226_c0_seq1.p1				
comp43227_c0_seq1.p2	sp|P03959|ATKA_ECOLI_Potassium-transporting_ATPase_A_chain_OS=Escherichia_coli_(strain_K12)_GN=kdpA_PE=3_SV=1	2.00E-62	GO:0000166,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006811,GO:0006813,GO:0006813,GO:0006813,GO:0006813,GO:0008152,GO:0008556,GO:0008556,GO:0008556,GO:0008556,GO:0016020,GO:0016020,GO:0016021,GO:0016787,GO:0030955,GO:0071805,GO:0071805,GO:0071805,GO:0071805	nucleotide binding,ATP binding,plasma membrane,plasma membrane,plasma membrane,plasma membrane,plasma membrane,transport,ion transport,potassium ion transport,potassium ion transport,potassium ion transport,potassium ion transport,metabolic process,potassium-transporting ATPase activity,potassium-transporting ATPase activity,potassium-transporting ATPase activity,potassium-transporting ATPase activity,membrane,membrane,integral component of membrane,hydrolase activity,potassium ion binding,potassium ion transmembrane transport,potassium ion transmembrane transport,potassium ion transmembrane transport,potassium ion transmembrane transport
comp4324_c0_seq1.p1				
comp43245_c0_seq1.p1				
comp43256_c0_seq1.p1				
comp43260_c0_seq1.p1				
comp43261_c0_seq1.p1				
comp43266_c0_seq1.p1	sp|P67654|KDSC_SHIFL_3-deoxy-D-manno-octulosonate_8-phosphate_phosphatase_KdsC_OS=Shigella_flexneri_GN=kdsC_PE=3_SV=1	8.00E-117	GO:0009103,GO:0009103,GO:0009103,GO:0009103,GO:0016311,GO:0016311,GO:0016787,GO:0019143,GO:0019143,GO:0046872	lipopolysaccharide biosynthetic process,lipopolysaccharide biosynthetic process,lipopolysaccharide biosynthetic process,lipopolysaccharide biosynthetic process,dephosphorylation,dephosphorylation,hydrolase activity,3-deoxy-manno-octulosonate-8-phosphatase activity,3-deoxy-manno-octulosonate-8-phosphatase activity,metal ion binding
comp43278_c0_seq1.p1				
comp43291_c0_seq1.p1				
comp43310_c0_seq1.p1				
comp43362_c0_seq1.p1	sp|P34091|RL6_MESCR_60S_ribosomal_protein_L6_OS=Mesembryanthemum_crystallinum_GN=RPL6_PE=2_SV=1	4.00E-42	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0030529	structural constituent of ribosome,intracellular,ribosome,ribosome,translation,ribonucleoprotein complex
comp43429_c0_seq1.p2				
comp43447_c0_seq1.p1	sp|P00072|CYC_FAGES_Cytochrome_c_OS=Fagopyrum_esculentum_PE=1_SV=1	7.00E-48	GO:0005506,GO:0005739,GO:0005758,GO:0009055,GO:0020037,GO:0046872,GO:0055114,GO:0070469	iron ion binding,mitochondrion,mitochondrial intermembrane space,electron carrier activity,heme binding,metal ion binding,oxidation-reduction process,respiratory chain
comp43500_c0_seq1.p1				
comp43502_c0_seq1.p1				
comp43531_c0_seq1.p2	sp|P36181|HSP80_SOLLC_Heat_shock_cognate_protein_80_OS=Solanum_lycopersicum_GN=HSC80_PE=2_SV=1	0	GO:0000166,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0006457,GO:0006950,GO:0051082	nucleotide binding,ATP binding,ATP binding,cytoplasm,cytoplasm,protein folding,response to stress,unfolded protein binding
comp43578_c0_seq1.p2	sp|Q94776|RL23_TRYCR_60S_ribosomal_protein_L23_OS=Trypanosoma_cruzi_GN=RPL23_PE=2_SV=1	1.00E-49	GO:0003735,GO:0005840,GO:0005840,GO:0006412,GO:0030529	structural constituent of ribosome,ribosome,ribosome,translation,ribonucleoprotein complex
comp43599_c0_seq1.p1				
comp43664_c0_seq1.p2				
comp43673_c0_seq1.p1				
comp43720_c0_seq1.p1				
comp43724_c0_seq1.p1				
comp43742_c0_seq1.p2				
comp43744_c0_seq1.p1	sp|P42915|YRAJ_ECOLI_Uncharacterized_outer_membrane_usher_protein_yraJ_OS=Escherichia_coli_(strain_K12)_GN=yraJ_PE=3_SV=1	1.00E-151	GO:0005215,GO:0006810,GO:0006810,GO:0006974,GO:0009279,GO:0009279,GO:0009279,GO:0009297,GO:0015473,GO:0016020,GO:0016020,GO:0016021,GO:0043711,GO:0055085	transporter activity,transport,transport,cellular response to DNA damage stimulus,cell outer membrane,cell outer membrane,cell outer membrane,pilus assembly,fimbrial usher porin activity,membrane,membrane,integral component of membrane,pilus organization,transmembrane transport
comp4375_c0_seq1.p1				
comp43786_c0_seq1.p1				
comp43807_c0_seq1.p2				
comp43811_c0_seq1.p1				
comp43826_c0_seq1.p1				
comp43835_c0_seq1.p2				
comp43856_c0_seq1.p1				
comp43869_c0_seq1.p1				
comp43873_c0_seq1.p1				
comp43882_c0_seq1.p2	sp|Q3Z5R3|LPXC_SHISS_UDP-3-O-[3-hydroxymyristoyl]_N-acetylglucosamine_deacetylase_OS=Shigella_sonnei_(strain_Ss046)_GN=lpxC_PE=3_SV=1	2.00E-72	GO:0006629,GO:0008759,GO:0008759,GO:0009245,GO:0009245,GO:0009245,GO:0016787	lipid metabolic process,UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase activity,UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase activity,lipid A biosynthetic process,lipid A biosynthetic process,lipid A biosynthetic process,hydrolase activity
comp43908_c0_seq1.p1				
comp43914_c0_seq1.p1				
comp43943_c0_seq1.p1				
comp43944_c0_seq1.p1	sp|P45842|RL34_AEDAL_60S_ribosomal_protein_L34_OS=Aedes_albopictus_GN=RpL34_PE=2_SV=2	7.00E-44	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0030529	structural constituent of ribosome,intracellular,ribosome,ribosome,translation,ribonucleoprotein complex
comp43946_c0_seq1.p2				
comp43957_c0_seq1.p1				
comp43960_c0_seq1.p1	sp|P61255|RL26_MOUSE_60S_ribosomal_protein_L26_OS=Mus_musculus_GN=Rpl26_PE=2_SV=1	6.00E-40	GO:0003735,GO:0005515,GO:0005515,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0015934,GO:0030529	structural constituent of ribosome,protein binding,protein binding,intracellular,ribosome,ribosome,translation,large ribosomal subunit,ribonucleoprotein complex
comp44001_c0_seq1.p1	sp|P31828|PQQL_ECOLI_Probable_zinc_protease_pqqL_OS=Escherichia_coli_(strain_K12)_GN=pqqL_PE=3_SV=2	0	GO:0003824,GO:0004222,GO:0006508,GO:0006508,GO:0008233,GO:0008237,GO:0016787,GO:0046872,GO:0046872	catalytic activity,metalloendopeptidase activity,proteolysis,proteolysis,peptidase activity,metallopeptidase activity,hydrolase activity,metal ion binding,metal ion binding
comp44008_c0_seq1.p1				
comp44015_c0_seq1.p1				
comp44022_c0_seq1.p1	sp|P28303|DINF_ECOLI_DNA-damage-inducible_protein_F_OS=Escherichia_coli_(strain_K12)_GN=dinF_PE=2_SV=1	4.00E-42	GO:0005886,GO:0005886,GO:0005886,GO:0006855,GO:0015238,GO:0015297,GO:0016020,GO:0016020,GO:0016021,GO:0055085	plasma membrane,plasma membrane,plasma membrane,drug transmembrane transport,drug transmembrane transporter activity,antiporter activity,membrane,membrane,integral component of membrane,transmembrane transport
comp44073_c0_seq1.p1				
comp4409_c0_seq1.p1	sp|Q54IP0|DNJC7_DICDI_DnaJ_homolog_subfamily_C_member_7_homolog_OS=Dictyostelium_discoideum_GN=dnajc7_PE=1_SV=1	4.00E-29	GO:0045335	phagocytic vesicle
comp44110_c0_seq1.p1				
comp4412_c0_seq1.p1	sp|Q9LIK5|CML11_ARATH_Calmodulin-like_protein_11_OS=Arabidopsis_thaliana_GN=CML11_PE=2_SV=1	4.00E-16	GO:0005509,GO:0008150,GO:0030048,GO:0046872,GO:0051645,GO:0051646,GO:0060151	calcium ion binding,biological_process,actin filament-based movement,metal ion binding,Golgi localization,mitochondrion localization,peroxisome localization
comp44127_c0_seq1.p1	sp|B2TW38|ARNA_SHIB3_Putative_bifunctional_polymyxin_resistance_protein_ArnA_OS=Shigella_boydii_serotype_18_(strain_CDC_3083-94_/_BS512)_GN=arnA_PE=5_SV=1	3.00E-127	GO:0003824,GO:0003824,GO:0006629,GO:0008152,GO:0009058,GO:0009103,GO:0009103,GO:0009245,GO:0016491,GO:0016740,GO:0016742,GO:0046677,GO:0050662,GO:0055114	catalytic activity,catalytic activity,lipid metabolic process,metabolic process,biosynthetic process,lipopolysaccharide biosynthetic process,lipopolysaccharide biosynthetic process,lipid A biosynthetic process,oxidoreductase activity,transferase activity,hydroxymethyl-, formyl- and related transferase activity,response to antibiotic,coenzyme binding,oxidation-reduction process
comp44139_c0_seq1.p1				
comp4416_c0_seq1.p2	sp|Q95276|RL5_PIG_60S_ribosomal_protein_L5_(Fragment)_OS=Sus_scrofa_GN=RPL5_PE=2_SV=3	4.00E-52	GO:0003723,GO:0003735,GO:0005622,GO:0005634,GO:0005730,GO:0005737,GO:0005737,GO:0005840,GO:0005840,GO:0006412,GO:0008097,GO:0019843,GO:0030529	RNA binding,structural constituent of ribosome,intracellular,nucleus,nucleolus,cytoplasm,cytoplasm,ribosome,ribosome,translation,5S rRNA binding,rRNA binding,ribonucleoprotein complex
comp44182_c0_seq1.p1				
comp44184_c0_seq1.p1	sp|Q754C8|EF2_ASHGO_Elongation_factor_2_OS=Ashbya_gossypii_(strain_ATCC_10895_/_CBS_109.51_/_FGSC_9923_/_NRRL_Y-1056)_GN=EFT1_PE=3_SV=1	1.00E-105	GO:0000166,GO:0003746,GO:0003924,GO:0005525,GO:0005525,GO:0005737,GO:0005737,GO:0006184,GO:0006412,GO:0006414,GO:0045901	nucleotide binding,translation elongation factor activity,GTPase activity,GTP binding,GTP binding,cytoplasm,cytoplasm,GTP catabolic process,translation,translational elongation,positive regulation of translational elongation
comp44207_c0_seq1.p1				
comp44211_c0_seq1.p1				
comp44213_c0_seq1.p1				
comp44230_c0_seq1.p1				
comp4427_c0_seq1.p2				
comp44297_c0_seq1.p1				
comp44303_c0_seq1.p1				
comp44318_c0_seq1.p1				
comp44406_c0_seq1.p1				
comp44505_c0_seq1.p1				
comp44508_c0_seq1.p1				
comp44509_c0_seq1.p1				
comp44595_c0_seq1.p1				
comp44611_c0_seq1.p1	sp|Q3UTQ8|CDKL5_MOUSE_Cyclin-dependent_kinase-like_5_OS=Mus_musculus_GN=Cdkl5_PE=2_SV=1	7.00E-63	GO:0000166,GO:0001764,GO:0004672,GO:0004674,GO:0004674,GO:0004693,GO:0005524,GO:0005524,GO:0005634,GO:0005634,GO:0005634,GO:0005737,GO:0006468,GO:0016301,GO:0016301,GO:0016301,GO:0016310,GO:0016740,GO:0016772,GO:0032587,GO:0032839,GO:0032855,GO:0044294,GO:0045773,GO:0046777,GO:0048365,GO:0050773,GO:0050775,GO:0051726	nucleotide binding,neuron migration,protein kinase activity,protein serine/threonine kinase activity,protein serine/threonine kinase activity,cyclin-dependent protein serine/threonine kinase activity,ATP binding,ATP binding,nucleus,nucleus,nucleus,cytoplasm,protein phosphorylation,kinase activity,kinase activity,kinase activity,phosphorylation,transferase activity,transferase activity, transferring phosphorus-containing groups,ruffle membrane,dendrite cytoplasm,positive regulation of Rac GTPase activity,dendritic growth cone,positive regulation of axon extension,protein autophosphorylation,Rac GTPase binding,regulation of dendrite development,positive regulation of dendrite morphogenesis,regulation of cell cycle
comp44646_c0_seq1.p1				
comp44655_c0_seq1.p1				
comp44787_c0_seq1.p1	sp|P0ADS9|YGGN_ECOLI_Uncharacterized_protein_yggN_OS=Escherichia_coli_(strain_K12)_GN=yggN_PE=4_SV=1	9.00E-93		
comp44797_c0_seq1.p1				
comp44807_c0_seq1.p1				
comp44809_c0_seq1.p1				
comp44826_c0_seq1.p1	sp|P0ACL9|PDHR_ECOLI_Pyruvate_dehydrogenase_complex_repressor_OS=Escherichia_coli_(strain_K12)_GN=pdhR_PE=1_SV=1	2.00E-157	GO:0003677,GO:0003700,GO:0003700,GO:0003700,GO:0003700,GO:0003700,GO:0006351,GO:0006355,GO:0006355,GO:0045892,GO:0045892,GO:0045892,GO:0045892,GO:0045893,GO:0045893,GO:0045893,GO:0045893,GO:0045893	DNA binding,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,sequence-specific DNA binding transcription factor activity,transcription, DNA-templated,regulation of transcription, DNA-templated,regulation of transcription, DNA-templated,negative regulation of transcription, DNA-templated,negative regulation of transcription, DNA-templated,negative regulation of transcription, DNA-templated,negative regulation of transcription, DNA-templated,positive regulation of transcription, DNA-templated,positive regulation of transcription, DNA-templated,positive regulation of transcription, DNA-templated,positive regulation of transcription, DNA-templated,positive regulation of transcription, DNA-templated
comp44827_c0_seq1.p1				
comp44831_c0_seq1.p1				
comp44843_c0_seq1.p1				
comp44845_c0_seq1.p1				
comp44846_c0_seq1.p1	sp|Q46851|YGHZ_ECOLI_Uncharacterized_protein_yghZ_OS=Escherichia_coli_(strain_K12)_GN=yghZ_PE=1_SV=1	3.00E-65	GO:0006974,GO:0009438,GO:0016491,GO:0016616,GO:0055114	cellular response to DNA damage stimulus,methylglyoxal metabolic process,oxidoreductase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,oxidation-reduction process
comp44847_c0_seq1.p1				
comp44869_c0_seq1.p2				
comp44871_c0_seq1.p1	sp|A0AUS0|WSDU1_DANRE_WD_repeat,_SAM_and_U-box_domain-containing_protein_1_OS=Danio_rerio_GN=wdsub1_PE=2_SV=1	4.00E-16	GO:0004842,GO:0016567	ubiquitin-protein transferase activity,protein ubiquitination
comp44886_c0_seq1.p2	sp|Q1R535|YSAB_ECOUT_Uncharacterized_lipoprotein_ysaB_OS=Escherichia_coli_(strain_UTI89_/_UPEC)_GN=ysaB_PE=4_SV=1	5.00E-66	GO:0005886,GO:0005886,GO:0016020	plasma membrane,plasma membrane,membrane
comp44898_c0_seq1.p1				
comp44902_c0_seq1.p1	sp|P22523|MUKB_ECOLI_Chromosome_partition_protein_MukB_OS=Escherichia_coli_(strain_K12)_GN=mukB_PE=1_SV=2	6.00E-174	GO:0000166,GO:0000796,GO:0003677,GO:0003677,GO:0003677,GO:0003677,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005524,GO:0005525,GO:0005737,GO:0005737,GO:0006260,GO:0007049,GO:0007059,GO:0007059,GO:0007059,GO:0007059,GO:0007059,GO:0007059,GO:0007059,GO:0007062,GO:0009295,GO:0009295,GO:0030261,GO:0030261,GO:0030261,GO:0030261,GO:0042802,GO:0051301,GO:0051301	nucleotide binding,condensin complex,DNA binding,DNA binding,DNA binding,DNA binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,ATP binding,ATP binding,GTP binding,cytoplasm,cytoplasm,DNA replication,cell cycle,chromosome segregation,chromosome segregation,chromosome segregation,chromosome segregation,chromosome segregation,chromosome segregation,chromosome segregation,sister chromatid cohesion,nucleoid,nucleoid,chromosome condensation,chromosome condensation,chromosome condensation,chromosome condensation,identical protein binding,cell division,cell division
comp44902_c0_seq1.p3	sp|P22525|YCBB_ECOLI_Probable_L,D-transpeptidase_YcbB_OS=Escherichia_coli_(strain_K12)_GN=ycbB_PE=3_SV=2	2.00E-90	GO:0006508,GO:0006974,GO:0008360,GO:0009252,GO:0009252,GO:0016020,GO:0016020,GO:0016021,GO:0016740,GO:0016740,GO:0016755,GO:0016757,GO:0016787,GO:0016807,GO:0043164,GO:0044036,GO:0071555,GO:0071972	proteolysis,cellular response to DNA damage stimulus,regulation of cell shape,peptidoglycan biosynthetic process,peptidoglycan biosynthetic process,membrane,membrane,integral component of membrane,transferase activity,transferase activity,transferase activity, transferring amino-acyl groups,transferase activity, transferring glycosyl groups,hydrolase activity,cysteine-type carboxypeptidase activity,Gram-negative-bacterium-type cell wall biogenesis,cell wall macromolecule metabolic process,cell wall organization,peptidoglycan L,D-transpeptidase activity
comp4491_c0_seq1.p1				
comp45013_c0_seq1.p1				
comp45014_c0_seq1.p1	sp|Q1R5L1|GLPG_ECOUT_Rhomboid_protease_glpG_OS=Escherichia_coli_(strain_UTI89_/_UPEC)_GN=glpG_PE=3_SV=1	0	GO:0004252,GO:0004252,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006508,GO:0006508,GO:0006508,GO:0008233,GO:0008236,GO:0016020,GO:0016021,GO:0016021,GO:0016787	serine-type endopeptidase activity,serine-type endopeptidase activity,plasma membrane,plasma membrane,plasma membrane,plasma membrane,proteolysis,proteolysis,proteolysis,peptidase activity,serine-type peptidase activity,membrane,integral component of membrane,integral component of membrane,hydrolase activity
comp45021_c0_seq1.p3				
comp45033_c0_seq1.p1	sp|P03018|UVRD_ECOLI_DNA_helicase_II_OS=Escherichia_coli_(strain_K12)_GN=uvrD_PE=1_SV=1	6.00E-121	GO:0000166,GO:0003677,GO:0003677,GO:0003678,GO:0004003,GO:0004386,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005524,GO:0005524,GO:0005737,GO:0005829,GO:0006200,GO:0006260,GO:0006268,GO:0006281,GO:0006289,GO:0006289,GO:0006298,GO:0006298,GO:0006974,GO:0009432,GO:0009432,GO:0015616,GO:0016787,GO:0016787,GO:0017116,GO:0017116,GO:0031297,GO:0031297,GO:0031297,GO:0031297,GO:0032508,GO:0051260,GO:0051260,GO:0070581	nucleotide binding,DNA binding,DNA binding,DNA helicase activity,ATP-dependent DNA helicase activity,helicase activity,protein binding,protein binding,protein binding,protein binding,protein binding,ATP binding,ATP binding,cytoplasm,cytosol,ATP catabolic process,DNA replication,DNA unwinding involved in DNA replication,DNA repair,nucleotide-excision repair,nucleotide-excision repair,mismatch repair,mismatch repair,cellular response to DNA damage stimulus,SOS response,SOS response,DNA translocase activity,hydrolase activity,hydrolase activity,single-stranded DNA-dependent ATP-dependent DNA helicase activity,single-stranded DNA-dependent ATP-dependent DNA helicase activity,replication fork processing,replication fork processing,replication fork processing,replication fork processing,DNA duplex unwinding,protein homooligomerization,protein homooligomerization,rolling circle DNA replication
comp45036_c0_seq1.p1				
comp45046_c0_seq1.p1				
comp45055_c0_seq1.p1				
comp45081_c0_seq1.p1				
comp45098_c0_seq1.p1				
comp45132_c0_seq1.p1				
comp45148_c0_seq1.p1	sp|Q9ZPJ8|AMT12_ARATH_Ammonium_transporter_1_member_2_OS=Arabidopsis_thaliana_GN=AMT1-2_PE=1_SV=1	3.00E-13	GO:0005886,GO:0006810,GO:0008519,GO:0009624,GO:0010264,GO:0015696,GO:0015696,GO:0015696,GO:0015843,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0072488	plasma membrane,transport,ammonium transmembrane transporter activity,response to nematode,myo-inositol hexakisphosphate biosynthetic process,ammonium transport,ammonium transport,ammonium transport,methylammonium transport,membrane,membrane,membrane,integral component of membrane,ammonium transmembrane transport
comp45162_c0_seq1.p1				
comp4517_c0_seq1.p2	sp|Q32DS7|MENC_SHIDS_o-succinylbenzoate_synthase_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=menC_PE=3_SV=1	2.00E-69	GO:0000287,GO:0000287,GO:0003824,GO:0008152,GO:0009234,GO:0009234,GO:0009234,GO:0009234,GO:0016829,GO:0016836,GO:0016836,GO:0046872	magnesium ion binding,magnesium ion binding,catalytic activity,metabolic process,menaquinone biosynthetic process,menaquinone biosynthetic process,menaquinone biosynthetic process,menaquinone biosynthetic process,lyase activity,hydro-lyase activity,hydro-lyase activity,metal ion binding
comp4518_c0_seq1.p1	sp|P37657|YHJS_ECOLI_Uncharacterized_protein_yhjS_OS=Escherichia_coli_(strain_K12)_GN=yhjS_PE=4_SV=1	1.00E-65		
comp45201_c0_seq1.p1	sp|Q39575|DYHG_CHLRE_Dynein_gamma_chain,_flagellar_outer_arm_OS=Chlamydomonas_reinhardtii_GN=ODA2_PE=1_SV=1	1.00E-151	GO:0000166,GO:0003774,GO:0003777,GO:0005524,GO:0005524,GO:0005737,GO:0005856,GO:0005874,GO:0005929,GO:0006200,GO:0007018,GO:0008152,GO:0008152,GO:0016887,GO:0030030,GO:0030286,GO:0030286,GO:0031514,GO:0042995	nucleotide binding,motor activity,microtubule motor activity,ATP binding,ATP binding,cytoplasm,cytoskeleton,microtubule,cilium,ATP catabolic process,microtubule-based movement,metabolic process,metabolic process,ATPase activity,cell projection organization,dynein complex,dynein complex,motile cilium,cell projection
comp45219_c0_seq1.p1				
comp45269_c0_seq1.p1	sp|Q612F5|PCCA_CAEBR_Propionyl-CoA_carboxylase_alpha_chain,_mitochondrial_OS=Caenorhabditis_briggsae_GN=pcca-1_PE=3_SV=1	6.00E-70	GO:0000166,GO:0003824,GO:0004075,GO:0004658,GO:0005524,GO:0005524,GO:0005739,GO:0005759,GO:0008152,GO:0016874,GO:0016874,GO:0046872	nucleotide binding,catalytic activity,biotin carboxylase activity,propionyl-CoA carboxylase activity,ATP binding,ATP binding,mitochondrion,mitochondrial matrix,metabolic process,ligase activity,ligase activity,metal ion binding
comp45297_c0_seq1.p1				
comp45298_c0_seq1.p1				
comp45300_c0_seq1.p1	sp|P62912|RL32_RAT_60S_ribosomal_protein_L32_OS=Rattus_norvegicus_GN=Rpl32_PE=1_SV=2	1.00E-46	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0016020,GO:0022625,GO:0022625,GO:0030529,GO:0044822	structural constituent of ribosome,intracellular,ribosome,ribosome,translation,membrane,cytosolic large ribosomal subunit,cytosolic large ribosomal subunit,ribonucleoprotein complex,poly(A) RNA binding
comp45317_c0_seq1.p2	sp|Q54Q51|RS16_DICDI_40S_ribosomal_protein_S16_OS=Dictyostelium_discoideum_GN=rps16_PE=3_SV=1	1.00E-59	GO:0003735,GO:0003735,GO:0005840,GO:0005840,GO:0006412,GO:0006412,GO:0030529,GO:0044351	structural constituent of ribosome,structural constituent of ribosome,ribosome,ribosome,translation,translation,ribonucleoprotein complex,macropinocytosis
comp45327_c0_seq1.p1				
comp45329_c0_seq1.p1				
comp45330_c0_seq1.p1				
comp45343_c0_seq1.p1	sp|P15977|MALQ_ECOLI_4-alpha-glucanotransferase_OS=Escherichia_coli_(strain_K12)_GN=malQ_PE=3_SV=2	2.00E-147	GO:0000025,GO:0000025,GO:0000025,GO:0004134,GO:0004134,GO:0004134,GO:0005737,GO:0005737,GO:0005829,GO:0005975,GO:0005975,GO:0005977,GO:0005977,GO:0005977,GO:0016740,GO:0016757	maltose catabolic process,maltose catabolic process,maltose catabolic process,4-alpha-glucanotransferase activity,4-alpha-glucanotransferase activity,4-alpha-glucanotransferase activity,cytoplasm,cytoplasm,cytosol,carbohydrate metabolic process,carbohydrate metabolic process,glycogen metabolic process,glycogen metabolic process,glycogen metabolic process,transferase activity,transferase activity, transferring glycosyl groups
comp45348_c0_seq1.p1				
comp45353_c0_seq1.p2				
comp45358_c0_seq1.p1	sp|Q4KTG9|RL17_SUBDO_60S_ribosomal_protein_L17_OS=Suberites_domuncula_GN=RPL17_PE=2_SV=1	5.00E-56	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0015934,GO:0030529	structural constituent of ribosome,intracellular,ribosome,ribosome,translation,large ribosomal subunit,ribonucleoprotein complex
comp45450_c0_seq1.p1				
comp45487_c0_seq1.p1				
comp45518_c0_seq1.p1				
comp45542_c0_seq1.p1				
comp45575_c0_seq1.p1				
comp45577_c0_seq1.p1	sp|P76573|YFGI_ECOLI_Uncharacterized_protein_yfgI_OS=Escherichia_coli_(strain_K12)_GN=yfgI_PE=4_SV=1	3.00E-98	GO:0006974	cellular response to DNA damage stimulus
comp4558_c0_seq1.p1				
comp45600_c0_seq1.p1				
comp45603_c0_seq1.p1	sp|B7N421|HEM1_ECOLU_Glutamyl-tRNA_reductase_OS=Escherichia_coli_O17:K52:H18_(strain_UMN026_/_ExPEC)_GN=hemA_PE=3_SV=1	9.00E-101	GO:0006779,GO:0006779,GO:0006782,GO:0008883,GO:0008883,GO:0008883,GO:0016491,GO:0033014,GO:0050661,GO:0055114,GO:0055114	porphyrin-containing compound biosynthetic process,porphyrin-containing compound biosynthetic process,protoporphyrinogen IX biosynthetic process,glutamyl-tRNA reductase activity,glutamyl-tRNA reductase activity,glutamyl-tRNA reductase activity,oxidoreductase activity,tetrapyrrole biosynthetic process,NADP binding,oxidation-reduction process,oxidation-reduction process
comp45609_c0_seq1.p1				
comp45649_c0_seq1.p1				
comp45670_c0_seq1.p2				
comp45694_c0_seq1.p1	sp|P0DJ14|RL7A_TETTH_60S_ribosomal_protein_L7a_OS=Tetrahymena_thermophila_GN=RPL7A_PE=1_SV=1	3.00E-27	GO:0005840,GO:0030529,GO:0030529,GO:0042254	ribosome,ribonucleoprotein complex,ribonucleoprotein complex,ribosome biogenesis
comp45836_c0_seq1.p1	sp|P04636|MDHM_RAT_Malate_dehydrogenase,_mitochondrial_OS=Rattus_norvegicus_GN=Mdh2_PE=1_SV=2	2.00E-63	GO:0003824,GO:0005515,GO:0005634,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005739,GO:0005743,GO:0005759,GO:0005759,GO:0005886,GO:0005975,GO:0006099,GO:0006099,GO:0006107,GO:0006108,GO:0006108,GO:0006108,GO:0006108,GO:0006475,GO:0006475,GO:0006734,GO:0016491,GO:0016491,GO:0016615,GO:0016615,GO:0016616,GO:0030060,GO:0030060,GO:0030060,GO:0030060,GO:0030060,GO:0043621,GO:0044262,GO:0044822,GO:0046554,GO:0055114,GO:0055114,GO:0070062	catalytic activity,protein binding,nucleus,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrion,mitochondrial inner membrane,mitochondrial matrix,mitochondrial matrix,plasma membrane,carbohydrate metabolic process,tricarboxylic acid cycle,tricarboxylic acid cycle,oxaloacetate metabolic process,malate metabolic process,malate metabolic process,malate metabolic process,malate metabolic process,internal protein amino acid acetylation,internal protein amino acid acetylation,NADH metabolic process,oxidoreductase activity,oxidoreductase activity,malate dehydrogenase activity,malate dehydrogenase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,L-malate dehydrogenase activity,L-malate dehydrogenase activity,L-malate dehydrogenase activity,L-malate dehydrogenase activity,L-malate dehydrogenase activity,protein self-association,cellular carbohydrate metabolic process,poly(A) RNA binding,malate dehydrogenase (NADP+) activity,oxidation-reduction process,oxidation-reduction process,extracellular vesicular exosome
comp45846_c0_seq1.p1	sp|P75821|YBJS_ECOLI_Uncharacterized_protein_ybjS_OS=Escherichia_coli_(strain_K12)_GN=ybjS_PE=4_SV=2	1.00E-142	GO:0003824,GO:0008152,GO:0050662	catalytic activity,metabolic process,coenzyme binding
comp45858_c0_seq1.p1				
comp45906_c0_seq1.p1				
comp45943_c0_seq1.p1				
comp45977_c0_seq1.p1				
comp45979_c0_seq1.p1				
comp46010_c0_seq1.p1	sp|P37653|BCSA_ECOLI_Cellulose_synthase_catalytic_subunit_[UDP-forming]_OS=Escherichia_coli_(strain_K12)_GN=bcsA_PE=1_SV=3	3.00E-165	GO:0005886,GO:0005886,GO:0005886,GO:0006011,GO:0016020,GO:0016020,GO:0016021,GO:0016740,GO:0016757,GO:0016759,GO:0016760,GO:0030244,GO:0035438,GO:0090540	plasma membrane,plasma membrane,plasma membrane,UDP-glucose metabolic process,membrane,membrane,integral component of membrane,transferase activity,transferase activity, transferring glycosyl groups,cellulose synthase activity,cellulose synthase (UDP-forming) activity,cellulose biosynthetic process,cyclic-di-GMP binding,bacterial cellulose biosynthetic process
comp46012_c0_seq1.p1				
comp46040_c0_seq1.p1				
comp46051_c0_seq1.p1				
comp46055_c0_seq1.p1				
comp46101_c0_seq1.p2	sp|Q7RVI1|RS5_NEUCR_40S_ribosomal_protein_S5_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=rps-5_PE=3_SV=2	3.00E-33	GO:0003723,GO:0003735,GO:0005840,GO:0006412,GO:0015935,GO:0030529	RNA binding,structural constituent of ribosome,ribosome,translation,small ribosomal subunit,ribonucleoprotein complex
comp46105_c0_seq1.p1	sp|Q3YVD7|METE_SHISS_5-methyltetrahydropteroyltriglutamate--homocysteine_methyltransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=metE_PE=3_SV=1	2.00E-62	GO:0003871,GO:0003871,GO:0003871,GO:0008168,GO:0008270,GO:0008652,GO:0008652,GO:0009086,GO:0009086,GO:0009086,GO:0016740,GO:0032259,GO:0046872	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity,5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity,5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity,methyltransferase activity,zinc ion binding,cellular amino acid biosynthetic process,cellular amino acid biosynthetic process,methionine biosynthetic process,methionine biosynthetic process,methionine biosynthetic process,transferase activity,methylation,metal ion binding
comp46113_c0_seq1.p1				
comp46120_c0_seq1.p2	sp|A0BD73|RL72_PARTE_60S_ribosomal_protein_L7_2_OS=Paramecium_tetraurelia_GN=Rpl7-2_PE=3_SV=1	8.00E-41	GO:0003723,GO:0005840,GO:0030529	RNA binding,ribosome,ribonucleoprotein complex
comp46130_c0_seq1.p1				
comp46132_c0_seq1.p1				
comp46133_c0_seq1.p1				
comp46134_c0_seq1.p1	sp|P81701|PRXV_ASCNO_Vanadium-dependent_bromoperoxidase_OS=Ascophyllum_nodosum_PE=1_SV=1	1.00E-101	GO:0003824,GO:0004601,GO:0004601,GO:0016020,GO:0016491,GO:0046872,GO:0055114,GO:0055114	catalytic activity,peroxidase activity,peroxidase activity,membrane,oxidoreductase activity,metal ion binding,oxidation-reduction process,oxidation-reduction process
comp46144_c0_seq1.p2	sp|P60868|RS20_RAT_40S_ribosomal_protein_S20_OS=Rattus_norvegicus_GN=Rps20_PE=3_SV=1	3.00E-50	GO:0002181,GO:0003723,GO:0003735,GO:0003735,GO:0005622,GO:0005737,GO:0005737,GO:0005840,GO:0005840,GO:0006412,GO:0015935,GO:0022627,GO:0030529	cytoplasmic translation,RNA binding,structural constituent of ribosome,structural constituent of ribosome,intracellular,cytoplasm,cytoplasm,ribosome,ribosome,translation,small ribosomal subunit,cytosolic small ribosomal subunit,ribonucleoprotein complex
comp46159_c0_seq1.p1				
comp46161_c0_seq1.p1	sp|P0AAA8|WZXE_SHIFL_Protein_wzxE_OS=Shigella_flexneri_GN=wzxE_PE=3_SV=1	1.00E-142	GO:0000271,GO:0005886,GO:0005886,GO:0005886,GO:0009246,GO:0016020,GO:0016020,GO:0016021	polysaccharide biosynthetic process,plasma membrane,plasma membrane,plasma membrane,enterobacterial common antigen biosynthetic process,membrane,membrane,integral component of membrane
comp46165_c0_seq1.p2				
comp46177_c0_seq1.p1	sp|Q22000|PDE4_CAEEL_Probable_3',5'-cyclic_phosphodiesterase_pde-4_OS=Caenorhabditis_elegans_GN=pde-4_PE=2_SV=2	2.00E-16	GO:0004114,GO:0004114,GO:0004115,GO:0006198,GO:0007165,GO:0008081,GO:0016787,GO:0030431,GO:0040013,GO:0043951,GO:0045202,GO:0046872	3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-nucleotide phosphodiesterase activity,3',5'-cyclic-AMP phosphodiesterase activity,cAMP catabolic process,signal transduction,phosphoric diester hydrolase activity,hydrolase activity,sleep,negative regulation of locomotion,negative regulation of cAMP-mediated signaling,synapse,metal ion binding
comp46180_c0_seq1.p1				
comp46182_c0_seq1.p1	sp|P52647|NIFJ_ECOLI_Probable_pyruvate-flavodoxin_oxidoreductase_OS=Escherichia_coli_(strain_K12)_GN=ydbK_PE=3_SV=2	3.00E-117	GO:0003824,GO:0005506,GO:0006979,GO:0008152,GO:0016491,GO:0016491,GO:0016903,GO:0022900,GO:0030976,GO:0043873,GO:0046872,GO:0051536,GO:0051536,GO:0051539,GO:0055114,GO:0055114,GO:0055114	catalytic activity,iron ion binding,response to oxidative stress,metabolic process,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the aldehyde or oxo group of donors,electron transport chain,thiamine pyrophosphate binding,pyruvate-flavodoxin oxidoreductase activity,metal ion binding,iron-sulfur cluster binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process
comp46183_c0_seq1.p1				
comp46194_c0_seq1.p1	sp|Q8H715|ATG8_PHYIN_Autophagy-related_protein_8_OS=Phytophthora_infestans_GN=ATG8_PE=3_SV=1	2.00E-63	GO:0000421,GO:0005773,GO:0005774,GO:0006810,GO:0006914,GO:0015031,GO:0016020,GO:0031410,GO:0033110	autophagic vacuole membrane,vacuole,vacuolar membrane,transport,autophagy,protein transport,membrane,cytoplasmic vesicle,Cvt vesicle membrane
comp46195_c0_seq1.p1				
comp46202_c0_seq1.p1	sp|Q7TQE7|K0895_MOUSE_Uncharacterized_protein_KIAA0895_OS=Mus_musculus_GN=Kiaa0895_PE=2_SV=2	1.00E-29	GO:0003674,GO:0005575,GO:0008150	molecular_function,cellular_component,biological_process
comp46223_c0_seq1.p1	sp|Q83JJ8|PAT_SHIFL_Putrescine_aminotransferase_OS=Shigella_flexneri_GN=patA_PE=3_SV=5	2.00E-123	GO:0003824,GO:0008483,GO:0008483,GO:0008483,GO:0009447,GO:0009447,GO:0009447,GO:0016740,GO:0030170,GO:0030170,GO:0033094,GO:0033094	catalytic activity,transaminase activity,transaminase activity,transaminase activity,putrescine catabolic process,putrescine catabolic process,putrescine catabolic process,transferase activity,pyridoxal phosphate binding,pyridoxal phosphate binding,butane-1,4-diamine:2-oxoglutarate aminotransferase activity,butane-1,4-diamine:2-oxoglutarate aminotransferase activity
comp46223_c0_seq1.p2	sp|P42589|YGJH_ECOLI_tRNA-binding_protein_ygjH_OS=Escherichia_coli_(strain_K12)_GN=ygjH_PE=1_SV=1	3.00E-72	GO:0000049,GO:0000049,GO:0003723	tRNA binding,tRNA binding,RNA binding
comp46235_c0_seq1.p1				
comp4625_c0_seq1.p1				
comp46257_c0_seq1.p1				
comp46267_c0_seq1.p1				
comp46268_c0_seq1.p1				
comp46280_c0_seq1.p1				
comp46295_c0_seq1.p2				
comp46296_c0_seq1.p1	sp|P0ABC6|HFLC_SHIFL_Protein_HflC_OS=Shigella_flexneri_GN=hflC_PE=3_SV=1	2.00E-48	GO:0005886,GO:0005886,GO:0005886,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0052547	plasma membrane,plasma membrane,plasma membrane,membrane,membrane,integral component of membrane,integral component of membrane,regulation of peptidase activity
comp46326_c0_seq1.p1	sp|Q7Z494|NPHP3_HUMAN_Nephrocystin-3_OS=Homo_sapiens_GN=NPHP3_PE=1_SV=1	9.00E-15	GO:0001822,GO:0001947,GO:0001947,GO:0003283,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005515,GO:0005929,GO:0005929,GO:0005929,GO:0007368,GO:0016055,GO:0030324,GO:0035469,GO:0042995,GO:0045494,GO:0048496,GO:0060027,GO:0060271,GO:0060271,GO:0060287,GO:0060993,GO:0071908,GO:0071909,GO:0071910,GO:0072189,GO:0072372,GO:0090090,GO:2000095,GO:2000167	kidney development,heart looping,heart looping,atrial septum development,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,protein binding,cilium,cilium,cilium,determination of left/right symmetry,Wnt signaling pathway,lung development,determination of pancreatic left/right asymmetry,cell projection,photoreceptor cell maintenance,maintenance of organ identity,convergent extension involved in gastrulation,cilium morphogenesis,cilium morphogenesis,epithelial cilium movement involved in determination of left/right asymmetry,kidney morphogenesis,determination of intestine left/right asymmetry,determination of stomach left/right asymmetry,determination of liver left/right asymmetry,ureter development,primary cilium,negative regulation of canonical Wnt signaling pathway,regulation of Wnt signaling pathway, planar cell polarity pathway,regulation of planar cell polarity pathway involved in neural tube closure
comp46333_c0_seq1.p1				
comp46337_c0_seq1.p1	sp|P10978|POLX_TOBAC_Retrovirus-related_Pol_polyprotein_from_transposon_TNT_1-94_OS=Nicotiana_tabacum_PE=2_SV=1	3.00E-11	GO:0003676,GO:0003964,GO:0003964,GO:0004190,GO:0004518,GO:0004519,GO:0006278,GO:0006278,GO:0006508,GO:0008233,GO:0008270,GO:0015074,GO:0016740,GO:0016779,GO:0016787,GO:0046872,GO:0090305,GO:0090305	nucleic acid binding,RNA-directed DNA polymerase activity,RNA-directed DNA polymerase activity,aspartic-type endopeptidase activity,nuclease activity,endonuclease activity,RNA-dependent DNA replication,RNA-dependent DNA replication,proteolysis,peptidase activity,zinc ion binding,DNA integration,transferase activity,nucleotidyltransferase activity,hydrolase activity,metal ion binding,nucleic acid phosphodiester bond hydrolysis,nucleic acid phosphodiester bond hydrolysis
comp46346_c0_seq1.p1	sp|Q8T2K9|MASY_DICDI_Malate_synthase_OS=Dictyostelium_discoideum_GN=masA_PE=2_SV=2	4.00E-152	GO:0003824,GO:0004474,GO:0004474,GO:0005575,GO:0006097,GO:0006097,GO:0006097,GO:0006099,GO:0016740,GO:0044351	catalytic activity,malate synthase activity,malate synthase activity,cellular_component,glyoxylate cycle,glyoxylate cycle,glyoxylate cycle,tricarboxylic acid cycle,transferase activity,macropinocytosis
comp46381_c0_seq1.p1				
comp46394_c0_seq1.p1				
comp46397_c0_seq1.p2				
comp46405_c0_seq1.p1	sp|Q32CG3|CYSJ_SHIDS_Sulfite_reductase_[NADPH]_flavoprotein_alpha-component_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=cysJ_PE=3_SV=1	6.00E-109	GO:0000103,GO:0000103,GO:0004783,GO:0004783,GO:0004783,GO:0005506,GO:0008652,GO:0010181,GO:0016491,GO:0016491,GO:0019344,GO:0019344,GO:0050660,GO:0055114,GO:0055114,GO:0055114,GO:0070814,GO:0070814	sulfate assimilation,sulfate assimilation,sulfite reductase (NADPH) activity,sulfite reductase (NADPH) activity,sulfite reductase (NADPH) activity,iron ion binding,cellular amino acid biosynthetic process,FMN binding,oxidoreductase activity,oxidoreductase activity,cysteine biosynthetic process,cysteine biosynthetic process,flavin adenine dinucleotide binding,oxidation-reduction process,oxidation-reduction process,oxidation-reduction process,hydrogen sulfide biosynthetic process,hydrogen sulfide biosynthetic process
comp46431_c0_seq1.p1	sp|Q9LH76|RHM3_ARATH_Probable_rhamnose_biosynthetic_enzyme_3_OS=Arabidopsis_thaliana_GN=RHM3_PE=1_SV=1	2.00E-21	GO:0003824,GO:0003824,GO:0005829,GO:0008152,GO:0008460,GO:0008831,GO:0009225,GO:0009506,GO:0010253,GO:0010280,GO:0010280,GO:0016491,GO:0016829,GO:0016853,GO:0045226,GO:0050377,GO:0050662,GO:0055114	catalytic activity,catalytic activity,cytosol,metabolic process,dTDP-glucose 4,6-dehydratase activity,dTDP-4-dehydrorhamnose reductase activity,nucleotide-sugar metabolic process,plasmodesma,UDP-rhamnose biosynthetic process,UDP-L-rhamnose synthase activity,UDP-L-rhamnose synthase activity,oxidoreductase activity,lyase activity,isomerase activity,extracellular polysaccharide biosynthetic process,UDP-glucose 4,6-dehydratase activity,coenzyme binding,oxidation-reduction process
comp46433_c0_seq1.p1				
comp46433_c0_seq1.p3				
comp46436_c0_seq1.p2	sp|Q4WI01|RS21_ASPFU_40S_ribosomal_protein_S21_OS=Neosartorya_fumigata_(strain_ATCC_MYA-4609_/_Af293_/_CBS_101355_/_FGSC_A1100)_GN=rps21_PE=3_SV=1	4.00E-16	GO:0003735,GO:0005622,GO:0005737,GO:0005737,GO:0005840,GO:0005840,GO:0006364,GO:0006412,GO:0030529	structural constituent of ribosome,intracellular,cytoplasm,cytoplasm,ribosome,ribosome,rRNA processing,translation,ribonucleoprotein complex
comp46455_c0_seq1.p1				
comp46471_c0_seq1.p1	sp|Q3Z586|MHPB_SHISS_2,3-dihydroxyphenylpropionate/2,3-dihydroxicinnamic_acid_1,2-dioxygenase_OS=Shigella_sonnei_(strain_Ss046)_GN=mhpB_PE=3_SV=1	5.00E-69	GO:0005506,GO:0005506,GO:0006725,GO:0008198,GO:0016491,GO:0016491,GO:0019380,GO:0019439,GO:0019439,GO:0019439,GO:0047070,GO:0047070,GO:0047070,GO:0051213,GO:0055114,GO:0055114	iron ion binding,iron ion binding,cellular aromatic compound metabolic process,ferrous iron binding,oxidoreductase activity,oxidoreductase activity,3-phenylpropionate catabolic process,aromatic compound catabolic process,aromatic compound catabolic process,aromatic compound catabolic process,3-carboxyethylcatechol 2,3-dioxygenase activity,3-carboxyethylcatechol 2,3-dioxygenase activity,3-carboxyethylcatechol 2,3-dioxygenase activity,dioxygenase activity,oxidation-reduction process,oxidation-reduction process
comp46489_c0_seq1.p1				
comp46496_c0_seq1.p1				
comp46502_c0_seq1.p1	sp|Q3YUZ6|RPOC_SHISS_DNA-directed_RNA_polymerase_subunit_beta'_OS=Shigella_sonnei_(strain_Ss046)_GN=rpoC_PE=3_SV=1	4.00E-78	GO:0003677,GO:0003677,GO:0003899,GO:0003899,GO:0003899,GO:0003899,GO:0006351,GO:0006351,GO:0016740,GO:0016779	DNA binding,DNA binding,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,DNA-directed RNA polymerase activity,transcription, DNA-templated,transcription, DNA-templated,transferase activity,nucleotidyltransferase activity
comp46506_c0_seq1.p1				
comp46545_c0_seq1.p1	sp|P0A8Y7|YIDA_SHIFL_Phosphatase_YidA_OS=Shigella_flexneri_GN=yidA_PE=3_SV=1	9.00E-78	GO:0000287,GO:0003824,GO:0008152,GO:0016311,GO:0016787,GO:0016787,GO:0016791,GO:0046872,GO:0050308,GO:0050308	magnesium ion binding,catalytic activity,metabolic process,dephosphorylation,hydrolase activity,hydrolase activity,phosphatase activity,metal ion binding,sugar-phosphatase activity,sugar-phosphatase activity
comp46568_c0_seq1.p1	sp|P62725|YEIH_SHIFL_UPF0324_membrane_protein_yeiH_OS=Shigella_flexneri_GN=yeiH_PE=3_SV=1	2.00E-77	GO:0005886,GO:0005886,GO:0016020,GO:0016021,GO:0016021	plasma membrane,plasma membrane,membrane,integral component of membrane,integral component of membrane
comp46610_c0_seq1.p1	sp|Q5I0R6|RL22L_XENTR_60S_ribosomal_protein_L22-like_1_OS=Xenopus_tropicalis_GN=rpl22l1_PE=2_SV=1	1.00E-27	GO:0003735,GO:0005622,GO:0005840,GO:0005840,GO:0006412,GO:0030529	structural constituent of ribosome,intracellular,ribosome,ribosome,translation,ribonucleoprotein complex
comp46625_c0_seq1.p1	sp|P37691|YIBQ_ECOLI_Uncharacterized_protein_yibQ_OS=Escherichia_coli_(strain_K12)_GN=yibQ_PE=4_SV=2	1.00E-103	GO:0003824,GO:0005975,GO:0016810	catalytic activity,carbohydrate metabolic process,hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds
comp46681_c0_seq1.p1				
comp46687_c0_seq1.p1				
comp46695_c0_seq1.p1				
comp46710_c0_seq1.p1				
comp46717_c0_seq1.p1				
comp46723_c0_seq1.p4	sp|P0C6B8|SVEP1_RAT_Sushi,_von_Willebrand_factor_type_A,_EGF_and_pentraxin_domain-containing_protein_1_OS=Rattus_norvegicus_GN=Svep1_PE=1_SV=1	2.00E-27	GO:0003682,GO:0005509,GO:0005576,GO:0005576,GO:0005737,GO:0005737,GO:0007155,GO:0016020,GO:0016020	chromatin binding,calcium ion binding,extracellular region,extracellular region,cytoplasm,cytoplasm,cell adhesion,membrane,membrane
comp46743_c0_seq1.p1	sp|P59739|CYAA_SHIFL_Adenylate_cyclase_OS=Shigella_flexneri_GN=cyaA_PE=3_SV=1	0	GO:0000166,GO:0004016,GO:0004016,GO:0005524,GO:0005737,GO:0005737,GO:0006171,GO:0006171,GO:0016829	nucleotide binding,adenylate cyclase activity,adenylate cyclase activity,ATP binding,cytoplasm,cytoplasm,cAMP biosynthetic process,cAMP biosynthetic process,lyase activity
comp46747_c0_seq1.p1				
comp46767_c0_seq1.p1				
comp46794_c0_seq1.p1				
comp46817_c0_seq1.p1				
comp46830_c0_seq1.p1				
comp46838_c0_seq1.p1				
comp46854_c0_seq1.p1	sp|P42911|PTPD_ECOLI_N-acetylgalactosamine_permease_IID_component_OS=Escherichia_coli_(strain_K12)_GN=agaD_PE=4_SV=1	3.00E-59	GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0008643,GO:0009401,GO:0009401,GO:0016020,GO:0016021,GO:0016021	plasma membrane,plasma membrane,plasma membrane,transport,carbohydrate transport,phosphoenolpyruvate-dependent sugar phosphotransferase system,phosphoenolpyruvate-dependent sugar phosphotransferase system,membrane,integral component of membrane,integral component of membrane
comp46854_c0_seq1.p2	sp|P42910|PTPC1_ECOLI_N-acetylgalactosamine_permease_IIC_component_1_OS=Escherichia_coli_(strain_K12)_GN=agaC_PE=1_SV=1	2.00E-12	GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0008643,GO:0009401,GO:0009401,GO:0016020,GO:0016021,GO:0016021	plasma membrane,plasma membrane,plasma membrane,transport,carbohydrate transport,phosphoenolpyruvate-dependent sugar phosphotransferase system,phosphoenolpyruvate-dependent sugar phosphotransferase system,membrane,integral component of membrane,integral component of membrane
comp46860_c0_seq1.p1	sp|B6HYY8|CAIC_ECOSE_Probable_crotonobetaine/carnitine-CoA_ligase_OS=Escherichia_coli_(strain_SE11)_GN=caiC_PE=3_SV=2	0	GO:0003824,GO:0008152,GO:0009437,GO:0009437,GO:0016405,GO:0016874,GO:0016878,GO:0051108,GO:0051109	catalytic activity,metabolic process,carnitine metabolic process,carnitine metabolic process,CoA-ligase activity,ligase activity,acid-thiol ligase activity,carnitine-CoA ligase activity,crotonobetaine-CoA ligase activity
comp46870_c0_seq1.p2				
comp46877_c0_seq1.p1	sp|Q3YUA6|PYRB_SHISS_Aspartate_carbamoyltransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=pyrB_PE=3_SV=1	0	GO:0004070,GO:0004070,GO:0004070,GO:0006207,GO:0006221,GO:0006221,GO:0006520,GO:0016597,GO:0016740,GO:0016743,GO:0044205	aspartate carbamoyltransferase activity,aspartate carbamoyltransferase activity,aspartate carbamoyltransferase activity,'de novo' pyrimidine nucleobase biosynthetic process,pyrimidine nucleotide biosynthetic process,pyrimidine nucleotide biosynthetic process,cellular amino acid metabolic process,amino acid binding,transferase activity,carboxyl- or carbamoyltransferase activity,'de novo' UMP biosynthetic process
comp46954_c0_seq1.p2				
comp46977_c0_seq1.p1	sp|Q8CG45|ARK72_RAT_Aflatoxin_B1_aldehyde_reductase_member_2_OS=Rattus_norvegicus_GN=Akr7a2_PE=1_SV=2	5.00E-47	GO:0004032,GO:0004033,GO:0004033,GO:0005737,GO:0005737,GO:0005739,GO:0005794,GO:0005794,GO:0005795,GO:0016491,GO:0016616,GO:0055114	alditol:NADP+ 1-oxidoreductase activity,aldo-keto reductase (NADP) activity,aldo-keto reductase (NADP) activity,cytoplasm,cytoplasm,mitochondrion,Golgi apparatus,Golgi apparatus,Golgi stack,oxidoreductase activity,oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,oxidation-reduction process
comp46988_c0_seq1.p2				
comp47001_c0_seq1.p1				
comp47007_c0_seq1.p1				
comp4703_c0_seq1.p1				
comp47044_c0_seq1.p1	sp|P08903|H32_ENCAL_Histone_H3.2_OS=Encephalartos_altensteinii_PE=1_SV=2	1.00E-32	GO:0000786,GO:0000786,GO:0003677,GO:0003677,GO:0005634,GO:0005634,GO:0005694,GO:0005694,GO:0046982	nucleosome,nucleosome,DNA binding,DNA binding,nucleus,nucleus,chromosome,chromosome,protein heterodimerization activity
comp47054_c0_seq1.p1	sp|P53533|CLPB1_SYNE7_Chaperone_protein_ClpB_1_OS=Synechococcus_elongatus_(strain_PCC_7942)_GN=clpB1_PE=2_SV=3	2.00E-63	GO:0000166,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0009408,GO:0016485,GO:0019538	nucleotide binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,response to heat,protein processing,protein metabolic process
comp47099_c0_seq1.p1				
comp4718_c0_seq1.p2				
comp47183_c0_seq1.p1				
comp47185_c0_seq1.p1				
comp47201_c0_seq1.p1				
comp47202_c0_seq1.p2	sp|Q03168|ASPP_AEDAE_Lysosomal_aspartic_protease_OS=Aedes_aegypti_GN=AAEL006169_PE=1_SV=2	4.00E-21	GO:0004190,GO:0004190,GO:0005764,GO:0005764,GO:0006508,GO:0006508,GO:0008233,GO:0016787	aspartic-type endopeptidase activity,aspartic-type endopeptidase activity,lysosome,lysosome,proteolysis,proteolysis,peptidase activity,hydrolase activity
comp47207_c0_seq1.p2				
comp47213_c0_seq1.p1				
comp47245_c0_seq1.p1				
comp47250_c0_seq1.p1				
comp47262_c0_seq1.p1	sp|Q5RC59|BT3L4_PONAB_Transcription_factor_BTF3_homolog_4_OS=Pongo_abelii_GN=BTF3L4_PE=2_SV=1	1.00E-30		
comp47314_c0_seq1.p3				
comp47330_c0_seq1.p1	sp|P77338|KEFA_ECOLI_Potassium_efflux_system_KefA_OS=Escherichia_coli_(strain_K12)_GN=kefA_PE=1_SV=1	1.00E-153	GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006811,GO:0006813,GO:0008381,GO:0009992,GO:0016020,GO:0016020,GO:0016021,GO:0034220,GO:0055085	plasma membrane,plasma membrane,plasma membrane,transport,ion transport,potassium ion transport,mechanically-gated ion channel activity,cellular water homeostasis,membrane,membrane,integral component of membrane,ion transmembrane transport,transmembrane transport
comp47332_c0_seq1.p1	sp|Q5JH71|GLMS_PYRKO_Glucosamine--fructose-6-phosphate_aminotransferase_[isomerizing]_OS=Pyrococcus_kodakaraensis_(strain_ATCC_BAA-918_/_JCM_12380_/_KOD1)_GN=glmS_PE=3_SV=3	6.00E-53	GO:0004360,GO:0004360,GO:0004360,GO:0005737,GO:0005737,GO:0005737,GO:0005975,GO:0005975,GO:0006541,GO:0006541,GO:0008152,GO:0008483,GO:0016051,GO:0016740,GO:0030246	glutamine-fructose-6-phosphate transaminase (isomerizing) activity,glutamine-fructose-6-phosphate transaminase (isomerizing) activity,glutamine-fructose-6-phosphate transaminase (isomerizing) activity,cytoplasm,cytoplasm,cytoplasm,carbohydrate metabolic process,carbohydrate metabolic process,glutamine metabolic process,glutamine metabolic process,metabolic process,transaminase activity,carbohydrate biosynthetic process,transferase activity,carbohydrate binding
comp47366_c0_seq1.p1	sp|Q3YVG9|WZYE_SHISS_Putative_ECA_polymerase_OS=Shigella_sonnei_(strain_Ss046)_GN=wzyE_PE=3_SV=1	3.00E-72	GO:0005886,GO:0005886,GO:0005886,GO:0009246,GO:0009246,GO:0016020,GO:0016021,GO:0016021	plasma membrane,plasma membrane,plasma membrane,enterobacterial common antigen biosynthetic process,enterobacterial common antigen biosynthetic process,membrane,membrane,integral component of membrane,integral component of membrane
comp47434_c0_seq1.p1	sp|P37661|EPTB_ECOLI_Phosphoethanolamine_transferase_eptB_OS=Escherichia_coli_(strain_K12)_GN=eptB_PE=1_SV=3	7.00E-122	GO:0003824,GO:0005886,GO:0005886,GO:0005886,GO:0006629,GO:0008152,GO:0008484,GO:0009103,GO:0009245,GO:0009245,GO:0016020,GO:0016021,GO:0016021,GO:0016740,GO:0043838	catalytic activity,plasma membrane,plasma membrane,plasma membrane,lipid metabolic process,metabolic process,sulfuric ester hydrolase activity,lipopolysaccharide biosynthetic process,lipid A biosynthetic process,lipid A biosynthetic process,membrane,integral component of membrane,integral component of membrane,transferase activity,phosphatidylethanolamine:Kdo2-lipid A phosphoethanolamine transferase activity
comp47470_c0_seq1.p1				
comp47480_c0_seq1.p1				
comp47591_c0_seq1.p1				
comp47595_c0_seq1.p1				
comp47598_c0_seq1.p1	sp|Q9FLF0|RS92_ARATH_40S_ribosomal_protein_S9-2_OS=Arabidopsis_thaliana_GN=RPS9C_PE=2_SV=1	7.00E-46	GO:0003723,GO:0003723,GO:0003735,GO:0003735,GO:0005622,GO:0005829,GO:0005840,GO:0006412,GO:0009506,GO:0015935,GO:0016020,GO:0019843,GO:0019843,GO:0019843,GO:0022627,GO:0030529,GO:0045903,GO:0005794	RNA binding,RNA binding,structural constituent of ribosome,structural constituent of ribosome,intracellular,cytosol,ribosome,translation,plasmodesma,small ribosomal subunit,membrane,rRNA binding,rRNA binding,rRNA binding,cytosolic small ribosomal subunit,ribonucleoprotein complex,positive regulation of translational fidelity,Golgi apparatus

comp47607_c0_seq1.p2		
comp47607_c0_seq1.p3		
comp47623_c0_seq1.p2	sp|P10713|CON10_NEUCR_Conidiation-specific_protein_10_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=con-10_PE=2_SV=1	6.00E-33
comp47633_c0_seq1.p1		
comp47638_c0_seq1.p1	sp|P00363|FRDA_ECOLI_Fumarate_reductase_flavoprotein_subunit_OS=Escherichia_coli_(strain_K12)_GN=frdA_PE=1_SV=3	0
comp47640_c0_seq1.p2		
comp47650_c0_seq1.p1	sp|P75792|SUPH_ECOLI_Sugar_phosphatase_SupH_OS=Escherichia_coli_(strain_K12)_GN=supH_PE=1_SV=1	3.00E-93
comp47650_c0_seq1.p2	sp|P75791|YBIU_ECOLI_Uncharacterized_protein_ybiU_OS=Escherichia_coli_(strain_K12)_GN=ybiU_PE=1_SV=1	5.00E-91
comp47664_c0_seq1.p1	sp|Q58455|Y1055_METJA_Uncharacterized_protein_MJ1055_OS=Methanocaldococcus_jannaschii_(strain_ATCC_43067_/_DSM_2661_/_JAL-1_/_JCM_10045_/_NBRC_100440)_GN=MJ1055_PE=3_SV=1	1.00E-43
comp47677_c0_seq1.p1	sp|P28629|ADIA_ECOLI_Biodegradative_arginine_decarboxylase_OS=Escherichia_coli_(strain_K12)_GN=adiA_PE=1_SV=1	0
comp47692_c0_seq1.p1		
comp47697_c0_seq1.p1		
comp47701_c0_seq1.p2		
comp47704_c0_seq1.p1		
comp47712_c0_seq1.p1	sp|Q3Z583|BGAL_SHISS_Beta-galactosidase_OS=Shigella_sonnei_(strain_Ss046)_GN=lacZ_PE=3_SV=1	1.00E-106
comp47718_c0_seq1.p2	sp|P28178|PK2_DICDI_Protein_kinase_2_OS=Dictyostelium_discoideum_GN=pkgB_PE=1_SV=2	8.00E-17
comp47731_c0_seq1.p1	sp|P0ACY1|YDJA_ECOLI_Putative_NAD(P)H_nitroreductase_ydjA_OS=Escherichia_coli_(strain_K12)_GN=ydjA_PE=1_SV=1	2.00E-82
comp47763_c0_seq1.p1	sp|P28306|YCEG_ECOLI_UPF0755_protein_yceG_OS=Escherichia_coli_(strain_K12)_GN=yceG_PE=1_SV=2	4.00E-68
comp47764_c0_seq1.p1	sp|P0AAZ4|RARA_ECOLI_Replication-associated_recombination_protein_A_OS=Escherichia_coli_(strain_K12)_GN=rarA_PE=1_SV=1	2.00E-135
comp47775_c0_seq1.p1	sp|Q4R6F8|TCPB_MACFA_T-complex_protein_1_subunit_beta_OS=Macaca_fascicularis_GN=CCT2_PE=2_SV=3	8.00E-36
comp47794_c0_seq1.p1		
comp47798_c0_seq1.p2	sp|Q54MV7|NDUAC_DICDI_NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_12_OS=Dictyostelium_discoideum_GN=ndufa12_PE=2_SV=2	1.00E-13
comp47799_c0_seq1.p1	sp|Q9P2E2|KIF17_HUMAN_Kinesin-like_protein_KIF17_OS=Homo_sapiens_GN=KIF17_PE=1_SV=3	1.00E-45
comp47801_c0_seq1.p1	sp|Q3Z3V3|GSIB_SHISS_Glutathione-binding_protein_gsiB_OS=Shigella_sonnei_(strain_Ss046)_GN=gsiB_PE=3_SV=1	7.00E-178
comp47824_c0_seq1.p2		
comp47830_c0_seq1.p1	sp|Q15751|HERC1_HUMAN_Probable_E3_ubiquitin-protein_ligase_HERC1_OS=Homo_sapiens_GN=HERC1_PE=1_SV=2	4.00E-14
comp47856_c0_seq1.p1		
comp47869_c0_seq1.p1		
comp47898_c0_seq1.p1		
comp47918_c0_seq1.p1	sp|Q9N3B0|ARMET_CAEEL_MANF/CDNF-like_protein_OS=Caenorhabditis_elegans_GN=Y54G2A.23_PE=3_SV=2	1.00E-24
comp47927_c0_seq1.p1		
comp47947_c0_seq1.p1		
comp47948_c0_seq1.p1	sp|Q31TC2|ULAR_SHIBS_HTH-type_transcriptional_regulator_UlaR_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=ulaR_PE=3_SV=1	3.00E-107
comp47954_c0_seq1.p1	sp|Q42290|MPPB_ARATH_Probable_mitochondrial-processing_peptidase_subunit_beta_OS=Arabidopsis_thaliana_GN=At3g02090_PE=1_SV=2	1.00E-29
comp47957_c0_seq1.p1	sp|Q9DA80|RSH3B_MOUSE_Radial_spoke_head_protein_3_homolog_B_OS=Mus_musculus_GN=Rsph3b_PE=2_SV=1	3.00E-33
comp47971_c0_seq1.p1	sp|P32099|LPLA_ECOLI_Lipoate-protein_ligase_A_OS=Escherichia_coli_(strain_K12)_GN=lplA_PE=1_SV=3	5.00E-132
comp47971_c0_seq1.p2	sp|P39410|YJJJ_ECOLI_Putative_kinase_YjjJ_OS=Escherichia_coli_(strain_K12)_GN=yjjJ_PE=3_SV=1	7.00E-102
comp47973_c0_seq1.p1	sp|B7ND45|CCA_ECOLU_Multifunctional_CCA_protein_OS=Escherichia_coli_O17:K52:H18_(strain_UMN026_/_ExPEC)_GN=cca_PE=3_SV=1	2.00E-152
comp48002_c0_seq1.p1		
comp48009_c0_seq1.p1		
comp48028_c0_seq1.p1		
comp48029_c0_seq1.p1		
comp48034_c0_seq1.p1		
comp48043_c0_seq1.p2	sp|O74538|RL27B_SCHPO_60S_ribosomal_protein_L27-B_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpl27b_PE=2_SV=1	3.00E-30
comp48048_c0_seq1.p1	sp|P75747|ABRB_ECOLI_Protein_AbrB_OS=Escherichia_coli_(strain_K12)_GN=abrB_PE=3_SV=2	2.00E-99
comp48090_c0_seq1.p1		
comp48097_c0_seq1.p1	sp|Q32BQ4|TTDT_SHIDS_L-tartrate/succinate_antiporter_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=ttdT_PE=3_SV=1	3.00E-112
comp48099_c0_seq1.p1		
comp4814_c0_seq1.p1	sp|Q46814|XDHD_ECOLI_Probable_hypoxanthine_oxidase_XdhD_OS=Escherichia_coli_(strain_K12)_GN=xdhD_PE=3_SV=1	2.00E-81
comp48148_c0_seq1.p1	sp|P0A9P3|DLDH_SHIFL_Dihydrolipoyl_dehydrogenase_OS=Shigella_flexneri_GN=lpdA_PE=3_SV=2	1.00E-112
comp48149_c0_seq1.p2	sp|P0A9M0|LON_ECOLI_Lon_protease_OS=Escherichia_coli_(strain_K12)_GN=lon_PE=1_SV=1	7.00E-64
comp48180_c0_seq1.p2		
comp48189_c0_seq1.p1		
comp48232_c0_seq1.p1		
comp48266_c0_seq1.p1		
comp48280_c0_seq1.p1	sp|P11454|ENTF_ECOLI_Enterobactin_synthase_component_F_OS=Escherichia_coli_(strain_K12)_GN=entF_PE=1_SV=3	0
comp48307_c0_seq1.p2		
comp48321_c0_seq1.p1		
comp48336_c0_seq1.p1		
comp48349_c0_seq1.p1		
comp48351_c0_seq1.p1		
comp4837_c0_seq1.p1	sp|P09152|NARG_ECOLI_Respiratory_nitrate_reductase_1_alpha_chain_OS=Escherichia_coli_(strain_K12)_GN=narG_PE=1_SV=4	1.00E-68
comp48371_c0_seq1.p1		
comp48404_c0_seq1.p1		
comp48409_c0_seq1.p1	sp|P76460|ATOE_ECOLI_Short-chain_fatty_acids_transporter_OS=Escherichia_coli_(strain_K12)_GN=atoE_PE=1_SV=1	5.00E-150
comp48413_c0_seq1.p1	sp|Q0VA61|HYOU1_XENTR_Hypoxia_up-regulated_protein_1_(Fragment)_OS=Xenopus_tropicalis_GN=hyou1_PE=2_SV=2	8.00E-31
comp48414_c0_seq1.p1		
comp48421_c0_seq1.p1	sp|Q3YW95|GLGC_SHISS_Glucose-1-phosphate_adenylyltransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=glgC_PE=3_SV=1	3.00E-115
comp48437_c0_seq1.p1	sp|Q9P2D7|DYH1_HUMAN_Dynein_heavy_chain_1,_axonemal_OS=Homo_sapiens_GN=DNAH1_PE=1_SV=4	4.00E-74
comp48444_c0_seq1.p1		
comp48454_c0_seq1.p1		
comp48467_c0_seq1.p1		
comp48482_c0_seq1.p1		
comp48494_c0_seq1.p1		
comp48498_c0_seq1.p1		
comp48504_c0_seq1.p1		
comp48505_c0_seq1.p3		
comp48522_c0_seq1.p1		
comp48531_c0_seq1.p1	sp|A8LHA4|Y4929_FRASN_Putative_S-adenosyl-L-methionine-dependent_methyltransferase_Franean1_4929_OS=Frankia_sp._(strain_EAN1pec)_GN=Franean1_4929_PE=3_SV=2	2.00E-21
comp48551_c0_seq1.p1	sp|Q46841|YGHQ_ECOLI_Inner_membrane_protein_yghQ_OS=Escherichia_coli_(strain_K12)_GN=yghQ_PE=1_SV=2	3.00E-92
comp48553_c0_seq1.p2		
comp48591_c0_seq1.p1		
comp48621_c0_seq1.p1		
comp48650_c0_seq1.p1		
comp48682_c0_seq1.p1	sp|P0AG92|SECD_SHIFL_Protein_translocase_subunit_SecD_OS=Shigella_flexneri_GN=secD_PE=3_SV=1	5.00E-102
comp48696_c0_seq1.p1		
comp48701_c0_seq1.p1	sp|Q98SP7|BBS2_DANRE_Bardet-Biedl_syndrome_2_protein_homolog_OS=Danio_rerio_GN=bbs2_PE=2_SV=1	2.00E-35
comp48717_c0_seq1.p2	sp|P47836|RS4_CHICK_40S_ribosomal_protein_S4_OS=Gallus_gallus_GN=RPS4_PE=2_SV=2	2.00E-119
comp48721_c0_seq1.p1		
comp48732_c0_seq1.p1		
comp4874_c0_seq1.p2		
comp48744_c0_seq1.p1	sp|P77129|YLBE_ECOLI_Uncharacterized_protein_ylbE_OS=Escherichia_coli_(strain_K12)_GN=ylbE_PE=4_SV=1	0
comp48766_c0_seq1.p1	sp|P0AGE8|YIEF_SHIFL_Uncharacterized_protein_yieF_OS=Shigella_flexneri_GN=yieF_PE=3_SV=1	6.00E-75
comp48781_c0_seq1.p1	sp|Q2U5T5|VAC8_ASPOR_Vacuolar_protein_8_OS=Aspergillus_oryzae_(strain_ATCC_42149_/_RIB_40)_GN=vac8_PE=3_SV=1	4.00E-17
comp48800_c0_seq1.p1	sp|B1LPB5|RIMM_ECOSM_Ribosome_maturation_factor_RimM_OS=Escherichia_coli_(strain_SMS-3-5_/_SECEC)_GN=rimM_PE=3_SV=1	6.00E-122
comp48804_c0_seq1.p2	sp|Q9HZP6|ETFB_PSEAE_Electron_transfer_flavoprotein_subunit_beta_OS=Pseudomonas_aeruginosa_(strain_ATCC_15692_/_PAO1_/_1C_/_PRS_101_/_LMG_12228)_GN=etfB_PE=3_SV=1	6.00E-30
comp48861_c0_seq1.p1		
comp48863_c0_seq1.p1	sp|P0AA78|EXUT_ECOLI_Hexuronate_transporter_OS=Escherichia_coli_(strain_K12)_GN=exuT_PE=1_SV=1	8.00E-91
comp48913_c0_seq1.p1		
comp48974_c0_seq1.p2		
comp48974_c0_seq1.p4		
comp49067_c0_seq1.p1		
comp49084_c0_seq1.p1	sp|P13458|SBCC_ECOLI_Nuclease_sbcCD_subunit_C_OS=Escherichia_coli_(strain_K12)_GN=sbcC_PE=1_SV=1	2.00E-64
comp49091_c0_seq1.p2	sp|P52235|DSBA_SHIFL_Thiol:disulfide_interchange_protein_DsbA_OS=Shigella_flexneri_GN=dsbA_PE=1_SV=2	2.00E-104
comp49104_c0_seq1.p3		
comp49123_c0_seq1.p2	sp|P14407|FUMB_ECOLI_Fumarate_hydratase_class_I,_anaerobic_OS=Escherichia_coli_(strain_K12)_GN=fumB_PE=1_SV=2	1.00E-52
comp49196_c0_seq1.p1		
comp49210_c0_seq1.p2		
comp49210_c0_seq1.p3		
comp49211_c0_seq1.p1		
comp4922_c0_seq1.p1	sp|P69681|AMTB_ECOLI_Ammonia_channel_OS=Escherichia_coli_(strain_K12)_GN=amtB_PE=1_SV=1	4.00E-42
comp49260_c0_seq1.p1		
comp49305_c0_seq1.p2	sp|P41351|TBA_TETTH_Tubulin_alpha_chain_OS=Tetrahymena_thermophila_PE=1_SV=1	2.00E-153
comp49347_c0_seq1.p1		
comp49354_c0_seq1.p1		
comp49356_c0_seq1.p2		
comp49365_c0_seq1.p1	sp|Q9SB41|GLPT2_ARATH_Putative_glycerol-3-phosphate_transporter_2_OS=Arabidopsis_thaliana_GN=At4g25220_PE=2_SV=1	1.00E-20
comp49367_c0_seq1.p1	sp|Q54Z60|ACSA_DICDI_Acetyl-coenzyme_A_synthetase_OS=Dictyostelium_discoideum_GN=acsA_PE=3_SV=1	2.00E-175
comp49376_c0_seq1.p1	sp|P62494|RB11A_RAT_Ras-related_protein_Rab-11A_OS=Rattus_norvegicus_GN=Rab11a_PE=1_SV=3	3.00E-74
comp49397_c0_seq1.p1	sp|P0ACQ4|OXYR_ECOLI_Hydrogen_peroxide-inducible_genes_activator_OS=Escherichia_coli_(strain_K12)_GN=oxyR_PE=1_SV=1	7.00E-134
comp49405_c0_seq1.p1		
comp49406_c0_seq1.p1	sp|P75829|YBJX_ECOLI_Uncharacterized_protein_ybjX_OS=Escherichia_coli_(strain_K12)_GN=ybjX_PE=4_SV=1	0
comp49406_c0_seq1.p2	sp|P75830|MACA_ECOLI_Macrolide-specific_efflux_protein_macA_OS=Escherichia_coli_(strain_K12)_GN=macA_PE=1_SV=2	6.00E-106
comp49406_c0_seq1.p3	sp|P75828|YBJD_ECOLI_Uncharacterized_protein_ybjD_OS=Escherichia_coli_(strain_K12)_GN=ybjD_PE=4_SV=1	6.00E-63
comp49417_c0_seq1.p1	sp|P0AF31|NARL_SHIFL_Nitrate/nitrite_response_regulator_protein_narL_OS=Shigella_flexneri_GN=narL_PE=3_SV=1	1.00E-90
comp49419_c0_seq1.p1	sp|Q31WK6|SPRT_SHIBS_Protein_sprT_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=sprT_PE=3_SV=1	2.00E-114
comp49421_c0_seq1.p1	sp|P55084|ECHB_HUMAN_Trifunctional_enzyme_subunit_beta,_mitochondrial_OS=Homo_sapiens_GN=HADHB_PE=1_SV=3	6.00E-46
comp49435_c0_seq1.p3		
comp49442_c0_seq1.p1		
comp49445_c0_seq1.p1	sp|P04968|ILVA_ECOLI_L-threonine_dehydratase_biosynthetic_IlvA_OS=Escherichia_coli_(strain_K12)_GN=ilvA_PE=1_SV=1	5.00E-178
comp49455_c0_seq1.p1		
comp49456_c0_seq1.p1		
comp49465_c0_seq1.p2	sp|P39342|YJGR_ECOLI_Uncharacterized_protein_yjgR_OS=Escherichia_coli_(strain_K12)_GN=yjgR_PE=4_SV=1	7.00E-75
comp49484_c0_seq1.p2	sp|P90519|EF1A_CRYPV_Elongation_factor_1-alpha_OS=Cryptosporidium_parvum_PE=2_SV=1	1.00E-16
comp49487_c0_seq1.p1	sp|Q9SLG9|PI5K5_ARATH_Phosphatidylinositol_4-phosphate_5-kinase_5_OS=Arabidopsis_thaliana_GN=PIP5K5_PE=2_SV=1	3.00E-25
comp49495_c0_seq1.p1	sp|Q3YUV0|MALK_SHISS_Maltose/maltodextrin_import_ATP-binding_protein_MalK_OS=Shigella_sonnei_(strain_Ss046)_GN=malK_PE=3_SV=1	0
comp49496_c0_seq1.p2		
comp49520_c0_seq1.p1	sp|P16694|YJDA_ECOLI_Uncharacterized_protein_yjdA_OS=Escherichia_coli_(strain_K12)_GN=yjdA_PE=4_SV=2	1.00E-153
comp49526_c0_seq1.p1	sp|Q7DFU6|YGHX_ECOLI_Putative_uncharacterized_protein_yghX_OS=Escherichia_coli_(strain_K12)_GN=yghX_PE=5_SV=3	7.00E-134
comp49532_c0_seq1.p2	sp|Q3YXF0|MLTC_SHISS_Membrane-bound_lytic_murein_transglycosylase_C_OS=Shigella_sonnei_(strain_Ss046)_GN=mltC_PE=3_SV=2	1.00E-73
comp49539_c0_seq1.p1	sp|Q3YWV8|RL15_SHISS_50S_ribosomal_protein_L15_OS=Shigella_sonnei_(strain_Ss046)_GN=rplO_PE=3_SV=1	5.00E-47
comp49539_c0_seq1.p3	sp|P0AGA5|SECY_SHIFL_Protein_translocase_subunit_SecY_OS=Shigella_flexneri_GN=secY_PE=3_SV=1	5.00E-59
comp49547_c0_seq1.p1		
comp49560_c0_seq1.p2		
comp49561_c0_seq1.p1	sp|O14727|APAF_HUMAN_Apoptotic_protease-activating_factor_1_OS=Homo_sapiens_GN=APAF1_PE=1_SV=2	3.00E-12
comp49568_c0_seq1.p2		
comp49596_c0_seq1.p1		
comp4960_c0_seq1.p1	sp|P33650|FEOB_ECOLI_Ferrous_iron_transport_protein_B_OS=Escherichia_coli_(strain_K12)_GN=feoB_PE=1_SV=1	2.00E-70
comp49607_c0_seq1.p2		
comp49610_c0_seq2.p1		
comp49625_c0_seq1.p1	sp|O65493|XCP1_ARATH_Xylem_cysteine_proteinase_1_OS=Arabidopsis_thaliana_GN=XCP1_PE=1_SV=1	3.00E-30
comp49629_c0_seq1.p1		
comp49630_c0_seq1.p1		
comp49632_c0_seq1.p1	sp|P76561|YPFH_ECOLI_Esterase_YpfH_OS=Escherichia_coli_(strain_K12)_GN=ypfH_PE=3_SV=2	2.00E-125
comp49643_c0_seq1.p1		
comp49645_c0_seq1.p1	sp|P14377|ZRAS_ECOLI_Sensor_protein_ZraS_OS=Escherichia_coli_(strain_K12)_GN=zraS_PE=1_SV=2	5.00E-107
comp49645_c0_seq1.p2	sp|P14375|ZRAR_ECOLI_Transcriptional_regulatory_protein_ZraR_OS=Escherichia_coli_(strain_K12)_GN=zraR_PE=1_SV=2	8.00E-74
comp49653_c0_seq1.p1		
comp49655_c0_seq1.p1	sp|Q3YV90|YIHY_SHISS_UPF0761_membrane_protein_yihY_OS=Shigella_sonnei_(strain_Ss046)_GN=yihY_PE=3_SV=1	2.00E-167
comp49655_c0_seq1.p2	sp|P0A8Y4|YIHX_SHIFL_Phosphatase_yihX_OS=Shigella_flexneri_GN=yihX_PE=3_SV=1	2.00E-69
comp49677_c0_seq1.p1		
comp49688_c0_seq1.p2		
comp49717_c0_seq1.p2	sp|P36967|SUCA_DICDI_Succinyl-CoA_ligase_[ADP/GDP-forming]_subunit_alpha,_mitochondrial_OS=Dictyostelium_discoideum_GN=scsA_PE=1_SV=3	5.00E-25
comp49720_c0_seq1.p1	sp|P27278|NADR_ECOLI_Trifunctional_NAD_biosynthesis/regulator_protein_NadR_OS=Escherichia_coli_(strain_K12)_GN=nadR_PE=1_SV=2	2.00E-90
comp49731_c0_seq1.p1		
comp49754_c0_seq1.p1		
comp49764_c0_seq1.p1	sp|P75780|FIU_ECOLI_Catecholate_siderophore_receptor_Fiu_OS=Escherichia_coli_(strain_K12)_GN=fiu_PE=1_SV=1	0
comp49783_c0_seq1.p1	sp|Q6QNM1|KC1_TOXGO_Casein_kinase_I_OS=Toxoplasma_gondii_PE=2_SV=1	1.00E-121
comp49806_c0_seq1.p1		
comp49820_c0_seq1.p1	sp|P22731|LIVF_ECOLI_High-affinity_branched-chain_amino_acid_transport_ATP-binding_protein_LivF_OS=Escherichia_coli_(strain_K12)_GN=livF_PE=1_SV=2	7.00E-105
comp49828_c0_seq1.p1		
comp49830_c0_seq1.p1	sp|Q9DAK2|PACRG_MOUSE_Parkin_coregulated_gene_protein_homolog_OS=Mus_musculus_GN=Pacrg_PE=1_SV=1	2.00E-57
comp49834_c0_seq1.p1	sp|P0ABT8|YIJE_ECOLI_Uncharacterized_inner_membrane_transporter_yijE_OS=Escherichia_coli_(strain_K12)_GN=yijE_PE=1_SV=1	5.00E-77
comp49834_c0_seq1.p2	sp|P0A967|CHEW_SHIFL_Chemotaxis_protein_CheW_OS=Shigella_flexneri_GN=cheW_PE=3_SV=1	4.00E-58
comp49901_c0_seq1.p1		
comp49921_c0_seq1.p1		
comp49932_c0_seq1.p1		
comp49943_c0_seq1.p1	sp|P63487|ALLA_SHIFL_Ureidoglycolate_hydrolase_OS=Shigella_flexneri_GN=allA_PE=1_SV=1	8.00E-115
comp49946_c0_seq1.p1	sp|P75617|YAAW_ECOLI_UPF0174_protein_yaaW_OS=Escherichia_coli_(strain_K12)_GN=yaaW_PE=3_SV=1	1.00E-59
comp49968_c0_seq1.p2		
comp49970_c0_seq1.p1	sp|O59865|RS24B_SCHPO_40S_ribosomal_protein_S24-B_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rps24b_PE=2_SV=3	5.00E-36
comp50008_c0_seq1.p1		
comp50032_c0_seq1.p1	sp|B6I2X6|BIOH_ECOSE_Pimelyl-[acyl-carrier_protein]_methyl_ester_esterase_OS=Escherichia_coli_(strain_SE11)_GN=bioH_PE=3_SV=1	1.00E-91
comp50035_c0_seq1.p1	sp|Q8GKZ1|HISX_SALEN_Histidinol_dehydrogenase_(Fragment)_OS=Salmonella_enteritidis_GN=hisD_PE=3_SV=1	8.00E-59
comp50052_c0_seq1.p1	sp|Q8ZBY6|FADE_YERPE_Acyl-coenzyme_A_dehydrogenase_OS=Yersinia_pestis_GN=fadE_PE=3_SV=1	2.00E-22
comp50078_c0_seq1.p2	sp|Q3Z0A6|THIM_SHISS_Hydroxyethylthiazole_kinase_OS=Shigella_sonnei_(strain_Ss046)_GN=thiM_PE=3_SV=1	2.00E-64
comp50085_c0_seq1.p1		
comp50090_c0_seq1.p1		
comp50122_c0_seq1.p1	sp|P07862|DDLB_ECOLI_D-alanine--D-alanine_ligase_B_OS=Escherichia_coli_(strain_K12)_GN=ddlB_PE=1_SV=3	5.00E-119
comp50122_c0_seq1.p2	sp|Q83MF8|MURC_SHIFL_UDP-N-acetylmuramate--L-alanine_ligase_OS=Shigella_flexneri_GN=murC_PE=3_SV=1	8.00E-72
comp50168_c0_seq1.p1	sp|P77599|YFCS_ECOLI_Uncharacterized_fimbrial_chaperone_yfcS_OS=Escherichia_coli_(strain_K12)_GN=yfcS_PE=3_SV=1	4.00E-86
comp50176_c0_seq1.p1		
comp50177_c0_seq1.p1	sp|P0C6F1|DYH2_MOUSE_Dynein_heavy_chain_2,_axonemal_OS=Mus_musculus_GN=Dnah2_PE=2_SV=1	4.00E-75
comp50178_c0_seq1.p1	sp|Q40302|CALM_MACPY_Calmodulin_OS=Macrocystis_pyrifera_PE=2_SV=3	1.00E-37
comp50183_c0_seq1.p2	sp|O13672|RL8_SCHPO_60S_ribosomal_protein_L8_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpl8_PE=1_SV=3	4.00E-33
comp50185_c0_seq1.p1	sp|Q83IH7|OPGB_SHIFL_Phosphoglycerol_transferase_I_OS=Shigella_flexneri_GN=mdoB_PE=3_SV=1	1.00E-107
comp50188_c0_seq1.p1	sp|P0A947|RIMI_SHIFL_Ribosomal-protein-alanine_acetyltransferase_OS=Shigella_flexneri_GN=rimI_PE=3_SV=1	2.00E-101
comp50219_c0_seq1.p1	sp|Q9C0G6|DYH6_HUMAN_Dynein_heavy_chain_6,_axonemal_OS=Homo_sapiens_GN=DNAH6_PE=1_SV=3	1.00E-94
comp50236_c0_seq1.p1		
comp50242_c0_seq1.p1	sp|P45955|YBGF_ECOLI_Uncharacterized_protein_YbgF_OS=Escherichia_coli_(strain_K12)_GN=ybgF_PE=1_SV=2	1.00E-98
comp50252_c0_seq1.p1		
comp50273_c0_seq1.p1		
comp50274_c0_seq1.p1		
comp50305_c0_seq1.p1	sp|B7NRS7|THIC_ECO7I_Phosphomethylpyrimidine_synthase_OS=Escherichia_coli_O7:K1_(strain_IAI39_/_ExPEC)_GN=thiC_PE=3_SV=1	2.00E-110
comp50311_c0_seq1.p1		
comp50326_c0_seq1.p1		
comp50337_c0_seq1.p1	sp|P28903|NRDD_ECOLI_Anaerobic_ribonucleoside-triphosphate_reductase_OS=Escherichia_coli_(strain_K12)_GN=nrdD_PE=1_SV=2	1.00E-137
comp50354_c0_seq1.p2	sp|P62302|RS13_SOYBN_40S_ribosomal_protein_S13_OS=Glycine_max_GN=RPS13_PE=2_SV=1	3.00E-85
comp5036_c0_seq1.p1	sp|P05704|MCP3_ECOLI_Methyl-accepting_chemotaxis_protein_III_OS=Escherichia_coli_(strain_K12)_GN=trg_PE=1_SV=3	2.00E-38
comp50363_c0_seq1.p1		
comp50378_c0_seq1.p1	sp|Q6BEX0|YTFR_ECOLI_Uncharacterized_ABC_transporter_ATP-binding_protein_YtfR_OS=Escherichia_coli_(strain_K12)_GN=ytfR_PE=3_SV=1	2.00E-118
comp50385_c0_seq1.p1		
comp50386_c0_seq1.p1	sp|P00934|THRC_ECOLI_Threonine_synthase_OS=Escherichia_coli_(strain_K12)_GN=thrC_PE=1_SV=1	0
comp50393_c0_seq1.p1		
comp50439_c0_seq1.p1		
comp50441_c0_seq1.p1	sp|P55354|NOEL_RHISN_GDP-mannose_4,6-dehydratase_OS=Rhizobium_sp._(strain_NGR234)_GN=noeL_PE=3_SV=1	2.00E-141
comp50525_c0_seq1.p1	sp|P25204|RS8_LEIMA_40S_ribosomal_protein_S8_OS=Leishmania_major_GN=RPS8A_PE=3_SV=1	3.00E-53
comp50543_c0_seq1.p1		
comp50571_c0_seq1.p1		
comp50586_c0_seq1.p1	sp|P75892|RUTG_ECOLI_Putative_pyrimidine_permease_RutG_OS=Escherichia_coli_(strain_K12)_GN=rutG_PE=1_SV=2	4.00E-57
comp50589_c0_seq1.p1	sp|P30844|BASS_ECOLI_Sensor_protein_BasS_OS=Escherichia_coli_(strain_K12)_GN=basS_PE=1_SV=1	3.00E-64
comp5059_c0_seq1.p1	sp|Q3YXW5|GCST_SHISS_Aminomethyltransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=gcvT_PE=3_SV=1	1.00E-40
comp50603_c0_seq1.p1	sp|Q98TX1|THIO_OPHHA_Thioredoxin_OS=Ophiophagus_hannah_GN=TXN_PE=3_SV=3	1.00E-22
comp50653_c0_seq1.p1		
comp50696_c0_seq1.p1		
comp50744_c0_seq1.p1	sp|P0ABH7|CISY_ECOLI_Citrate_synthase_OS=Escherichia_coli_(strain_K12)_GN=gltA_PE=1_SV=1	4.00E-101
comp50747_c0_seq1.p1		
comp50753_c0_seq1.p1		
comp50766_c0_seq1.p1		
comp50814_c0_seq1.p1	sp|Q325R4|MATB_SHIBS_Fimbrillin_matB_homolog_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=matB_PE=3_SV=1	3.00E-106
comp50820_c0_seq1.p1	sp|Q9Z899|PMP6_CHLPN_Probable_outer_membrane_protein_pmp6_OS=Chlamydia_pneumoniae_GN=pmp6_PE=3_SV=2	5.00E-11
comp50857_c0_seq1.p2		
comp50867_c0_seq1.p1		
comp50893_c0_seq1.p1		
comp50904_c0_seq1.p1	sp|P27837|YIFK_ECOLI_Probable_transport_protein_YifK_OS=Escherichia_coli_(strain_K12)_GN=yifK_PE=1_SV=4	1.00E-110
comp50904_c0_seq1.p2	sp|Q3YVG8|WECG_SHISS_Probable_UDP-N-acetyl-D-mannosaminuronic_acid_transferase_OS=Shigella_sonnei_(strain_Ss046)_GN=wecG_PE=3_SV=1	2.00E-139
comp50922_c0_seq1.p1	sp|P75747|ABRB_ECOLI_Protein_AbrB_OS=Escherichia_coli_(strain_K12)_GN=abrB_PE=3_SV=2	1.00E-82
comp50926_c0_seq1.p1		
comp50949_c0_seq1.p1	sp|P0ABQ0|COABC_ECOLI_Coenzyme_A_biosynthesis_bifunctional_protein_CoaBC_OS=Escherichia_coli_(strain_K12)_GN=coaBC_PE=1_SV=2	2.00E-126
comp50983_c0_seq1.p2		
comp51011_c0_seq1.p1		
comp51055_c0_seq1.p1	sp|P0ADT5|YGIC_ECOLI_Uncharacterized_protein_ygiC_OS=Escherichia_coli_(strain_K12)_GN=ygiC_PE=4_SV=1	0
comp51080_c0_seq1.p1		
comp51100_c0_seq1.p1	sp|P0AFP4|YBBO_ECOLI_Uncharacterized_oxidoreductase_ybbO_OS=Escherichia_coli_(strain_K12)_GN=ybbO_PE=3_SV=1	2.00E-106
comp51120_c0_seq1.p1	sp|P0A9T5|TAS_SHIFL_Protein_tas_OS=Shigella_flexneri_GN=tas_PE=3_SV=1	8.00E-89
comp51147_c0_seq1.p1	sp|Q00218|AROG_ARATH_Phospho-2-dehydro-3-deoxyheptonate_aldolase_2,_chloroplastic_OS=Arabidopsis_thaliana_GN=DHS2_PE=2_SV=2	9.00E-100
comp51163_c0_seq1.p1	sp|P0AF44|YJBB_SHIFL_Uncharacterized_protein_yjbB_OS=Shigella_flexneri_GN=yjbB_PE=4_SV=1	2.00E-46
comp51182_c0_seq1.p1		
comp51185_c0_seq1.p1		
comp51196_c0_seq1.p1	sp|P0C6F1|DYH2_MOUSE_Dynein_heavy_chain_2,_axonemal_OS=Mus_musculus_GN=Dnah2_PE=2_SV=1	1.00E-100
comp51223_c0_seq1.p1	sp|Q3Z5S7|RSMH_SHISS_Ribosomal_RNA_small_subunit_methyltransferase_H_OS=Shigella_sonnei_(strain_Ss046)_GN=rsmH_PE=3_SV=1	8.00E-110
comp51236_c0_seq1.p1	sp|Q7Z4L9|PPR42_HUMAN_Protein_phosphatase_1_regulatory_subunit_42_OS=Homo_sapiens_GN=PPP1R42_PE=2_SV=2	9.00E-15
comp51294_c0_seq1.p1	sp|P40618|HMGB3_CHICK_High_mobility_group_protein_B3_OS=Gallus_gallus_GN=HMGB3_PE=2_SV=2	9.00E-20
comp51333_c0_seq1.p1	sp|Q9FDZ9|RL212_ARATH_60S_ribosomal_protein_L21-2_OS=Arabidopsis_thaliana_GN=RPL21E_PE=2_SV=1	1.00E-50
comp51346_c0_seq1.p1	sp|Q8FJN9|YBHO_ECOL6_Putative_cardiolipin_synthase_YbhO_OS=Escherichia_coli_O6_GN=ybhO_PE=3_SV=1	0
comp51400_c0_seq1.p1	sp|Q3Z586|MHPB_SHISS_2,3-dihydroxyphenylpropionate/2,3-dihydroxicinnamic_acid_1,2-dioxygenase_OS=Shigella_sonnei_(strain_Ss046)_GN=mhpB_PE=3_SV=1	7.00E-135
comp51430_c0_seq1.p2		
comp51464_c0_seq1.p1		
comp51519_c0_seq1.p1		
comp51584_c0_seq1.p1	sp|Q86C65|TOR_DICDI_Target_of_rapamycin_OS=Dictyostelium_discoideum_GN=tor_PE=1_SV=1	1.00E-14
comp51601_c0_seq1.p1	sp|Q31Y50|PTYBC_SHIBS_PTS_system_N-acetylmuramic_acid-specific_EIIBC_component_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=murP_PE=3_SV=1	4.00E-120
comp51613_c0_seq1.p1	sp|P36879|YADG_ECOLI_Uncharacterized_ABC_transporter_ATP-binding_protein_YadG_OS=Escherichia_coli_(strain_K12)_GN=yadG_PE=3_SV=1	3.00E-95
comp51616_c0_seq1.p1	sp|Q3YX74|RBFA_SHISS_Ribosome-binding_factor_A_OS=Shigella_sonnei_(strain_Ss046)_GN=rbfA_PE=3_SV=1	5.00E-70
comp51658_c0_seq1.p1		
comp51687_c0_seq1.p1	sp|Q83LX5|SYL_SHIFL_Leucine--tRNA_ligase_OS=Shigella_flexneri_GN=leuS_PE=3_SV=2	0
comp51707_c0_seq1.p1		
comp51713_c0_seq1.p1		
comp51725_c0_seq1.p2		
comp51740_c0_seq1.p1	sp|O75000|RL12_SCHPO_60S_ribosomal_protein_L12_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpl1201_PE=1_SV=1	3.00E-73
comp51743_c0_seq1.p1		
comp51744_c0_seq1.p2	sp|P77774|YFGL_ECOLI_Lipoprotein_yfgL_OS=Escherichia_coli_(strain_K12)_GN=yfgL_PE=1_SV=1	5.00E-68
comp51744_c0_seq1.p3	sp|P76576|YFGM_ECOLI_UPF0070_protein_yfgM_OS=Escherichia_coli_(strain_K12)_GN=yfgM_PE=3_SV=1	1.00E-71
comp51751_c0_seq1.p1	sp|P05804|BGLR_ECOLI_Beta-glucuronidase_OS=Escherichia_coli_(strain_K12)_GN=uidA_PE=1_SV=2	6.00E-132
comp51752_c0_seq1.p1	sp|Q54D63|RL6_DICDI_60S_ribosomal_protein_L6_OS=Dictyostelium_discoideum_GN=rpl6_PE=1_SV=1	1.00E-36
comp51755_c0_seq1.p1	sp|P0AD65|PBP2_ECOLI_Penicillin-binding_protein_2_OS=Escherichia_coli_(strain_K12)_GN=mrdA_PE=3_SV=1	5.00E-100
comp51763_c0_seq1.p1		
comp51767_c0_seq1.p1	sp|P37909|YBGD_ECOLI_Uncharacterized_fimbrial-like_protein_ybgD_OS=Escherichia_coli_(strain_K12)_GN=ybgD_PE=3_SV=2	5.00E-57
comp51776_c0_seq1.p1		
comp51777_c0_seq1.p1		
comp51810_c0_seq1.p1		
comp51818_c0_seq1.p1		
comp51849_c0_seq1.p1	sp|P75783|YBIO_ECOLI_Uncharacterized_MscS_family_protein_YbiO_OS=Escherichia_coli_(strain_K12)_GN=ybiO_PE=3_SV=2	0
comp51857_c0_seq1.p1		
comp51864_c0_seq1.p1		
comp51865_c0_seq1.p1	sp|P33898|G3P3_ECOLI_Putative_glyceraldehyde-3-phosphate_dehydrogenase_C_OS=Escherichia_coli_(strain_K12)_GN=gapC_PE=5_SV=2	7.00E-109
comp5187_c0_seq1.p1	sp|P37679|SGBU_ECOLI_Putative_L-ribulose-5-phosphate_3-epimerase_sgbU_OS=Escherichia_coli_(strain_K12)_GN=sgbU_PE=3_SV=2	3.00E-79
comp51875_c0_seq1.p1		
comp51899_c0_seq1.p1	sp|P31466|PURP_ECOLI_Probable_adenine_permease_PurP_OS=Escherichia_coli_(strain_K12)_GN=purP_PE=1_SV=2	8.00E-147
comp51916_c0_seq1.p1		
comp51919_c0_seq1.p1	sp|Q54F10|NDUV2_DICDI_NADH_dehydrogenase_[ubiquinone]_flavoprotein_2,_mitochondrial_OS=Dictyostelium_discoideum_GN=ndufv2_PE=3_SV=1	1.00E-32
comp51921_c0_seq1.p1		
comp51939_c0_seq1.p2		
comp51940_c0_seq1.p2	sp|Q3Z5I8|EFTS_SHISS_Elongation_factor_Ts_OS=Shigella_sonnei_(strain_Ss046)_GN=tsf_PE=3_SV=1	9.00E-69
comp51960_c0_seq1.p1		
comp51965_c0_seq1.p1		
comp51978_c0_seq1.p1		
comp51987_c0_seq1.p2	sp|Q9U7D0|H4_MASBA_Histone_H4_OS=Mastigamoeba_balamuthi_PE=3_SV=3	3.00E-50
comp51995_c0_seq1.p1	sp|P0ACR0|ALLS_ECOLI_HTH-type_transcriptional_activator_AllS_OS=Escherichia_coli_(strain_K12)_GN=allS_PE=1_SV=1	1.00E-119
comp52001_c0_seq1.p1	sp|P26701|VPI_BPP2_Tail_protein_I_OS=Enterobacteria_phage_P2_GN=I_PE=4_SV=1	2.00E-52
comp52020_c0_seq1.p2		
comp52036_c0_seq1.p1	sp|P0ACC0|HEMY_SHIFL_Protein_hemY_OS=Shigella_flexneri_GN=hemY_PE=3_SV=1	0
comp52058_c0_seq1.p1	sp|P77726|YAJR_ECOLI_Inner_membrane_transport_protein_yajR_OS=Escherichia_coli_(strain_K12)_GN=yajR_PE=1_SV=2	6.00E-74
comp52069_c0_seq1.p1		
comp52085_c0_seq1.p1		
comp52086_c0_seq1.p1		
comp52095_c0_seq1.p1	sp|Q3Z5K2|CLCA_SHISS_H(+)/Cl(-)_exchange_transporter_ClcA_OS=Shigella_sonnei_(strain_Ss046)_GN=clcA_PE=3_SV=1	2.00E-66
comp52096_c0_seq1.p1	sp|P78976|SAR1_HYPJE_Small_COPII_coat_GTPase_sar1_OS=Hypocrea_jecorina_GN=sar1_PE=3_SV=1	3.00E-75
comp52098_c0_seq1.p1	sp|O46629|ECHB_BOVIN_Trifunctional_enzyme_subunit_beta,_mitochondrial_OS=Bos_taurus_GN=HADHB_PE=2_SV=1	8.00E-45
comp52101_c0_seq1.p2	sp|Q9Z0R9|FADS2_MOUSE_Fatty_acid_desaturase_2_OS=Mus_musculus_GN=Fads2_PE=2_SV=1	6.00E-15
comp52114_c0_seq1.p1	sp|P15043|RECQ_ECOLI_ATP-dependent_DNA_helicase_recQ_OS=Escherichia_coli_(strain_K12)_GN=recQ_PE=1_SV=5	4.00E-131
comp52116_c0_seq1.p1	sp|Q9XI91|IF5A1_ARATH_Eukaryotic_translation_initiation_factor_5A-1_OS=Arabidopsis_thaliana_GN=At1g13950_PE=2_SV=1	1.00E-45
comp52124_c0_seq1.p1		
comp52165_c0_seq1.p1	sp|P32689|YJBH_ECOLI_Uncharacterized_lipoprotein_yjbH_OS=Escherichia_coli_(strain_K12)_GN=yjbH_PE=4_SV=1	4.00E-153
comp52170_c0_seq1.p1	sp|Q8WXX0|DYH7_HUMAN_Dynein_heavy_chain_7,_axonemal_OS=Homo_sapiens_GN=DNAH7_PE=1_SV=2	3.00E-64
comp52175_c0_seq1.p1	sp|P0AAE2|PROY_ECOLI_Proline-specific_permease_ProY_OS=Escherichia_coli_(strain_K12)_GN=proY_PE=1_SV=1	1.00E-78
comp52179_c0_seq1.p1	sp|Q9WTV5|PSMD9_RAT_26S_proteasome_non-ATPase_regulatory_subunit_9_OS=Rattus_norvegicus_GN=Psmd9_PE=1_SV=1	2.00E-11
comp52180_c0_seq1.p1		
comp52182_c0_seq1.p1		
comp52200_c0_seq1.p2	sp|P37902|GLTI_ECOLI_Glutamate/aspartate_periplasmic-binding_protein_OS=Escherichia_coli_(strain_K12)_GN=gltI_PE=1_SV=2	5.00E-72

comp52202_c0_seq1.p1				
comp52226_c0_seq1.p2				
comp52237_c0_seq1.p1				
comp52248_c0_seq1.p1	sp|P0ADP8|YIGP_SHIFL_Uncharacterized_protein_yigP_OS=Shigella_flexneri_GN=yigP_PE=4_SV=1	2.00E-110		
comp52267_c0_seq1.p1	sp|P0AD30|YFCA_ECOLI_UPF0721_transmembrane_protein_yfcA_OS=Escherichia_coli_(strain_K12)_GN=yfcA_PE=1_SV=1	5.00E-125	GO:0005886,GO:0005886,GO:0005886,GO:0009408,GO:0016020,GO:0016021,GO:0016021	[illegible]
comp52291_c0_seq1.p1				
comp52294_c0_seq1.p1	sp|P32151|YIIG_ECOLI_Uncharacterized_protein_yiiG_OS=Escherichia_coli_(strain_K12)_GN=yiiG_PE=4_SV=1	1.00E-120		
comp52309_c0_seq1.p1				
comp5231_c0_seq1.p2				
comp52311_c0_seq1.p1				
comp52330_c0_seq1.p1				
comp52332_c0_seq1.p1	sp|P00579|RPOD_ECOLI_RNA_polymerase_sigma_factor_rpoD_OS=Escherichia_coli_(strain_K12)_GN=rpoD_PE=1_SV=2	2.00E-104	[illegible]	[illegible]
comp52340_c0_seq1.p1				
comp52353_c0_seq1.p2				
comp52355_c0_seq1.p1	sp|O23087|ECA2_ARATH_Calcium-transporting_ATPase_2,_endoplasmic_reticulum-type_OS=Arabidopsis_thaliana_GN=ECA2_PE=2_SV=1	9.00E-20	[illegible]	[illegible]
comp52359_c0_seq1.p1				
comp52362_c0_seq1.p1	sp|Q32EB4|YEGS_SHIDS_Probable_lipid_kinase_YegS_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=yegS_PE=3_SV=1	3.00E-91	[illegible]	[illegible]
comp52427_c0_seq1.p1	sp|P46852|YHHW_ECOLI_Quercetin_2,3-dioxygenase_OS=Escherichia_coli_(strain_K12)_GN=yhhW_PE=1_SV=1	2.00E-105	GO:0008127,GO:0008127,GO:0016491,GO:0046872,GO:0051213,GO:0055114	[illegible]
comp52443_c0_seq1.p1				
comp52461_c0_seq1.p2				
comp52469_c0_seq1.p1				
comp52482_c0_seq1.p1				
comp52512_c0_seq1.p1				
comp52544_c0_seq1.p1	sp|P62282|RS11_RAT_40S_ribosomal_protein_S11_OS=Rattus_norvegicus_GN=Rps11_PE=1_SV=3	4.00E-52	[illegible]	[illegible]
comp52571_c0_seq1.p2	sp|P77329|HYFG_ECOLI_Hydrogenase-4_component_G_OS=Escherichia_coli_(strain_K12)_GN=hyfG_PE=1_SV=1	3.00E-69	[illegible]	[illegible]
comp52588_c0_seq1.p2				
comp52598_c0_seq1.p1				
comp52634_c0_seq1.p1	sp|P10873|TBA_TOXGO_Tubulin_alpha_chain_OS=Toxoplasma_gondii_PE=3_SV=1	3.00E-133	[illegible]	[illegible]
comp52638_c0_seq1.p1				
comp52652_c0_seq1.p1	sp|P00961|SYGB_ECOLI_Glycine--tRNA_ligase_beta_subunit_OS=Escherichia_coli_(strain_K12)_GN=glyS_PE=1_SV=4	2.00E-65	[illegible]	[illegible]
comp52657_c0_seq1.p1				
comp52673_c0_seq1.p1				
comp52678_c0_seq1.p1				
comp52701_c0_seq1.p1	sp|P46889|FTSK_ECOLI_DNA_translocase_FtsK_OS=Escherichia_coli_(strain_K12)_GN=ftsK_PE=1_SV=2	1.00E-173	[illegible]	[illegible]
comp52742_c0_seq1.p1				
comp52756_c0_seq1.p1	sp|P05825|FEPA_ECOLI_Ferrienterobactin_receptor_OS=Escherichia_coli_(strain_K12)_GN=fepA_PE=1_SV=2	2.00E-106	[illegible]	[illegible]
comp52761_c0_seq1.p1				
comp52784_c0_seq1.p1				
comp52799_c0_seq1.p1	sp|P0AEP7|GCL_ECOLI_Glyoxylate_carboligase_OS=Escherichia_coli_(strain_K12)_GN=gcl_PE=1_SV=2	2.00E-85	[illegible]	[illegible]
comp52801_c0_seq1.p1	sp|Q3YYG6|SYA_SHISS_Alanine--tRNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=alaS_PE=3_SV=1	3.00E-67	[illegible]	[illegible]
comp52803_c0_seq1.p1	sp|P14130|RS14_DROME_40S_ribosomal_protein_S14_OS=Drosophila_melanogaster_GN=RpS14a_PE=1_SV=1	8.00E-81	[illegible]	[illegible]
comp52814_c0_seq1.p1				
comp52829_c0_seq1.p1	sp|P30845|EPTA_ECOLI_Phosphoethanolamine_transferase_eptA_OS=Escherichia_coli_(strain_K12)_GN=eptA_PE=1_SV=2	0	[illegible]	[illegible]
comp52836_c0_seq1.p1	sp|P76537|YFEY_ECOLI_Uncharacterized_protein_yfeY_OS=Escherichia_coli_(strain_K12)_GN=yfeY_PE=1_SV=1	2.00E-68		
comp52842_c0_seq1.p2				
comp52849_c0_seq1.p1				
comp52858_c0_seq1.p1				
comp52861_c0_seq1.p1				
comp52873_c0_seq1.p1	sp|P0CB39|CPTA_ECOLI_Phosphoethanolamine_transferase_CptA_OS=Escherichia_coli_(strain_K12)_GN=cptA_PE=1_SV=1	5.00E-134	[illegible]	[illegible]
comp52881_c0_seq1.p1	sp|P15047|ENTA_ECOLI_2,3-dihydro-2,3-dihydroxybenzoate_dehydrogenase_OS=Escherichia_coli_(strain_K12)_GN=entA_PE=1_SV=1	6.00E-136	[illegible]	[illegible]
comp52895_c0_seq1.p1	sp|P0A9V9|YIHU_SHIFL_Uncharacterized_oxidoreductase_yihU_OS=Shigella_flexneri_GN=yihU_PE=3_SV=1	4.00E-53	[illegible]	[illegible]
comp52896_c0_seq1.p1	sp|P77716|YCJP_ECOLI_Inner_membrane_ABC_transporter_permease_protein_ycjP_OS=Escherichia_coli_(strain_K12)_GN=ycjP_PE=1_SV=1	4.00E-112	[illegible]	[illegible]
comp52907_c0_seq1.p1				
comp5292_c0_seq1.p1				
comp52929_c0_seq1.p2				
comp52950_c0_seq1.p1	sp|P17078|RL35_RAT_60S_ribosomal_protein_L35_OS=Rattus_norvegicus_GN=Rpl35_PE=1_SV=3	2.00E-37	[illegible]	[illegible]
comp52976_c0_seq1.p1				
comp52981_c0_seq1.p2	sp|Q3YVU1|SYGA_SHISS_Glycine--tRNA_ligase_alpha_subunit_OS=Shigella_sonnei_(strain_Ss046)_GN=glyQ_PE=3_SV=1	7.00E-61	[illegible]	[illegible]
comp52982_c0_seq1.p2				
comp53013_c0_seq1.p1				
comp53050_c0_seq1.p1	sp|P67067|WECC_SHIFL_UDP-N-acetyl-D-mannosamine_dehydrogenase_OS=Shigella_flexneri_GN=wecC_PE=3_SV=1	1.00E-63	[illegible]	[illegible]
comp53065_c0_seq1.p1	sp|P37047|CDAR_ECOLI_Carbohydrate_diacid_regulator_OS=Escherichia_coli_(strain_K12)_GN=cdaR_PE=1_SV=2	8.00E-152	[illegible]	[illegible]
comp53077_c0_seq1.p1	sp|Q3YY95|CYSI_SHISS_Sulfite_reductase_[NADPH]_hemoprotein_beta-component_OS=Shigella_sonnei_(strain_Ss046)_GN=cysI_PE=3_SV=1	6.00E-145	[illegible]	[illegible]
comp53134_c0_seq1.p1	sp|P32701|YJCC_ECOLI_Uncharacterized_membrane_protein_YjcC_OS=Escherichia_coli_(strain_K12)_GN=yjcC_PE=1_SV=2	0	[illegible]	[illegible]
comp53152_c0_seq1.p2				
comp53188_c0_seq1.p1				
comp53204_c0_seq1.p1				
comp5321_c0_seq1.p1	sp|P30851|RNR_SHIFL_Ribonuclease_R_OS=Shigella_flexneri_GN=rnr_PE=3_SV=4	7.00E-90	[illegible]	[illegible]
comp53223_c0_seq1.p1				
comp53230_c0_seq1.p1	sp|Q3YU08|LPLA_SHISS_Lipoate-protein_ligase_A_OS=Shigella_sonnei_(strain_Ss046)_GN=lplA_PE=3_SV=1	1.00E-109	[illegible]	[illegible]
comp53245_c0_seq1.p1	sp|P46474|YHDP_ECOLI_Uncharacterized_protein_yhdP_OS=Escherichia_coli_(strain_K12)_GN=yhdP_PE=4_SV=4	1.00E-144		
comp53265_c0_seq1.p1				
comp53283_c0_seq1.p4				
comp53314_c0_seq1.p1				
comp53332_c0_seq1.p3	sp|P0A9C2|GLPA_SHIFL_Anaerobic_glycerol-3-phosphate_dehydrogenase_subunit_A_OS=Shigella_flexneri_GN=glpA_PE=3_SV=1	3.00E-67	[illegible]	[illegible]
comp53334_c0_seq1.p2				
comp53340_c0_seq1.p2				
comp53341_c0_seq1.p1				
comp53409_c0_seq1.p1				
comp53412_c0_seq1.p1				
comp53414_c0_seq1.p1	sp|P76072|STFR_ECOLI_Side_tail_fiber_protein_homolog_from_lambdoid_prophage_Rac_OS=Escherichia_coli_(strain_K12)_GN=stfR_PE=3_SV=2	2.00E-11	[illegible]	[illegible]
comp53415_c0_seq1.p1	sp|P63687|CTPF_MYCTU_Probable_cation-transporting_ATPase_F_OS=Mycobacterium_tuberculosis_GN=ctpF_PE=1_SV=1	4.00E-53		
comp53417_c0_seq1.p1	sp|P09127|HEMX_ECOLI_Putative_uroporphyrinogen-III_C-methyltransferase_OS=Escherichia_coli_(strain_K12)_GN=hemX_PE=1_SV=1	0	[illegible]	[illegible]
comp53443_c0_seq1.p2	sp|Q3Z1Z4|PDXH_SHISS_Pyridoxine/pyridoxamine_5'-phosphate_oxidase_OS=Shigella_sonnei_(strain_Ss046)_GN=pdxH_PE=3_SV=1	8.00E-71	[illegible]	[illegible]
comp53450_c0_seq1.p2	sp|P32802|TMN1_YEAST_Transmembrane_9_superfamily_member_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=EMP70_PE=1_SV=2	2.00E-13	[illegible]	[illegible]
comp53461_c0_seq1.p1				
comp53479_c0_seq1.p2				
comp53504_c0_seq1.p1				
comp53529_c0_seq1.p1				
comp53535_c0_seq1.p1				
comp53581_c0_seq1.p1				
comp53595_c0_seq1.p1				
comp53601_c0_seq1.p1	sp|O03986|HS904_ARATH_Heat_shock_protein_90-4_OS=Arabidopsis_thaliana_GN=HSP90-4_PE=2_SV=1	2.00E-52	[illegible]	[illegible]
comp53615_c0_seq1.p1				
comp53644_c0_seq1.p1	sp|Q9LPG6|RHM2_ARATH_Probable_rhamnose_biosynthetic_enzyme_2_OS=Arabidopsis_thaliana_GN=RHM2_PE=1_SV=1	2.00E-91	[illegible]	[illegible]
comp53657_c0_seq1.p2	sp|P24156|L2CC_DROME_Protein_l(2)37Cc_OS=Drosophila_melanogaster_GN=l(2)37Cc_PE=2_SV=2	1.00E-46	[illegible]	[illegible]
comp53746_c0_seq1.p1	sp|P0AFB7|NTRB_SHIFL_Nitrogen_regulation_protein_NR(II)_OS=Shigella_flexneri_GN=glnL_PE=3_SV=1	7.00E-99	[illegible]	[illegible]
comp53746_c0_seq1.p2	sp|P0AFB8|NTRC_ECOLI_Nitrogen_regulation_protein_NR(I)_OS=Escherichia_coli_(strain_K12)_GN=glnG_PE=3_SV=1	6.00E-72	[illegible]	[illegible]
comp53771_c0_seq1.p2	sp|Q83JC4|EFTU_SHIFL_Elongation_factor_Tu_OS=Shigella_flexneri_GN=tufA_PE=3_SV=3	8.00E-57	[illegible]	[illegible]
comp53813_c0_seq1.p1				
comp53831_c0_seq1.p1	sp|P25549|ASLA_ECOLI_Arylsulfatase_OS=Escherichia_coli_(strain_K12)_GN=aslA_PE=3_SV=2	8.00E-173	[illegible]	[illegible]
comp53832_c0_seq1.p1	sp|P41093|RL18A_DROME_60S_ribosomal_protein_L18a_OS=Drosophila_melanogaster_GN=RpL18A_PE=1_SV=1	2.00E-65	[illegible]	[illegible]
comp53845_c0_seq1.p2	sp|Q3YY32|LGT_SHISS_Prolipoprotein_diacylglyceryl_transferase_OS=Shigella_sonnei_(strain_Ss046)_GN=lgt_PE=3_SV=1	5.00E-85	[illegible]	[illegible]
comp5387_c0_seq1.p1	sp|Q83Q35|ALX_SHIFL_Inner_membrane_protein_alx_OS=Shigella_flexneri_GN=alx_PE=3_SV=1	8.00E-73	[illegible]	[illegible]
comp53874_c0_seq1.p1				
comp53885_c0_seq1.p1	sp|B6I245|TUSD_ECOSE_Sulfurtransferase_TusD_OS=Escherichia_coli_(strain_SE11)_GN=tusD_PE=3_SV=1	2.00E-65	[illegible]	[illegible]
comp53918_c0_seq1.p1	sp|Q876G9|MYO2_SACBA_Myosin-2_OS=Saccharomyces_bayanus_GN=MYO2_PE=3_SV=2	1.00E-31	[illegible]	[illegible]
comp53920_c0_seq1.p2				
comp53944_c0_seq1.p1				
comp53951_c0_seq1.p1				
comp54020_c0_seq1.p1	sp|P0AC27|NIRC_SHIFL_Probable_nitrite_transporter_OS=Shigella_flexneri_GN=nirC_PE=3_SV=1	3.00E-93	[illegible]	[illegible]
comp54169_c0_seq1.p3				
comp54227_c0_seq1.p1				
comp54230_c0_seq1.p1	sp|P39405|FHUF_ECOLI_Ferric_iron_reductase_protein_fhuF_OS=Escherichia_coli_(strain_K12)_GN=fhuF_PE=1_SV=1	2.00E-67	[illegible]	[illegible]
comp54239_c0_seq1.p1				
comp54241_c0_seq1.p1	sp|O35678|MGLL_MOUSE_Monoglyceride_lipase_OS=Mus_musculus_GN=Mgll_PE=1_SV=1	1.00E-14	[illegible]	[illegible]
comp54244_c0_seq1.p1	sp|P03007|DPO3E_ECOLI_DNA_polymerase_III_subunit_epsilon_OS=Escherichia_coli_(strain_K12)_GN=dnaQ_PE=1_SV=1	4.00E-110	[illegible]	[illegible]
comp54252_c0_seq1.p1				
comp54276_c0_seq1.p1	sp|P0AFL3|PPIA_ECOLI_Peptidyl-prolyl_cis-trans_isomerase_A_OS=Escherichia_coli_(strain_K12)_GN=ppiA_PE=1_SV=1	4.00E-110	[illegible]	[illegible]
comp54279_c0_seq1.p1	sp|Q47146|FADE_ECOLI_Acyl-coenzyme_A_dehydrogenase_OS=Escherichia_coli_(strain_K12)_GN=fadE_PE=2_SV=2	1.00E-102	[illegible]	[illegible]
comp54292_c0_seq1.p1	sp|Q2SLW3|ADE_HAHCH_Adenine_deaminase_OS=Hahella_chejuensis_(strain_KCTC_2396)_GN=HCH_01503_PE=3_SV=1	2.00E-40	[illegible]	[illegible]
comp54293_c0_seq1.p1	sp|Q63164|DYH1_RAT_Dynein_heavy_chain_1,_axonemal_OS=Rattus_norvegicus_GN=Dnah1_PE=2_SV=2	7.00E-31	[illegible]	[illegible]
comp54299_c0_seq1.p1	sp|Q83IP5|LAMB_SHIFL_Maltoporin_OS=Shigella_flexneri_GN=lamB_PE=3_SV=4	1.00E-139	[illegible]	[illegible]
comp54312_c0_seq1.p2	sp|Q76NU3|TCPZ_DICDI_T-complex_protein_1_subunit_zeta_OS=Dictyostelium_discoideum_GN=cct6_PE=1_SV=1	3.00E-47	[illegible]	[illegible]
comp54337_c0_seq1.p1				
comp54340_c0_seq1.p2	sp|Q3Z1W3|TUS_SHISS_DNA_replication_terminus_site-binding_protein_OS=Shigella_sonnei_(strain_Ss046)_GN=tus_PE=3_SV=1	5.00E-84	[illegible]	[illegible]
comp54345_c0_seq1.p1				
comp54346_c0_seq1.p1				
comp54355_c0_seq1.p1				
comp54365_c0_seq1.p1	sp|Q3Z250|YDIA_SHISS_Putative_phosphotransferase_ydiA_OS=Shigella_sonnei_(strain_Ss046)_GN=ydiA_PE=3_SV=1	4.00E-151	[illegible]	[illegible]
comp54376_c0_seq1.p1	sp|Q39610|DYHA_CHLRE_Dynein_alpha_chain,_flagellar_outer_arm_OS=Chlamydomonas_reinhardtii_GN=ODA11_PE=3_SV=2	2.00E-16	[illegible]	[illegible]
comp54382_c0_seq1.p2				
comp54399_c0_seq1.p1	sp|P39263|YFCC_ECOLI_Uncharacterized_protein_yfcC_OS=Escherichia_coli_(strain_K12)_GN=yfcC_PE=4_SV=2	3.00E-140	[illegible]	[illegible]
comp54408_c0_seq1.p1				
comp54426_c0_seq1.p1	sp|P75820|AMID_ECOLI_N-acetylmuramoyl-L-alanine_amidase_AmiD_OS=Escherichia_coli_(strain_K12)_GN=amiD_PE=1_SV=1	0	[illegible]	[illegible]
comp54427_c0_seq1.p1	sp|P0ACR8|YFER_SHIFL_Uncharacterized_HTH-type_transcriptional_regulator_yfeR_OS=Shigella_flexneri_GN=yfeR_PE=4_SV=1	1.00E-152	[illegible]	[illegible]
comp54449_c0_seq1.p1	sp|P33346|YEHI_ECOLI_Uncharacterized_protein_yehI_OS=Escherichia_coli_(strain_K12)_GN=yehI_PE=4_SV=2	0		
comp54460_c0_seq1.p1				
comp54493_c0_seq1.p1				
comp54499_c0_seq1.p1	sp|Q71UH5|CALM_PYTSP_Calmodulin_OS=Pythium_splendens_PE=2_SV=1	5.00E-52	[illegible]	[illegible]
comp54509_c0_seq1.p1	sp|P49215|RS17_SOLLC_40S_ribosomal_protein_S17_OS=Solanum_lycopersicum_GN=RPS17_PE=2_SV=3	5.00E-46	[illegible]	[illegible]
comp54537_c0_seq1.p1				
comp5454_c0_seq1.p1				
comp54550_c0_seq1.p1				
comp54594_c0_seq1.p2	sp|Q3YVP5|MNMG_SHISS_tRNA_uridine_5-carboxymethylaminomethyl_modification_enzyme_MnmG_OS=Shigella_sonnei_(strain_Ss046)_GN=mnmG_PE=3_SV=1	5.00E-99	[illegible]	[illegible]
comp54606_c0_seq1.p1	sp|Q24VT7|HTPG_DESHY_Chaperone_protein_htpG_OS=Desulfitobacterium_hafniense_(strain_Y51)_GN=htpG_PE=3_SV=1	4.00E-29	[illegible]	[illegible]
comp54640_c0_seq1.p1				
comp54648_c0_seq1.p1				
comp54650_c0_seq1.p2	sp|Q3YVN5|ATPE_SHISS_ATP_synthase_epsilon_chain_OS=Shigella_sonnei_(strain_Ss046)_GN=atpC_PE=3_SV=1	2.00E-81	[illegible]	[illegible]
comp54650_c0_seq1.p3	sp|Q3YVN6|ATPB_SHISS_ATP_synthase_subunit_beta_OS=Shigella_sonnei_(strain_Ss046)_GN=atpD_PE=3_SV=1	4.00E-73	[illegible]	[illegible]
comp54666_c0_seq1.p1				
comp54677_c0_seq1.p1	sp|P37773|MPL_ECOLI_UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate_ligase_OS=Escherichia_coli_(strain_K12)_GN=mpl_PE=1_SV=3	2.00E-94	[illegible]	[illegible]
comp54683_c0_seq1.p2				
comp54689_c0_seq1.p1	sp|P11179|ODO2_BOVIN_Dihydrolipoyllysine-residue_succinyltransferase_component_of_2-oxoglutarate_dehydrogenase_complex,_mitochondrial_OS=Bos_taurus_GN=DLST_PE=1_SV=2	5.00E-71	[illegible]	[illegible]
comp54692_c0_seq1.p1	sp|P02362|RS7_XENLA_40S_ribosomal_protein_S7_OS=Xenopus_laevis_GN=rps7_PE=2_SV=2	4.00E-86	[illegible]	[illegible]
comp54693_c0_seq1.p1	sp|P30137|THIE_ECOLI_Thiamine-phosphate_synthase_OS=Escherichia_coli_(strain_K12)_GN=thiE_PE=1_SV=1	1.00E-58	[illegible]	[illegible]
comp54703_c0_seq1.p1	sp|P75733|YBFM_ECOLI_Uncharacterized_protein_ybfM_OS=Escherichia_coli_(strain_K12)_GN=ybfM_PE=4_SV=1	2.00E-118	[illegible]	[illegible]
comp54723_c0_seq1.p2	sp|P16273|PRPX_HORVU_Pathogen-related_protein_OS=Hordeum_vulgare_PE=2_SV=2	2.00E-14	[illegible]	[illegible]
comp54724_c0_seq1.p1				
comp54752_c0_seq1.p1	sp|Q31W53|GLMM_SHIBS_Phosphoglucosamine_mutase_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=glmM_PE=3_SV=1	0	[illegible]	[illegible]
comp54755_c0_seq1.p2	sp|Q9N9V4|RS25_LEIIN_40S_ribosomal_protein_S25_OS=Leishmania_infantum_GN=RPS25_PE=2_SV=1	3.00E-29	[illegible]	[illegible]
comp54765_c0_seq1.p1	sp|P76462|YFAP_ECOLI_Uncharacterized_protein_yfaP_OS=Escherichia_coli_(strain_K12)_GN=yfaP_PE=4_SV=1	3.00E-155		
comp54771_c0_seq1.p2	sp|Q9SQH9|AMT13_ARATH_Ammonium_transporter_1_member_3_OS=Arabidopsis_thaliana_GN=AMT1-3_PE=1_SV=2	8.00E-14	[illegible]	[illegible]
comp54780_c0_seq1.p1				
comp54783_c0_seq1.p2				
comp54790_c0_seq1.p1				
comp54799_c0_seq1.p1	sp|Q32J96|SELU_SHIDS_tRNA_2-selenouridine_synthase_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=selU_PE=3_SV=1	7.00E-89	[illegible]	[illegible]
comp54800_c0_seq1.p1	sp|P0AE55|BCP_SHIFL_Putative_peroxiredoxin_bcp_OS=Shigella_flexneri_GN=bcp_PE=3_SV=1	3.00E-74	[illegible]	[illegible]
comp54802_c0_seq1.p1				
comp54809_c0_seq1.p1				
comp54831_c0_seq1.p1				
comp54839_c0_seq1.p1				
comp5485_c0_seq1.p1				
comp54861_c0_seq1.p1	sp|P0ABK5|CYSK_ECOLI_Cysteine_synthase_A_OS=Escherichia_coli_(strain_K12)_GN=cysK_PE=1_SV=2	4.00E-93	[illegible]	[illegible]
comp54868_c0_seq1.p1	sp|P0AAF3|ARAG_ECOLI_Arabinose_import_ATP-binding_protein_AraG_OS=Escherichia_coli_(strain_K12)_GN=araG_PE=1_SV=1	3.00E-140	[illegible]	[illegible]
comp54874_c0_seq1.p1	sp|Q46803|YGEW_ECOLI_Uncharacterized_protein_ygeW_OS=Escherichia_coli_(strain_K12)_GN=ygeW_PE=1_SV=2	2.00E-126	[illegible]	[illegible]
comp54883_c0_seq1.p1	sp|P76422|THID_ECOLI_Hydroxymethylpyrimidine/phosphomethylpyrimidine_kinase_OS=Escherichia_coli_(strain_K12)_GN=thiD_PE=1_SV=1	4.00E-95	[illegible]	[illegible]
comp54887_c0_seq1.p1				
comp54889_c0_seq1.p1	sp|P32154|PTFLB_ECOLI_Fructose-like_PTS_system_EIIBC_component_OS=Escherichia_coli_(strain_K12)_GN=frvB_PE=3_SV=2	2.00E-49	[illegible]	[illegible]
comp54899_c0_seq1.p1	sp|B2TZP2|OPGB_SHIB3_Phosphoglycerol_transferase_I_OS=Shigella_boydii_serotype_18_(strain_CDC_3083-94_/_BS512)_GN=mdoB_PE=3_SV=1	4.00E-63	[illegible]	[illegible]
comp54923_c0_seq1.p1	sp|P35679|RL4A_SCHPO_60S_ribosomal_protein_L4-A_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rpl4a_PE=1_SV=2	1.00E-52	[illegible]	[illegible]
comp54924_c0_seq1.p1				
comp54939_c0_seq1.p1				
comp54950_c0_seq1.p2	sp|P0AES5|GYRA_SHIFL_DNA_gyrase_subunit_A_OS=Shigella_flexneri_GN=gyrA_PE=1_SV=1	7.00E-116	[illegible]	[illegible]
comp55019_c0_seq1.p2				
comp55033_c0_seq1.p1	sp|P18624|EF1A_DICDI_Elongation_factor_1-alpha_OS=Dictyostelium_discoideum_GN=eef1a1_PE=1_SV=2	1.00E-24		
comp55044_c0_seq1.p2				
comp55055_c0_seq1.p2				
comp55059_c0_seq1.p1	sp|P46142|YGGM_ECOLI_Uncharacterized_protein_yggM_OS=Escherichia_coli_(strain_K12)_GN=yggM_PE=4_SV=2	3.00E-132		
comp55097_c0_seq1.p1				
comp55106_c0_seq1.p2				
comp55117_c0_seq1.p1	sp|Q5HYA8|MKS3_HUMAN_Meckelin_OS=Homo_sapiens_GN=TMEM67_PE=1_SV=2	7.00E-15	[illegible]	[illegible]
comp55119_c0_seq1.p1				
comp55121_c0_seq1.p1	sp|P42904|PTPB2_ECOLI_N-acetylgalactosamine-specific_phosphotransferase_enzyme_IIB_component_2_OS=Escherichia_coli_(strain_K12)_GN=agaV_PE=4_SV=1	2.00E-100	[illegible]	[illegible]
comp55129_c0_seq1.p1	sp|Q43291|RL211_ARATH_60S_ribosomal_protein_L21-1_OS=Arabidopsis_thaliana_GN=RPL21A_PE=2_SV=2	4.00E-45	[illegible]	[illegible]
comp55175_c0_seq1.p1				
comp55203_c0_seq1.p1	sp|Q47622|SAPA_ECOLI_Peptide_transport_periplasmic_protein_sapA_OS=Escherichia_coli_(strain_K12)_GN=sapA_PE=3_SV=1	2.00E-69	[illegible]	[illegible]
comp55205_c0_seq1.p1	sp|Q02440|MYO5A_CHICK_Unconventional_myosin-Va_OS=Gallus_gallus_GN=MYO5A_PE=1_SV=1	8.00E-11	[illegible]	[illegible]
comp55208_c0_seq1.p1				
comp55211_c0_seq1.p1	sp|Q1R4E3|WECF_ECOUT_4-alpha-L-fucosyltransferase_OS=Escherichia_coli_(strain_UTI89_/_UPEC)_GN=wecF_PE=3_SV=1	4.00E-92	[illegible]	[illegible]
comp55211_c0_seq1.p2	sp|Q3YVG0|WZYE_SHISS_Putative_ECA_polymerase_OS=Shigella_sonnei_(strain_Ss046)_GN=wzyE_PE=3_SV=1	1.00E-59	[illegible]	[illegible]
comp55212_c0_seq1.p1				
comp55216_c0_seq1.p2	sp|P0AFZ9|TRKH_SHIFL_Trk_system_potassium_uptake_protein_trkH_OS=Shigella_flexneri_GN=trkH_PE=3_SV=1	2.00E-78	[illegible]	[illegible]
comp55220_c0_seq1.p1				
comp55242_c0_seq1.p1				
comp55245_c0_seq1.p1				
comp55248_c0_seq1.p1				
comp55309_c0_seq1.p1				
comp55338_c0_seq1.p1				
comp55354_c0_seq1.p2				
comp55367_c0_seq1.p1				
comp5540_c0_seq1.p1	sp|B2KI97|THOC2_RHIFE_THO_complex_subunit_2_OS=Rhinolophus_ferrumequinum_GN=THOC2_PE=3_SV=1	5.00E-23	[illegible]	[illegible]
comp55419_c0_seq1.p1	sp|P31471|YIEL_ECOLI_Uncharacterized_protein_yieL_OS=Escherichia_coli_(strain_K12)_GN=yieL_PE=1_SV=3	0	[illegible]	[illegible]
comp55427_c0_seq1.p1	sp|P0A9T3|SERA_SHIFL_D-3-phosphoglycerate_dehydrogenase_OS=Shigella_flexneri_GN=serA_PE=3_SV=2	4.00E-88	[illegible]	[illegible]
comp55433_c0_seq1.p1				
comp55455_c0_seq1.p1				
comp55481_c0_seq1.p1	sp|P33591|NIKB_ECOLI_Nickel_transport_system_permease_protein_nikB_OS=Escherichia_coli_(strain_K12)_GN=nikB_PE=1_SV=2	9.00E-76	[illegible]	[illegible]
comp55484_c0_seq1.p1	sp|P24230|RECG_ECOLI_ATP-dependent_DNA_helicase_recG_OS=Escherichia_coli_(strain_K12)_GN=recG_PE=1_SV=1	1.00E-163	[illegible]	[illegible]
comp55498_c0_seq1.p1	sp|P30177|YBIB_ECOLI_Uncharacterized_protein_ybiB_OS=Escherichia_coli_(strain_K12)_GN=ybiB_PE=3_SV=1	2.00E-91	[illegible]	[illegible]
comp55502_c0_seq1.p1	sp|Q8X826|DAMX_ECO57_Protein_damX_OS=Escherichia_coli_O157:H7_GN=damX_PE=4_SV=1	5.00E-74	[illegible]	[illegible]
comp55534_c0_seq1.p1	sp|P58234|RS19A_SCHPO_40S_ribosomal_protein_S19-A_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rps19a_PE=2_SV=1	2.00E-29	[illegible]	[illegible]
comp55535_c0_seq1.p1	sp|P21375|OSM1_YEAST_Osmotic_growth_protein_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=OSM1_PE=1_SV=3	5.00E-54	[illegible]	[illegible]
comp5554_c0_seq1.p1				
comp55540_c0_seq1.p1	sp|Q46904|YGCN_ECOLI_Probable_electron_transfer_flavoprotein-quinone_oxidoreductase_ygcN_OS=Escherichia_coli_(strain_K12)_GN=ygcN_PE=3_SV=2	1.00E-85	[illegible]	[illegible]
comp55554_c0_seq1.p1	sp|P0AB58|YCIM_ECOLI_Uncharacterized_protein_yciM_OS=Escherichia_coli_(strain_K12)_GN=yciM_PE=4_SV=1	5.00E-132	[illegible]	[illegible]
comp55570_c0_seq1.p2				
comp55583_c0_seq1.p1	sp|Q9SYM5|RHM1_ARATH_Probable_rhamnose_biosynthetic_enzyme_1_OS=Arabidopsis_thaliana_GN=RHM1_PE=1_SV=1	2.00E-51	[illegible]	[illegible]
comp55617_c0_seq1.p1				
comp55620_c0_seq1.p1	sp|Q9VQX4|PNCB_DROME_Nicotinate_phosphoribosyltransferase_OS=Drosophila_melanogaster_GN=CG3714_PE=2_SV=2	7.00E-78	[illegible]	[illegible]
comp55641_c0_seq1.p1				
comp55662_c0_seq1.p1				
comp55686_c0_seq1.p1				
comp55693_c0_seq1.p1	sp|P0A9H9|CHEZ_ECOLI_Protein_phosphatase_CheZ_OS=Escherichia_coli_(strain_K12)_GN=cheZ_PE=1_SV=1	2.00E-102	[illegible]	[illegible]
comp55729_c0_seq1.p1				
comp55784_c0_seq1.p1				
comp55791_c0_seq1.p1				
comp55802_c0_seq1.p1	sp|P31224|ACRB_ECOLI_Acriflavine_resistance_protein_B_OS=Escherichia_coli_(strain_K12)_GN=acrB_PE=1_SV=1	1.00E-35	[illegible]	[illegible]
comp55803_c0_seq1.p1	sp|O65082|RL15B_PICMA_60S_ribosomal_protein_L15-2_OS=Picea_mariana_GN=SB62_PE=2_SV=1	1.00E-74	[illegible]	[illegible]
comp55806_c0_seq1.p1	sp|Q66I24|ASSY_DANRE_Argininosuccinate_synthase_OS=Danio_rerio_GN=ass1_PE=2_SV=1	3.00E-59	[illegible]	[illegible]
comp55807_c0_seq1.p1	sp|Q3YUF5|ULAG_SHISS_Probable_L-ascorbate-6-phosphate_lactonase_ulaG_OS=Shigella_sonnei_(strain_Ss046)_GN=ulaG_PE=3_SV=2	3.00E-81	[illegible]	[illegible]
comp55812_c0_seq1.p1				
comp55813_c0_seq1.p1	sp|Q31XU9|HCAB_SHIBS_3-phenylpropionate-dihydrodiol/cinnamic_acid-dihydrodiol_dehydrogenase_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=hcaB_PE=3_SV=1	5.00E-159	[illegible]	[illegible]
comp55818_c0_seq1.p1				
comp55825_c0_seq1.p2				
comp55847_c0_seq1.p1				
comp55861_c0_seq1.p1	sp|Q8XA23|NADB_ECO57_L-aspartate_oxidase_OS=Escherichia_coli_O157:H7_GN=nadB_PE=3_SV=1	2.00E-101	[illegible]	[illegible]
comp55872_c0_seq1.p1	sp|Q5RAS0|ACADS_PONAB_Short-chain_specific_acyl-CoA_dehydrogenase,_mitochondrial_OS=Pongo_abelii_GN=ACADS_PE=2_SV=1	3.00E-50	[illegible]	[illegible]
comp55882_c0_seq1.p2				
comp55886_c0_seq1.p2				
comp55916_c0_seq1.p3				
comp55918_c0_seq1.p2	sp|P52647|NIFJ_ECOLI_Probable_pyruvate-flavodoxin_oxidoreductase_OS=Escherichia_coli_(strain_K12)_GN=ydbK_PE=3_SV=2	9.00E-98	[illegible]	[illegible]
comp55935_c0_seq1.p1				
comp55941_c0_seq1.p2				
comp55946_c0_seq1.p1	sp|P51817|PRKX_HUMAN_cAMP-dependent_protein_kinase_catalytic_subunit_PRKX_OS=Homo_sapiens_GN=PRKX_PE=1_SV=1	1.00E-79	[illegible]	[illegible]
comp55961_c0_seq1.p1				
comp55969_c0_seq1.p1				
comp55981_c0_seq1.p1				
comp55986_c0_seq1.p1				
comp55990_c0_seq1.p1	sp|Q04933|DLDH_TRYBB_Dihydrolipoyl_dehydrogenase_OS=Trypanosoma_brucei_brucei_PE=3_SV=1	6.00E-32	[illegible]	[illegible]
comp56003_c0_seq1.p1				
comp56012_c0_seq1.p2	sp|Q9SJL8|METK3_ARATH_S-adenosylmethionine_synthase_3_OS=Arabidopsis_thaliana_GN=METK3_PE=1_SV=1	2.00E-78	[illegible]	[illegible]
comp56018_c0_seq1.p1				
comp56020_c0_seq1.p1				
comp56038_c0_seq1.p1				
comp56049_c0_seq1.p1				
comp56064_c0_seq1.p1	sp|Q9C0G6|DYH6_HUMAN_Dynein_heavy_chain_6,_axonemal_OS=Homo_sapiens_GN=DNAH6_PE=1_SV=3	2.00E-66	[illegible]	[illegible]
comp56071_c0_seq1.p1				
comp56103_c0_seq1.p1				
comp56112_c0_seq1.p1				
comp56124_c0_seq1.p1				
comp56162_c0_seq1.p2				
comp56168_c0_seq1.p1	sp|P16681|PHNB_ECOLI_Protein_phnB_OS=Escherichia_coli_(strain_K12)_GN=phnB_PE=4_SV=1	9.00E-82		
comp56169_c0_seq1.p2	sp|Q3Z4W7|TIG_SHISS_Trigger_factor_OS=Shigella_sonnei_(strain_Ss046)_GN=tig_PE=3_SV=1	1.00E-179	[illegible]	[illegible]
comp56187_c0_seq1.p1				
comp56188_c0_seq1.p1	sp|B1IWX5|ILVD_ECOLC_Dihydroxy-acid_dehydratase_OS=Escherichia_coli_(strain_ATCC_8739_/_DSM_1576_/_Crooks)_GN=ilvD_PE=3_SV=1	0	[illegible]	[illegible]
comp56197_c0_seq1.p1	sp|P36889|SAHH_LEIDO_Adenosylhomocysteinase_OS=Leishmania_donovani_PE=3_SV=2	2.00E-48	[illegible]	[illegible]
comp56218_c0_seq1.p2				
comp56278_c0_seq1.p1	sp|Q8X878|KEFB_ECO57_Glutathione-regulated_potassium-efflux_system_protein_KefB_OS=Escherichia_coli_O157:H7_GN=kefB_PE=3_SV=1	2.00E-98	[illegible]	[illegible]
comp56348_c0_seq1.p1				
comp56358_c0_seq1.p1	sp|P60932|UPPP_ECOLI_Undecaprenyl-diphosphatase_OS=Escherichia_coli_(strain_K12)_GN=uppP_PE=1_SV=1	1.00E-69	[illegible]	[illegible]
comp56366_c0_seq1.p2				
comp56376_c0_seq1.p1	sp|P42037|RLA2_ALTAL_60S_acidic_ribosomal_protein_P2_OS=Alternaria_alternata_GN=ALTA5_PE=1_SV=1	1.00E-16	[illegible]	[illegible]
comp56383_c0_seq1.p1				
comp56387_c0_seq1.p1	sp|Q3Z146|PUUD_SHISS_Gamma-glutamyl-gamma-aminobutyrate_hydrolase_OS=Shigella_sonnei_(strain_Ss046)_GN=puuD_PE=3_SV=2	3.00E-64	[illegible]	[illegible]
comp56397_c0_seq1.p1				
comp56417_c0_seq1.p1				
comp56440_c0_seq1.p1				
comp56443_c0_seq1.p2	sp|P48501|TPIS_SCHMA_Triosephosphate_isomerase_OS=Schistosoma_mansoni_GN=TPI_PE=1_SV=1	2.00E-24	[illegible]	[illegible]
comp56492_c0_seq1.p1				
comp56556_c0_seq1.p1				
comp56558_c0_seq1.p1				
comp56566_c0_seq1.p1				
comp56569_c0_seq1.p1	sp|Q6T3U3|NPCL1_RAT_Niemann-Pick_C1-like_protein_1_OS=Rattus_norvegicus_GN=Npc1l1_PE=1_SV=1	4.00E-16	[illegible]	[illegible]
comp56578_c0_seq1.p1				
comp5660_c0_seq1.p1				
comp56607_c0_seq1.p1				
comp56622_c0_seq1.p1	sp|Q3Z5V6|SURA_SHISS_Chaperone_surA_OS=Shigella_sonnei_(strain_Ss046)_GN=surA_PE=3_SV=1	2.00E-87	[illegible]	[illegible]
comp56636_c0_seq1.p1	sp|P0AA88|DSBE_SHIFL_Thiol:disulfide_interchange_protein_DsbE_OS=Shigella_flexneri_GN=dsbE_PE=3_SV=1	3.00E-60	[illegible]	[illegible]
comp56639_c0_seq1.p1	sp|P51817|PRKX_HUMAN_cAMP-dependent_protein_kinase_catalytic_subunit_PRKX_OS=Homo_sapiens_GN=PRKX_PE=1_SV=1	3.00E-30	[illegible]	[illegible]
comp56680_c0_seq1.p1				
comp56682_c0_seq1.p1	sp|Q39610|DYHA_CHLRE_Dynein_alpha_chain,_flagellar_outer_arm_OS=Chlamydomonas_reinhardtii_GN=ODA11_PE=3_SV=2	2.00E-14	[illegible]	[illegible]
comp56685_c0_seq1.p1	sp|P0AGI1|RBSC_ECOLI_Ribose_transport_system_permease_protein_rbsC_OS=Escherichia_coli_(strain_K12)_GN=rbsC_PE=1_SV=1	5.00E-70	[illegible]	[illegible]
comp56700_c0_seq1.p1	sp|Q3YV47|HSLU_SHISS_ATP-dependent_protease_ATPase_subunit_HslU_OS=Shigella_sonnei_(strain_Ss046)_GN=hslU_PE=3_SV=1	8.00E-152	[illegible]	[illegible]
comp56702_c0_seq1.p2				
comp56752_c0_seq1.p2	sp|P36415|HS7C1_DICDI_Heat_shock_cognate_70_kDa_protein_1_OS=Dictyostelium_discoideum_GN=hspB_PE=1_SV=2	4.00E-62	[illegible]	[illegible]
comp56753_c0_seq1.p1				
comp56787_c0_seq1.p1				
comp56810_c0_seq1.p1				
comp56848_c0_seq1.p1	sp|P41123|RL13_RAT_60S_ribosomal_protein_L13_OS=Rattus_norvegicus_GN=Rpl13_PE=1_SV=2	7.00E-41	[illegible]	[illegible]
comp56865_c0_seq1.p1	sp|P32157|YIIM_ECOLI_Protein_yiiM_OS=Escherichia_coli_(strain_K12)_GN=yiiM_PE=1_SV=2	6.00E-82	[illegible]	[illegible]
comp56914_c0_seq1.p2				
comp56916_c0_seq1.p1				
comp56954_c0_seq1.p1				
comp56996_c0_seq1.p1	sp|P0A9K6|PHOL_SHIFL_PhoH-like_protein_OS=Shigella_flexneri_GN=ybeZ_PE=3_SV=2	2.00E-158	[illegible]	[illegible]
comp57021_c0_seq1.p1	sp|Q3Z4Z4|RISB_SHISS_6,7-dimethyl-8-ribityllumazine_synthase_OS=Shigella_sonnei_(strain_Ss046)_GN=ribH_PE=3_SV=1	2.00E-95	[illegible]	[illegible]
comp57023_c0_seq1.p2	sp|Q3Z135|RNB_SHISS_Exoribonuclease_2_OS=Shigella_sonnei_(strain_Ss046)_GN=rnb_PE=3_SV=1	1.00E-63	[illegible]	[illegible]
comp57104_c0_seq1.p1	sp|P07654|PSTA_ECOLI_Phosphate_transport_system_permease_protein_pstA_OS=Escherichia_coli_(strain_K12)_GN=pstA_PE=1_SV=1	3.00E-80	[illegible]	[illegible]
comp57154_c0_seq1.p2				
comp57173_c0_seq1.p1				
comp57192_c0_seq1.p1				
comp57238_c0_seq1.p1	sp|P34827|EF1B_TRYCR_25_kDa_elongation_factor_1-beta_OS=Trypanosoma_cruzi_PE=2_SV=1	2.00E-13	[illegible]	[illegible]
comp57241_c0_seq1.p1				
comp5725_c0_seq1.p1				
comp57282_c0_seq1.p1				
comp57359_c0_seq1.p1	sp|Q3YU31|DNAT_SHISS_Primosomal_protein_1_OS=Shigella_sonnei_(strain_Ss046)_GN=dnaT_PE=3_SV=1	1.00E-72	[illegible]	[illegible]
comp57382_c0_seq1.p1	sp|P24177|ACRD_ECOLI_Probable_aminoglycoside_efflux_pump_OS=Escherichia_coli_(strain_K12)_GN=acrD_PE=3_SV=3	1.00E-117	[illegible]	[illegible]
comp57387_c0_seq1.p1	sp|Q9LP24|Y1571_ARATH_Probable_leucine-rich_repeat_receptor-like_protein_kinase_At1g35710_OS=Arabidopsis_thaliana_GN=At1g35710_PE=2_SV=1	2.00E-56	[illegible]	[illegible]
comp57431_c0_seq1.p2				
comp57454_c0_seq1.p1	sp|P33934|NAPH_ECOLI_Ferredoxin-type_protein_napH_OS=Escherichia_coli_(strain_K12)_GN=napH_PE=4_SV=1	8.00E-116	[illegible]	[illegible]
comp57515_c0_seq1.p1				
comp5752_c0_seq1.p1	sp|P0AA40|RLUC_SHIFL_Ribosomal_large_subunit_pseudouridine_synthase_C_OS=Shigella_flexneri_GN=rluC_PE=3_SV=1	1.00E-45	[illegible]	[illegible]
comp57523_c0_seq1.p1				
comp57524_c0_seq1.p1				
comp57526_c0_seq1.p1	sp|P27643|SP5K_BACSU_Stage_V_sporulation_protein_K_OS=Bacillus_subtilis_GN=spoVK_PE=2_SV=3	5.00E-14	[illegible]	[illegible]
comp57527_c0_seq1.p1	sp|Q46814|XDHD_ECOLI_Probable_hypoxanthine_oxidase_XdhD_OS=Escherichia_coli_(strain_K12)_GN=xdhD_PE=3_SV=1	2.00E-103	[illegible]	[illegible]
comp57535_c0_seq1.p1				

comp57543_c0_seq1.p1	sp|Q31TY7|ACEK_SHIBS_Isocitrate_dehydrogenase_kinase/phosphatase_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=aceK_PE=3_SV=1	4.00E-66	[illegible]	[illegible]
comp57545_c0_seq1.p1	sp|P75823|LTAE_ECOLI_Low_specificity_L-threonine_aldolase_OS=Escherichia_coli_(strain_K12)_GN=ltaE_PE=1_SV=1	0	[illegible]	[illegible]
comp57546_c0_seq1.p1				
comp57554_c0_seq1.p1	sp|Q01233|HSP70_NEUCR_Heat_shock_70_kDa_protein_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=hsps-1_PE=2_SV=2	9.00E-72	[illegible]	[illegible]
comp57557_c0_seq1.p1				
comp57558_c0_seq1.p1	sp|Q54XM6|ETFD_DICDI_Electron_transfer_flavoprotein-ubiquinone_oxidoreductase,_mitochondrial_OS=Dictyostelium_discoideum_GN=etfdh_PE=3_SV=1	1.00E-29	[illegible]	[illegible]
comp57565_c0_seq1.p1	sp|Q62559|IFT52_MOUSE_Intraflagellar_transport_protein_52_homolog_OS=Mus_musculus_GN=Ift52_PE=1_SV=2	2.00E-35	[illegible]	[illegible]
comp57582_c0_seq1.p1				
comp57596_c0_seq2.p1	sp|P31691|ADT_ORYSJ_ADP,ATP_carrier_protein,_mitochondrial_OS=Oryza_sativa_subsp._japonica_GN=Os02g0718900_PE=2_SV=1	5.00E-63	[illegible]	[illegible]
comp57606_c0_seq1.p1				
comp57614_c0_seq1.p1	sp|Q326L3|TAL_SHIBS_Transaldolase_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=tal_PE=1_SV=1	8.00E-168	[illegible]	[illegible]
comp57619_c0_seq1.p1				
comp57629_c0_seq1.p1				
comp57631_c0_seq1.p1				
comp57640_c0_seq1.p1	sp|P52043|SCPC_ECOLI_Propionyl-CoA:succinate_CoA_transferase_OS=Escherichia_coli_(strain_K12)_GN=scpC_PE=1_SV=1	0	[illegible]	[illegible]
comp57646_c0_seq1.p1				
comp57677_c0_seq1.p1	sp|P22256|GABT_ECOLI_4-aminobutyrate_aminotransferase_GabT_OS=Escherichia_coli_(strain_K12)_GN=gabT_PE=1_SV=1	6.00E-101	[illegible]	[illegible]
comp57678_c0_seq1.p1	sp|P0A867|TALA_ECOLI_Transaldolase_A_OS=Escherichia_coli_(strain_K12)_GN=talA_PE=1_SV=1	2.00E-144	[illegible]	[illegible]
comp57686_c0_seq1.p1	sp|Q9CQR2|RS21_MOUSE_40S_ribosomal_protein_S21_OS=Mus_musculus_GN=Rps21_PE=2_SV=1	6.00E-43	[illegible]	[illegible]
comp57725_c0_seq1.p1	sp|Q8ZLS7|RLME_SALTY_Ribosomal_RNA_large_subunit_methyltransferase_E_OS=Salmonella_typhimurium_GN=rlmE_PE=3_SV=1	1.00E-100	[illegible]	[illegible]
comp57728_c0_seq1.p1				
comp57745_c0_seq1.p1	sp|Q4QQV8|CHMP5_RAT_Charged_multivesicular_body_protein_5_OS=Rattus_norvegicus_GN=Chmp5_PE=2_SV=1	6.00E-25	[illegible]	[illegible]
comp57754_c0_seq1.p1	sp|B1IQQ7|NANK_ECOLC_N-acetylmannosamine_kinase_OS=Escherichia_coli_(strain_ATCC_8739_/_DSM_1576_/_Crooks)_GN=nanK_PE=3_SV=1	1.00E-67	[illegible]	[illegible]
comp57755_c0_seq1.p1				
comp57756_c0_seq1.p1	sp|P39285|YJEP_ECOLI_Uncharacterized_MscS_family_protein_YjeP_OS=Escherichia_coli_(strain_K12)_GN=yjeP_PE=3_SV=3	3.00E-61	[illegible]	[illegible]
comp57762_c0_seq1.p1				
comp57776_c0_seq1.p2	sp|Q323D9|MDTC_SHIBS_Multidrug_resistance_protein_MdtC_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=mdtC_PE=3_SV=1	8.00E-43	[illegible]	[illegible]
comp57790_c0_seq1.p1	sp|P39365|SGCC_ECOLI_Putative_permease_IIC_component_OS=Escherichia_coli_(strain_K12)_GN=sgcC_PE=3_SV=1	2.00E-81	[illegible]	[illegible]
comp57794_c0_seq1.p1				
comp57797_c0_seq1.p1				
comp57804_c0_seq1.p1	sp|P26365|AMIB_ECOLI_N-acetylmuramoyl-L-alanine_amidase_AmiB_OS=Escherichia_coli_(strain_K12)_GN=amiB_PE=1_SV=2	8.00E-92	[illegible]	[illegible]
comp57805_c0_seq1.p1				
comp57818_c0_seq1.p1	sp|Q6MIV0|CLPB_BDEBA_Chaperone_protein_ClpB_OS=Bdellovibrio_bacteriovorus_(strain_ATCC_15356_/_DSM_50701_/_NCIB_9529_/_HD100)_GN=clpB_PE=3_SV=1	9.00E-33	[illegible]	[illegible]
comp57831_c0_seq1.p1				
comp57841_c0_seq1.p1	sp|P62302|RS13_SOYBN_40S_ribosomal_protein_S13_OS=Glycine_max_GN=RPS13_PE=2_SV=1	2.00E-53	[illegible]	[illegible]
comp57845_c0_seq1.p1				
comp57867_c0_seq1.p2	sp|Q54HS9|AP1M_DICDI_AP-1_complex_subunit_mu_OS=Dictyostelium_discoideum_GN=apm1_PE=1_SV=1	1.00E-76	[illegible]	[illegible]
comp57876_c0_seq1.p1				
comp57892_c0_seq1.p1				
comp57921_c0_seq1.p1	sp|P0AAG2|DPPD_SHIFL_Dipeptide_transport_ATP-binding_protein_DppD_OS=Shigella_flexneri_GN=dppD_PE=3_SV=1	5.00E-97	[illegible]	[illegible]
comp57927_c0_seq1.p1	sp|Q3Z2M2|YEBC_SHISS_Probable_transcriptional_regulatory_protein_YebC_OS=Shigella_sonnei_(strain_Ss046)_GN=yebC_PE=3_SV=1	6.00E-83	[illegible]	[illegible]
comp57938_c0_seq1.p1				
comp57946_c0_seq1.p1				
comp57956_c0_seq1.p1				
comp57973_c0_seq1.p1				
comp57979_c0_seq1.p1	sp|B6HYQ4|ATKC_ECOSE_Potassium-transporting_ATPase_C_chain_OS=Escherichia_coli_(strain_SE11)_GN=kdpC_PE=3_SV=1	8.00E-99	[illegible]	[illegible]
comp57979_c0_seq1.p3	sp|P21865|KDPD_ECOLI_Sensor_protein_KdpD_OS=Escherichia_coli_(strain_K12)_GN=kdpD_PE=1_SV=2	3.00E-86	[illegible]	[illegible]
comp57980_c0_seq1.p1	sp|B1LFX3|CAIT_ECOSM_L-carnitine/gamma-butyrobetaine_antiporter_OS=Escherichia_coli_(strain_SMS-3-5_/_SECEC)_GN=caiT_PE=3_SV=1	1.00E-74	[illegible]	[illegible]
comp57984_c0_seq1.p2				
comp57985_c0_seq1.p1	sp|P19800|RS14_TRYBB_40S_ribosomal_protein_S14_OS=Trypanosoma_brucei_brucei_GN=RPS14_PE=3_SV=1	3.00E-45	[illegible]	[illegible]
comp57986_c0_seq1.p1	sp|P18281|ACTO_ACACA_Actobindin_OS=Acanthamoeba_castellanii_PE=1_SV=2	4.00E-28	[illegible]	[illegible]
comp57994_c0_seq1.p1	sp|B1LK77|DUT_ECOSM_Deoxyuridine_5'-triphosphate_nucleotidohydrolase_OS=Escherichia_coli_(strain_SMS-3-5_/_SECEC)_GN=dut_PE=3_SV=1	1.00E-106	[illegible]	[illegible]
comp57996_c0_seq1.p1	sp|Q9UL16|CCD19_HUMAN_Coiled-coil_domain-containing_protein_19,_mitochondrial_OS=Homo_sapiens_GN=CCDC19_PE=1_SV=2	2.00E-14	[illegible]	[illegible]
comp57999_c0_seq1.p1				
comp58010_c0_seq1.p1	sp|Q325H8|THII_SHIBS_tRNA_sulfurtransferase_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=thiI_PE=3_SV=1	3.00E-61	[illegible]	[illegible]
comp58018_c0_seq1.p1				
comp5802_c0_seq1.p2				
comp58028_c0_seq1.p1				
comp58036_c0_seq1.p1				
comp58039_c0_seq1.p1	sp|P0AEL6|FEPB_ECOLI_Ferrienterobactin-binding_periplasmic_protein_OS=Escherichia_coli_(strain_K12)_GN=fepB_PE=1_SV=1	2.00E-111	[illegible]	[illegible]
comp58041_c0_seq1.p2	sp|P14375|ZRAR_ECOLI_Transcriptional_regulatory_protein_ZraR_OS=Escherichia_coli_(strain_K12)_GN=zraR_PE=1_SV=2	4.00E-131	[illegible]	[illegible]
comp58061_c0_seq1.p2	sp|P30859|ARTI_ECOLI_Putative_ABC_transporter_arginine-binding_protein_2_OS=Escherichia_coli_(strain_K12)_GN=artI_PE=1_SV=3	5.00E-69	[illegible]	[illegible]
comp58064_c0_seq1.p1				
comp58080_c0_seq1.p4				
comp58087_c0_seq1.p1	sp|P52061|RDGB_ECOLI_dITP/XTP_pyrophosphatase_OS=Escherichia_coli_(strain_K12)_GN=rdgB_PE=1_SV=1	9.00E-126	[illegible]	[illegible]
comp58089_c0_seq1.p1	sp|Q83MD6|DGTP_SHIFL_Deoxyguanosinetriphosphate_triphosphohydrolase_OS=Shigella_flexneri_GN=dgt_PE=3_SV=3	1.00E-59	[illegible]	[illegible]
comp58090_c0_seq1.p1				
comp58091_c0_seq1.p1	sp|P77454|GLSA1_ECOLI_Glutaminase_1_OS=Escherichia_coli_(strain_K12)_GN=glsA1_PE=1_SV=1	7.00E-65	[illegible]	[illegible]
comp58102_c0_seq1.p1	sp|P37690|ENVC_ECOLI_Murein_hydrolase_activator_EnvC_OS=Escherichia_coli_(strain_K12)_GN=envC_PE=1_SV=2	6.00E-64	[illegible]	[illegible]
comp58103_c0_seq1.p2	sp|P23482|HYFB_ECOLI_Hydrogenase-4_component_B_OS=Escherichia_coli_(strain_K12)_GN=hyfB_PE=1_SV=1	1.00E-76	[illegible]	[illegible]
comp58107_c0_seq1.p1				
comp58108_c0_seq1.p1				
comp58125_c0_seq1.p1				
comp58132_c0_seq1.p2				
comp58137_c0_seq1.p1	sp|Q3YVR0|DCTA_SHISS_C4-dicarboxylate_transport_protein_OS=Shigella_sonnei_(strain_Ss046)_GN=dctA_PE=3_SV=1	2.00E-168	[illegible]	[illegible]
comp58139_c0_seq1.p1	sp|Q3YZA3|EUTC_SHISS_Ethanolamine_ammonia-lyase_light_chain_OS=Shigella_sonnei_(strain_Ss046)_GN=eutC_PE=3_SV=1	3.00E-62	[illegible]	[illegible]
comp58143_c0_seq1.p1	sp|P49093|ASNS2_LOTJA_Asparagine_synthetase_[glutamine-hydrolyzing]_2_OS=Lotus_japonicus_GN=AS2_PE=2_SV=1	2.00E-47	[illegible]	[illegible]
comp58162_c0_seq1.p2				
comp58204_c0_seq1.p1	sp|P0AFF9|NUSA_SHIFL_Transcription_elongation_protein_nusA_OS=Shigella_flexneri_GN=nusA_PE=3_SV=1	9.00E-47	[illegible]	[illegible]
comp58220_c0_seq1.p2	sp|Q08277|HSP82_MAIZE_Heat_shock_protein_82_OS=Zea_mays_GN=HSP82_PE=3_SV=1	4.00E-23	[illegible]	[illegible]
comp58236_c0_seq1.p1				
comp58252_c0_seq1.p1	sp|P33222|YJFC_ECOLI_Uncharacterized_protein_yjfC_OS=Escherichia_coli_(strain_K12)_GN=yjfC_PE=4_SV=2	2.00E-157	[illegible]	[illegible]
comp58268_c0_seq1.p1	sp|Q5PQ44|CD022_XENLA_Uncharacterized_protein_C4orf22_homolog_OS=Xenopus_laevis_PE=2_SV=1	5.00E-56		
comp58281_c0_seq1.p1	sp|P20099|BISC_ECOLI_Biotin_sulfoxide_reductase_OS=Escherichia_coli_(strain_K12)_GN=bisC_PE=3_SV=3	7.00E-87	[illegible]	[illegible]
comp58302_c0_seq1.p1	sp|Q7UC56|NUOG_SHIFL_NADH-quinone_oxidoreductase_subunit_G_OS=Shigella_flexneri_GN=nuoG_PE=3_SV=3	5.00E-90	[illegible]	[illegible]
comp58309_c0_seq1.p1				
comp58310_c0_seq1.p1				
comp58319_c0_seq1.p1	sp|P0A9S0|FTSE_SHIFL_Cell_division_ATP-binding_protein_FtsE_OS=Shigella_flexneri_GN=ftsE_PE=3_SV=1	5.00E-76	[illegible]	[illegible]
comp58335_c0_seq1.p1				
comp58344_c0_seq1.p1				
comp58352_c0_seq1.p1	sp|A5PK63|RS17_BOVIN_40S_ribosomal_protein_S17_OS=Bos_taurus_GN=RPS17_PE=2_SV=1	3.00E-50	[illegible]	[illegible]
comp58360_c0_seq1.p1	sp|Q5UPD5|YL059_MIMIV_Putative_ankyrin_repeat_protein_L59_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L59_PE=4_SV=1	2.00E-12		
comp58367_c0_seq1.p1	sp|P77306|YQIK_ECOLI_Inner_membrane_protein_yqiK_OS=Escherichia_coli_(strain_K12)_GN=yqiK_PE=1_SV=1	8.00E-66	[illegible]	[illegible]
comp58370_c0_seq1.p1				
comp58375_c0_seq1.p1	sp|P19950|RS141_MAIZE_40S_ribosomal_protein_S14_OS=Zea_mays_PE=3_SV=1	5.00E-33	[illegible]	[illegible]
comp58376_c0_seq1.p1	sp|P09323|PTW3C_ECOLI_PTS_system_N-acetylglucosamine-specific_EIICBA_component_OS=Escherichia_coli_(strain_K12)_GN=nagE_PE=4_SV=1	5.00E-99	[illegible]	[illegible]
comp58381_c0_seq1.p1	sp|A5DE68|FAL1_PICGU_ATP-dependent_RNA_helicase_FAL1_OS=Meyerozyma_guilliermondii_(strain_ATCC_6260_/_CBS_566_/_DSM_6381_/_JCM_1539_/_NBRC_10279_/_NRRL_Y-324)_GN=FAL1_PE=3_SV=2	1.00E-109	[illegible]	[illegible]
comp58393_c0_seq1.p1	sp|Q54Q51|RS16_DICDI_40S_ribosomal_protein_S16_OS=Dictyostelium_discoideum_GN=rps16_PE=3_SV=1	2.00E-37	[illegible]	[illegible]
comp58394_c0_seq1.p2	sp|Q46948|YAJL_ECOLI_Chaperone_protein_YajL_OS=Escherichia_coli_(strain_K12)_GN=yajL_PE=1_SV=2	2.00E-135	[illegible]	[illegible]
comp58399_c0_seq1.p2	sp|O65050|RL15A_PICMA_60S_ribosomal_protein_L15-1_OS=Picea_mariana_GN=SB61_PE=2_SV=1	2.00E-24	[illegible]	[illegible]
comp58415_c0_seq1.p1	sp|Q9P7P8|DDH1_SCHPO_2-hydroxyacid_dehydrogenase_homolog_1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAC186.07c_PE=2_SV=1	1.00E-34	[illegible]	[illegible]
comp58417_c0_seq1.p1	sp|P0AD59|IVY_ECOLI_Inhibitor_of_vertebrate_lysozyme_OS=Escherichia_coli_(strain_K12)_GN=ivy_PE=1_SV=1	9.00E-98	[illegible]	[illegible]
comp58445_c0_seq1.p1	sp|P14081|SELB_ECOLI_Selenocysteine-specific_elongation_factor_OS=Escherichia_coli_(strain_K12)_GN=selB_PE=1_SV=3	7.00E-138	[illegible]	[illegible]
comp58446_c0_seq1.p2				
comp58451_c0_seq1.p2	sp|P49747|COMP_HUMAN_Cartilage_oligomeric_matrix_protein_OS=Homo_sapiens_GN=COMP_PE=1_SV=2	1.00E-30	[illegible]	[illegible]
comp58459_c0_seq1.p1				
comp58463_c0_seq1.p1	sp|P15640|PUR2_ECOLI_Phosphoribosylamine--glycine_ligase_OS=Escherichia_coli_(strain_K12)_GN=purD_PE=1_SV=2	1.00E-74	[illegible]	[illegible]
comp58467_c0_seq1.p1	sp|P31433|YICH_ECOLI_Uncharacterized_protein_yicH_OS=Escherichia_coli_(strain_K12)_GN=yicH_PE=4_SV=2	4.00E-73		
comp58498_c0_seq1.p1				
comp58500_c0_seq1.p1	sp|P32674|PFLD_ECOLI_Formate_acetyltransferase_2_OS=Escherichia_coli_(strain_K12)_GN=pflD_PE=3_SV=1	1.00E-142	[illegible]	[illegible]
comp58531_c0_seq1.p1	sp|P47990|XDH_CHICK_Xanthine_dehydrogenase/oxidase_OS=Gallus_gallus_GN=XDH_PE=1_SV=1	3.00E-16	[illegible]	[illegible]
comp58541_c0_seq1.p1				
comp58548_c0_seq1.p1	sp|B7M458|MDTB_ECO8A_Multidrug_resistance_protein_MdtB_OS=Escherichia_coli_O8_(strain_IAI1)_GN=mdtB_PE=2_SV=1	6.00E-72	[illegible]	[illegible]
comp58564_c0_seq1.p1	sp|Q46889|YGBK_ECOLI_Uncharacterized_protein_ygbK_OS=Escherichia_coli_(strain_K12)_GN=ygbK_PE=4_SV=1	1.00E-114		
comp58576_c0_seq1.p1	sp|P0AEC4|ARCB_SHIFL_Aerobic_respiration_control_sensor_protein_ArcB_OS=Shigella_flexneri_GN=arcB_PE=3_SV=1	8.00E-112	[illegible]	[illegible]
comp58577_c0_seq1.p1				
comp58584_c0_seq1.p2	sp|Q9FY66|RS152_ARATH_40S_ribosomal_protein_S15-2_OS=Arabidopsis_thaliana_GN=RPS15B_PE=2_SV=1	1.00E-23	[illegible]	[illegible]
comp58611_c0_seq1.p2	sp|P32140|YIHS_ECOLI_Uncharacterized_sugar_isomerase_yihS_OS=Escherichia_coli_(strain_K12)_GN=yihS_PE=1_SV=2	9.00E-83	[illegible]	[illegible]
comp58624_c0_seq1.p2				
comp58639_c0_seq1.p1				
comp58647_c0_seq1.p1	sp|Q9P2D7|DYH1_HUMAN_Dynein_heavy_chain_1,_axonemal_OS=Homo_sapiens_GN=DNAH1_PE=1_SV=4	9.00E-54	[illegible]	[illegible]
comp58660_c0_seq1.p1				
comp58672_c0_seq1.p1				
comp58673_c0_seq1.p1	sp|P0AE21|AMPM_SHIFL_Methionine_aminopeptidase_OS=Shigella_flexneri_GN=map_PE=3_SV=1	6.00E-69	[illegible]	[illegible]
comp58686_c0_seq1.p1	sp|Q9M3C3|R23A2_ARATH_60S_ribosomal_protein_L23a-2_OS=Arabidopsis_thaliana_GN=RPL23AB_PE=2_SV=1	7.00E-26	[illegible]	[illegible]
comp58691_c0_seq1.p1	sp|P71241|WCAJ_ECOLI_Putative_colanic_biosynthesis_UDP-glucose_lipid_carrier_transferase_OS=Escherichia_coli_(strain_K12)_GN=wcaJ_PE=1_SV=2	3.00E-108	[illegible]	[illegible]
comp58692_c0_seq1.p1				
comp58693_c0_seq1.p1				
comp58706_c0_seq1.p1	sp|P77396|YPDC_ECOLI_Uncharacterized_HTH-type_transcriptional_regulator_ypdC_OS=Escherichia_coli_(strain_K12)_GN=ypdC_PE=1_SV=1	0	[illegible]	[illegible]
comp58718_c0_seq1.p1				
comp58720_c0_seq1.p1	sp|B2TX75|PLSB_SHIB3_Glycerol-3-phosphate_acyltransferase_OS=Shigella_boydii_serotype_18_(strain_CDC_3083-94_/_BS512)_GN=plsB_PE=3_SV=1	3.00E-124	[illegible]	[illegible]
comp58735_c0_seq1.p2				
comp58750_c0_seq1.p1	sp|P0A8I4|YAAA_SHIFL_UPF0246_protein_yaaA_OS=Shigella_flexneri_GN=yaaA_PE=3_SV=1	6.00E-98		
comp58787_c0_seq1.p1				
comp58796_c0_seq1.p1	sp|P16688|PHNJ_ECOLI_Protein_phnJ_OS=Escherichia_coli_(strain_K12)_GN=phnJ_PE=3_SV=2	3.00E-168	[illegible]	[illegible]
comp58820_c0_seq1.p1	sp|Q08972|NEW1_YEAST_[NU+]_prion_formation_protein_1_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=NEW1_PE=1_SV=1	9.00E-21	[illegible]	[illegible]
comp58835_c0_seq1.p1				
comp58850_c0_seq1.p2	sp|P52095|DCLZ_ECOLI_Lysine_decarboxylase,_constitutive_OS=Escherichia_coli_(strain_K12)_GN=ldcC_PE=1_SV=2	2.00E-118	[illegible]	[illegible]
comp58859_c0_seq1.p1	sp|P0ABC7|HFLK_ECOLI_Modulator_of_FtsH_protease_HflK_OS=Escherichia_coli_(strain_K12)_GN=hflK_PE=1_SV=1	3.00E-120	[illegible]	[illegible]
comp58882_c0_seq1.p2	sp|Q46845|YGHU_ECOLI_Uncharacterized_GST-like_protein_yghU_OS=Escherichia_coli_(strain_K12)_GN=yghU_PE=1_SV=2	7.00E-85	[illegible]	[illegible]
comp58885_c0_seq1.p2	sp|Q3YVX7|GPMI_SHISS_2,3-bisphosphoglycerate-independent_phosphoglycerate_mutase_OS=Shigella_sonnei_(strain_Ss046)_GN=gpmI_PE=3_SV=1	7.00E-73	[illegible]	[illegible]
comp58890_c0_seq1.p1				
comp58921_c0_seq1.p1				
comp58931_c0_seq1.p1	sp|Q9ZPX5|DHSA2_ARATH_Succinate_dehydrogenase_[ubiquinone]_flavoprotein_subunit_2,_mitochondrial_OS=Arabidopsis_thaliana_GN=SDH1-2_PE=1_SV=1	5.00E-81	[illegible]	[illegible]
comp58955_c0_seq1.p1	sp|Q9C0G6|DYH6_HUMAN_Dynein_heavy_chain_6,_axonemal_OS=Homo_sapiens_GN=DNAH6_PE=1_SV=3	3.00E-70	[illegible]	[illegible]
comp59012_c0_seq1.p1				
comp59023_c0_seq1.p1				
comp59031_c0_seq1.p1	sp|Q08277|HSP82_MAIZE_Heat_shock_protein_82_OS=Zea_mays_GN=HSP82_PE=3_SV=1	1.00E-21	[illegible]	[illegible]
comp59061_c0_seq1.p1				
comp59100_c0_seq1.p2	sp|O42248|GBLP_DANRE_Guanine_nucleotide-binding_protein_subunit_beta-2-like_1_OS=Danio_rerio_GN=gnb2l1_PE=2_SV=1	2.00E-154	[illegible]	[illegible]
comp59110_c0_seq1.p1	sp|P31452|PTXC_ECOLI_Putative_permease_IIC_component_glvC_OS=Escherichia_coli_(strain_K12)_GN=glvC_PE=5_SV=2	7.00E-81	[illegible]	[illegible]
comp59130_c0_seq1.p1	sp|P27296|DING_ECOLI_Probable_ATP-dependent_helicase_dinG_OS=Escherichia_coli_(strain_K12)_GN=dinG_PE=3_SV=3	1.00E-121	[illegible]	[illegible]
comp59142_c0_seq1.p1				
comp59145_c0_seq1.p1	sp|P0AEC5|BARA_ECOLI_Signal_transduction_histidine-protein_kinase_BarA_OS=Escherichia_coli_(strain_K12)_GN=barA_PE=1_SV=1	2.00E-115	[illegible]	[illegible]
comp59156_c0_seq1.p2				
comp59161_c0_seq1.p1	sp|P07648|EX5C_ECOLI_Exodeoxyribonuclease_V_gamma_chain_OS=Escherichia_coli_(strain_K12)_GN=recC_PE=1_SV=1	6.00E-109	[illegible]	[illegible]
comp59177_c0_seq1.p1				
comp59188_c0_seq1.p1	sp|P36682|YACH_ECOLI_Uncharacterized_protein_yacH_OS=Escherichia_coli_(strain_K12)_GN=yacH_PE=4_SV=2	2.00E-61		
comp59196_c0_seq1.p1	sp|P24205|MSBB_ECOLI_Lipid_A_biosynthesis_(KDO)2-(lauroyl)-lipid_IVA_acyltransferase_OS=Escherichia_coli_(strain_K12)_GN=msbB_PE=1_SV=1	4.00E-109	[illegible]	[illegible]
comp59200_c0_seq1.p1				
comp59207_c0_seq1.p1	sp|P0AGF4|XYLE_ECOLI_D-xylose-proton_symporter_OS=Escherichia_coli_(strain_K12)_GN=xylE_PE=1_SV=1	0	[illegible]	[illegible]
comp59208_c0_seq1.p1	sp|Q9P2D7|DYH1_HUMAN_Dynein_heavy_chain_1,_axonemal_OS=Homo_sapiens_GN=DNAH1_PE=1_SV=4	3.00E-52	[illegible]	[illegible]
comp59224_c0_seq1.p1				
comp59239_c0_seq1.p1				
comp59249_c0_seq1.p1				
comp59253_c0_seq1.p1				
comp59302_c0_seq1.p1				
comp59312_c0_seq1.p2				
comp59324_c0_seq1.p1	sp|P06972|FHUB_ECOLI_Iron(3+)-hydroxamate_import_system_permease_protein_fhuB_OS=Escherichia_coli_(strain_K12)_GN=fhuB_PE=1_SV=2	1.00E-75	[illegible]	[illegible]
comp59325_c0_seq1.p2	sp|P36415|HS7C1_DICDI_Heat_shock_cognate_70_kDa_protein_1_OS=Dictyostelium_discoideum_GN=hspB_PE=1_SV=2	3.00E-109	[illegible]	[illegible]
comp59345_c0_seq1.p1	sp|Q5R9F9|NACA_PONAB_Nascent_polypeptide-associated_complex_subunit_alpha_OS=Pongo_abelii_GN=NACA_PE=2_SV=1	6.00E-19	[illegible]	[illegible]
comp59358_c0_seq1.p2				
comp59377_c0_seq1.p1	sp|P36547|EUTR_ECOLI_HTH-type_transcriptional_regulator_eutR_OS=Escherichia_coli_(strain_K12)_GN=eutR_PE=3_SV=2	2.00E-102	[illegible]	[illegible]
comp59393_c0_seq1.p1	sp|P16919|RHSD_ECOLI_Protein_rhsD_OS=Escherichia_coli_(strain_K12)_GN=rhsD_PE=2_SV=3	6.00E-73	[illegible]	[illegible]
comp59411_c0_seq1.p1				
comp59436_c0_seq1.p1	sp|Q5YLM1|DGLA_RAT_Sn1-specific_diacylglycerol_lipase_alpha_OS=Rattus_norvegicus_GN=Dagla_PE=2_SV=1	4.00E-16	[illegible]	[illegible]
comp59442_c0_seq1.p1	sp|P24181|ACRF_ECOLI_Acriflavine_resistance_protein_F_OS=Escherichia_coli_(strain_K12)_GN=acrF_PE=2_SV=2	0	[illegible]	[illegible]
comp59450_c0_seq1.p1	sp|B0G143|UCPB_DICDI_Mitochondrial_substrate_carrier_family_protein_ucpB_OS=Dictyostelium_discoideum_GN=ucpB_PE=3_SV=1	2.00E-37	[illegible]	[illegible]
comp59453_c0_seq1.p1	sp|Q3YXH4|MUG_SHISS_G/U_mismatch-specific_DNA_glycosylase_OS=Shigella_sonnei_(strain_Ss046)_GN=mug_PE=3_SV=1	1.00E-97	[illegible]	[illegible]
comp59462_c0_seq1.p1	sp|Q640T1|ALLC_XENTR_Allantoicase_OS=Xenopus_tropicalis_GN=allc_PE=2_SV=1	3.00E-16	[illegible]	[illegible]
comp5948_c0_seq1.p1	sp|Q83LK4|EFEB_SHIFL_Deferrochelatase/peroxidase_EfeB_OS=Shigella_flexneri_GN=efeB_PE=3_SV=1	4.00E-63	[illegible]	[illegible]
comp59480_c0_seq1.p1	sp|P16689|PHNM_ECOLI_Protein_phnM_OS=Escherichia_coli_(strain_K12)_GN=phnM_PE=4_SV=2	1.00E-53	[illegible]	[illegible]
comp59483_c0_seq1.p1				
comp59507_c0_seq1.p1	sp|P49200|RS201_ARATH_40S_ribosomal_protein_S20-1_OS=Arabidopsis_thaliana_GN=RPS20A_PE=1_SV=2	8.00E-28	[illegible]	[illegible]
comp59512_c0_seq1.p1				
comp59515_c0_seq1.p1				
comp59522_c0_seq1.p1	sp|Q3YWB4|RECF_SHISS_DNA_replication_and_repair_protein_recF_OS=Shigella_sonnei_(strain_Ss046)_GN=recF_PE=3_SV=1	2.00E-178	[illegible]	[illegible]
comp59527_c0_seq1.p2				
comp59533_c0_seq1.p1				
comp59536_c0_seq1.p1	sp|P62246|RS15A_RAT_40S_ribosomal_protein_S15a_OS=Rattus_norvegicus_GN=Rps15a_PE=1_SV=2	3.00E-42	[illegible]	[illegible]
comp59541_c0_seq1.p1	sp|Q83JE2|AAEB_SHIFL_p-hydroxybenzoic_acid_efflux_pump_subunit_AaeB_OS=Shigella_flexneri_GN=aaeB_PE=3_SV=1	2.00E-134	[illegible]	[illegible]
comp59583_c0_seq1.p1	sp|P17411|CHBF_ECOLI_6-phospho-beta-glucosidase_OS=Escherichia_coli_(strain_K12)_GN=chbF_PE=1_SV=4	0	[illegible]	[illegible]
comp59587_c0_seq1.p1				
comp59603_c0_seq1.p1				
comp59607_c0_seq1.p1	sp|P27859|TATD_ECOLI_Tat-linked_quality_control_protein_TatD_OS=Escherichia_coli_(strain_K12)_GN=tatD_PE=1_SV=3	4.00E-114	[illegible]	[illegible]
comp59607_c0_seq1.p2	sp|P69423|TATC_ECOLI_Sec-independent_protein_translocase_protein_TatC_OS=Escherichia_coli_(strain_K12)_GN=tatC_PE=1_SV=2	7.00E-54	[illegible]	[illegible]
comp59609_c0_seq1.p1	sp|P24211|RHSE_ECOLI_Putative_protein_rhsE_OS=Escherichia_coli_(strain_K12)_GN=rhsE_PE=5_SV=3	0	[illegible]	[illegible]
comp59635_c0_seq1.p1				
comp59646_c0_seq1.p1				
comp59663_c0_seq1.p1				
comp59668_c0_seq1.p1				
comp59701_c0_seq1.p1	sp|P0AG17|PUR1_SHIFL_Amidophosphoribosyltransferase_OS=Shigella_flexneri_GN=purF_PE=3_SV=2	9.00E-141	[illegible]	[illegible]
comp59707_c0_seq1.p2	sp|Q2KJC6|METK1_BOVIN_S-adenosylmethionine_synthase_isoform_type-1_OS=Bos_taurus_GN=MAT1A_PE=2_SV=1	9.00E-54	[illegible]	[illegible]
comp59708_c0_seq1.p1				
comp59717_c0_seq1.p1	sp|Q3Z476|SUCC_SHISS_Succinyl-CoA_ligase_[ADP-forming]_subunit_beta_OS=Shigella_sonnei_(strain_Ss046)_GN=sucC_PE=3_SV=1	2.00E-67	[illegible]	[illegible]
comp59722_c0_seq1.p1				
comp59740_c0_seq1.p2				
comp59763_c0_seq1.p1				
comp59765_c0_seq1.p1				
comp59795_c0_seq1.p1				
comp59797_c0_seq1.p1	sp|P69805|PTND_ECOLI_Mannose_permease_IID_component_OS=Escherichia_coli_(strain_K12)_GN=manZ_PE=1_SV=2	3.00E-58	[illegible]	[illegible]
comp59815_c0_seq1.p1	sp|Q3Z595|PROB_SHISS_Glutamate_5-kinase_OS=Shigella_sonnei_(strain_Ss046)_GN=proB_PE=3_SV=1	2.00E-145	[illegible]	[illegible]
comp59830_c0_seq1.p1	sp|P45546|YHFT_ECOLI_Uncharacterized_protein_yhfT_OS=Escherichia_coli_(strain_K12)_GN=yhfT_PE=4_SV=2	2.00E-71	[illegible]	[illegible]
comp59837_c0_seq1.p1				
comp59844_c0_seq1.p2				
comp59865_c0_seq1.p1	sp|Q5Y750|CP512_ARATH_Putative_sterol_14-demethylase-like_protein_OS=Arabidopsis_thaliana_GN=CYP51G2_PE=5_SV=1	2.00E-15	[illegible]	[illegible]
comp59924_c0_seq1.p1				
comp59949_c0_seq1.p1	sp|Q9JJ79|DYHC2_RAT_Cytoplasmic_dynein_2_heavy_chain_1_OS=Rattus_norvegicus_GN=Dync2h1_PE=1_SV=1	1.00E-59	[illegible]	[illegible]
comp59971_c0_seq1.p2	sp|P22232|FBRL_XENLA_rRNA_2'-O-methyltransferase_fibrillarin_OS=Xenopus_laevis_GN=fbl_PE=2_SV=1	1.00E-59	[illegible]	[illegible]
comp59999_c0_seq1.p1				
comp60001_c0_seq1.p1	sp|P78061|PUUA_ECOLI_Gamma-glutamylputrescine_synthetase_PuuA_OS=Escherichia_coli_(strain_K12)_GN=puuA_PE=1_SV=2	8.00E-95	[illegible]	[illegible]
comp60058_c0_seq1.p1	sp|P28634|YAEB_ECOLI_UPF0066_protein_yaeB_OS=Escherichia_coli_(strain_K12)_GN=yaeB_PE=1_SV=2	2.00E-102	[illegible]	[illegible]
comp60079_c0_seq1.p1	sp|P0ACJ5|YBAO_ECOLI_Uncharacterized_HTH-type_transcriptional_regulator_ybaO_OS=Escherichia_coli_(strain_K12)_GN=ybaO_PE=4_SV=1	2.00E-52	[illegible]	[illegible]
comp60082_c0_seq1.p1	sp|P77154|YCJT_ECOLI_Uncharacterized_glycosyl_hydrolase_ycjT_OS=Escherichia_coli_(strain_K12)_GN=ycjT_PE=3_SV=1	9.00E-54	[illegible]	[illegible]
comp60084_c0_seq1.p1	sp|P33924|YEJO_ECOLI_Putative_uncharacterized_outer_membrane_protein_YejO_OS=Escherichia_coli_(strain_K12)_GN=yejO_PE=5_SV=1	1.00E-106	[illegible]	[illegible]
comp60118_c0_seq2.p1				
comp60119_c0_seq1.p2	sp|B0G0Y5|MYBAA_DICDI_Myb-like_protein_AA_OS=Dictyostelium_discoideum_GN=mybAA_PE=3_SV=1	9.00E-13	[illegible]	[illegible]
comp60122_c0_seq1.p1				
comp60176_c0_seq1.p1	sp|P76226|YNJF_ECOLI_Inner_membrane_protein_YnjF_OS=Escherichia_coli_(strain_K12)_GN=ynjF_PE=1_SV=2	4.00E-98	[illegible]	[illegible]
comp60199_c0_seq1.p3				
comp60237_c0_seq1.p1	sp|P36938|PGM_ECOLI_Phosphoglucomutase_OS=Escherichia_coli_(strain_K12)_GN=pgm_PE=1_SV=1	2.00E-80	[illegible]	[illegible]
comp60243_c0_seq1.p1				
comp60280_c0_seq1.p1	sp|P0A9U2|YBHF_SHIFL_Uncharacterized_ABC_transporter_ATP-binding_protein_YbhF_OS=Shigella_flexneri_GN=ybhF_PE=3_SV=1	5.00E-108	[illegible]	[illegible]
comp60349_c0_seq1.p1				
comp60388_c0_seq1.p1				
comp60421_c0_seq1.p1				
comp60436_c0_seq1.p1	sp|P31907|HOXX_BRAJA_Hydrogenase_maturation_factor_hoxX_OS=Bradyrhizobium_japonicum_(strain_USDA_110)_GN=hoxX_PE=4_SV=2	4.00E-29	[illegible]	[illegible]
comp60446_c0_seq1.p1				
comp60448_c0_seq1.p2				
comp60459_c0_seq1.p1				
comp60461_c0_seq1.p1				
comp60482_c0_seq1.p1				
comp60483_c0_seq1.p1				
comp60492_c0_seq1.p1	sp|B7LPB7|GCSP_ESCF3_Glycine_dehydrogenase_[decarboxylating]_OS=Escherichia_fergusonii_(strain_ATCC_35469_/_DSM_13698_/_CDC_0568-73)_GN=gcvP_PE=3_SV=1	2.00E-129	[illegible]	[illegible]
comp60530_c0_seq1.p1				
comp60537_c0_seq1.p1				
comp60547_c0_seq1.p2	sp|P32007|ADT3_BOVIN_ADP/ATP_translocase_3_OS=Bos_taurus_GN=SLC25A6_PE=1_SV=3	3.00E-53	[illegible]	[illegible]
comp60564_c0_seq1.p1				
comp6062_c0_seq1.p1	sp|P35685|RL7A_ORYSJ_60S_ribosomal_protein_L7a_OS=Oryza_sativa_subsp._japonica_GN=RPL7A_PE=2_SV=1	8.00E-45	[illegible]	[illegible]
comp60622_c0_seq1.p1	sp|Q31WY2|GLNE_SHIBS_Glutamate-ammonia-ligase_adenylyltransferase_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=glnE_PE=3_SV=1	0	[illegible]	[illegible]
comp60628_c0_seq1.p1	sp|P77379|YKGD_ECOLI_Uncharacterized_HTH-type_transcriptional_regulator_ykgD_OS=Escherichia_coli_(strain_K12)_GN=ykgD_PE=4_SV=1	0	[illegible]	[illegible]
comp60655_c0_seq1.p1				
comp60663_c0_seq1.p1	sp|Q12574|TPIS_COPC7_Triosephosphate_isomerase_OS=Coprinopsis_cinerea_(strain_Okayama-7_/_130_/_ATCC_MYA-4618_/_FGSC_9003)_GN=TPI_PE=3_SV=2	7.00E-32	[illegible]	[illegible]
comp60698_c0_seq1.p1	sp|P24181|ACRF_ECOLI_Acriflavine_resistance_protein_F_OS=Escherichia_coli_(strain_K12)_GN=acrF_PE=2_SV=2	7.00E-134	[illegible]	[illegible]
comp60701_c0_seq1.p1				
comp60736_c0_seq1.p1	sp|Q875S0|EF2_LACKL_Elongation_factor_2_OS=Lachancea_kluyveri_GN=EFT2_PE=3_SV=1	6.00E-76	[illegible]	[illegible]
comp60754_c0_seq1.p2	sp|A0R3D6|Y5435_MYCS2_Putative_ligase_MSMEG_5435_OS=Mycobacterium_smegmatis_(strain_ATCC_700084_/_mc(2)155)_GN=MSMEG_5435_PE=1_SV=1	6.00E-18	[illegible]	[illegible]
comp60781_c0_seq1.p1	sp|Q3YW93|GLGB_SHISS_1,4-alpha-glucan_branching_enzyme_GlgB_OS=Shigella_sonnei_(strain_Ss046)_GN=glgB_PE=3_SV=1	1.00E-134	[illegible]	[illegible]
comp60791_c0_seq1.p2				
comp60792_c0_seq1.p1	sp|P76387|WZC_ECOLI_Tyrosine-protein_kinase_wzc_OS=Escherichia_coli_(strain_K12)_GN=wzc_PE=1_SV=2	2.00E-135	[illegible]	[illegible]
comp60802_c0_seq1.p1				
comp60845_c0_seq1.p1	sp|Q83MG0|MURE_SHIFL_UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate_ligase_OS=Shigella_flexneri_GN=murE_PE=3_SV=1	8.00E-71	[illegible]	[illegible]
comp60885_c0_seq1.p1	sp|P75867|LONH_ECOLI_Putative_Lon_protease_homolog_OS=Escherichia_coli_(strain_K12)_GN=ycbZ_PE=3_SV=1	6.00E-137	[illegible]	[illegible]
comp60896_c0_seq1.p1	sp|P39389|YJIR_ECOLI_Uncharacterized_HTH-type_transcriptional_regulator_yjiR_OS=Escherichia_coli_(strain_K12)_GN=yjiR_PE=1_SV=1	9.00E-133	[illegible]	[illegible]
comp60975_c0_seq1.p2				
comp6099_c0_seq1.p2	sp|P09180|RL4_DROME_60S_ribosomal_protein_L4_OS=Drosophila_melanogaster_GN=RpL4_PE=2_SV=2	2.00E-32	[illegible]	[illegible]
comp60990_c0_seq1.p1				
comp61012_c0_seq1.p2	sp|P16095|SDHL_ECOLI_L-serine_dehydratase_1_OS=Escherichia_coli_(strain_K12)_GN=sdaA_PE=1_SV=3	4.00E-96	[illegible]	[illegible]
comp61030_c0_seq1.p1	sp|B6HZX5|MHPC_ECOSE_2-hydroxy-6-oxononadienedioate/2-hydroxy-6-oxononatrienedioate_hydrolase_OS=Escherichia_coli_(strain_SE11)_GN=mhpC_PE=3_SV=2	4.00E-148	[illegible]	[illegible]
comp6104_c0_seq1.p1	sp|Q3Z261|SYFB_SHISS_Phenylalanine--tRNA_ligase_beta_subunit_OS=Shigella_sonnei_(strain_Ss046)_GN=pheT_PE=3_SV=1	1.00E-49	[illegible]	[illegible]
comp61045_c0_seq1.p1	sp|Q1R4G0|GPPA_ECOUT_Guanosine-5'-triphosphate,3'-diphosphate_pyrophosphatase_OS=Escherichia_coli_(strain_UTI89_/_UPEC)_GN=gppA_PE=3_SV=2	3.00E-105	[illegible]	[illegible]
comp61063_c0_seq1.p1				
comp61116_c0_seq1.p1	sp|Q3Z554|HOA_SHISS_4-hydroxy-2-oxovalerate_aldolase_OS=Shigella_sonnei_(strain_Ss046)_GN=mhpE_PE=3_SV=1	3.00E-97	[illegible]	[illegible]
comp61161_c0_seq1.p1	sp|Q9CUL5|IQCA1_MOUSE_IQ_and_AAA_domain-containing_protein_1_OS=Mus_musculus_GN=Iqca1_PE=2_SV=2	1.00E-20	[illegible]	[illegible]
comp61237_c0_seq1.p1				
comp61243_c0_seq1.p1				
comp61257_c0_seq1.p1	sp|P08372|PPDC_ECOLI_Prepilin_peptidase-dependent_protein_C_OS=Escherichia_coli_(strain_K12)_GN=ppdC_PE=3_SV=1	2.00E-57		
comp61270_c0_seq1.p1	sp|Q9XGL4|RL31_CYAPA_60S_ribosomal_protein_L31_OS=Cyanophora_paradoxa_GN=RPL31_PE=3_SV=1	3.00E-33	[illegible]	[illegible]
comp61284_c0_seq1.p1	sp|P76578|YFHM_ECOLI_Uncharacterized_lipoprotein_yfhM_OS=Escherichia_coli_(strain_K12)_GN=yfhM_PE=4_SV=1	7.00E-117	[illegible]	[illegible]
comp61312_c0_seq1.p1	sp|P64609|MLAE_SHIFL_Probable_phospholipid_ABC_transporter_permease_protein_mlaE_OS=Shigella_flexneri_GN=mlaE_PE=3_SV=1	2.00E-118	[illegible]	[illegible]
comp6134_c0_seq1.p1				
comp61365_c0_seq1.p1				
comp61375_c0_seq1.p2	sp|Q3YWK3|MDTL_SHISS_Multidrug_resistance_protein_MdtL_OS=Shigella_sonnei_(strain_Ss046)_GN=mdtL_PE=3_SV=1	4.00E-71	[illegible]	[illegible]
comp61404_c0_seq1.p1				
comp61449_c0_seq1.p1	sp|P23173|TNAB_ECOLI_Low_affinity_tryptophan_permease_OS=Escherichia_coli_(strain_K12)_GN=tnaB_PE=1_SV=1	2.00E-65	[illegible]	[illegible]
comp61492_c0_seq1.p1				
comp61494_c0_seq1.p1	sp|Q10101|RS7_SCHPO_40S_ribosomal_protein_S7_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=rps7_PE=1_SV=2	3.00E-29	[illegible]	[illegible]
comp61508_c0_seq1.p1				
comp61514_c0_seq1.p1	sp|P02931|OMPF_ECOLI_Outer_membrane_protein_F_OS=Escherichia_coli_(strain_K12)_GN=ompF_PE=1_SV=1	3.00E-145	[illegible]	[illegible]
comp61525_c0_seq1.p1				
comp61536_c0_seq1.p1				
comp61540_c0_seq1.p1	sp|P77243|PRPD_ECOLI_2-methylcitrate_dehydratase_OS=Escherichia_coli_(strain_K12)_GN=prpD_PE=1_SV=3	1.00E-109	[illegible]	[illegible]
comp61554_c0_seq1.p1	sp|B6IBG5|ASTB_ECOSE_N-succinylarginine_dihydrolase_OS=Escherichia_coli_(strain_SE11)_GN=astB_PE=3_SV=1	4.00E-90	[illegible]	[illegible]
comp61572_c0_seq1.p2	sp|Q4R4D3|RL10L_MACFA_60S_ribosomal_protein_L10-like_OS=Macaca_fascicularis_GN=RPL10L_PE=2_SV=1	3.00E-48	[illegible]	[illegible]
comp61618_c0_seq1.p1				
comp61620_c0_seq1.p1	sp|Q5JHG5|CPKA_PYRKO_Carbamate_kinase_OS=Pyrococcus_kodakaraensis_(strain_ATCC_BAA-918_/_JCM_12380_/_KOD1)_GN=cpkA_PE=3_SV=1	2.00E-43	[illegible]	[illegible]
comp61653_c0_seq1.p1				
comp61686_c0_seq1.p1	sp|P37344|PSPF_ECOLI_Psp_operon_transcriptional_activator_OS=Escherichia_coli_(strain_K12)_GN=pspF_PE=1_SV=2	9.00E-96	[illegible]	[illegible]
comp61702_c0_seq1.p1	sp|P31353|PMM_CANAL_Phosphomannomutase_OS=Candida_albicans_(strain_SC5314_/_ATCC_MYA-2876)_GN=PMM1_PE=1_SV=1	3.00E-55	[illegible]	[illegible]
comp61703_c0_seq1.p1	sp|O19072|OTC_PIG_Ornithine_carbamoyltransferase,_mitochondrial_(Fragment)_OS=Sus_scrofa_GN=OTC_PE=2_SV=1	4.00E-41	[illegible]	[illegible]
comp61742_c0_seq1.p1	sp|P62302|RS13_SOYBN_40S_ribosomal_protein_S13_OS=Glycine_max_GN=RPS13_PE=2_SV=1	3.00E-67	[illegible]	[illegible]
comp61763_c0_seq1.p1	sp|P76577|PBPC_ECOLI_Penicillin-binding_protein_1C_OS=Escherichia_coli_(strain_K12)_GN=pbpC_PE=3_SV=1	4.00E-118	[illegible]	[illegible]
comp61765_c0_seq1.p2				
comp61801_c0_seq1.p1	sp|P23842|YFEA_ECOLI_Uncharacterized_protein_YfeA_OS=Escherichia_coli_(strain_K12)_GN=yfeA_PE=2_SV=2	4.00E-129		
comp61812_c0_seq1.p1				
comp61831_c0_seq1.p1				
comp61832_c0_seq1.p1	sp|O15066|KIF3B_HUMAN_Kinesin-like_protein_KIF3B_OS=Homo_sapiens_GN=KIF3B_PE=1_SV=1	1.00E-41	[illegible]	[illegible]
comp61841_c0_seq1.p1	sp|P69794|PTQA_SHIFL_N,N'-diacetylchitobiose-specific_phosphotransferase_enzyme_IIA_component_OS=Shigella_flexneri_GN=chbA_PE=3_SV=1	4.00E-64	[illegible]	[illegible]
comp61854_c0_seq1.p1	sp|P37621|YHHS_ECOLI_UPF0226_protein_yhhS_OS=Escherichia_coli_(strain_K12)_GN=yhhS_PE=1_SV=2	4.00E-76	[illegible]	[illegible]
comp61860_c0_seq1.p1	sp|P51026|YI2A_ECOLX_Insertion_element_IS2A_uncharacterized_48.2_kDa_protein_OS=Escherichia_coli_PE=3_SV=2	1.00E-63	[illegible]	[illegible]
comp61875_c0_seq1.p1				
comp61898_c0_seq1.p1	sp|P0ABU6|ELBB_SHIFL_Enhancing_lycopene_biosynthesis_protein_2_OS=Shigella_flexneri_GN=elbB_PE=3_SV=1	4.00E-108	[illegible]	[illegible]
comp61915_c0_seq1.p1				
comp61922_c0_seq1.p1	sp|P90526|RS3_DICDI_40S_ribosomal_protein_S3_OS=Dictyostelium_discoideum_GN=rps3_PE=1_SV=1	9.00E-39	[illegible]	[illegible]
comp61939_c0_seq1.p1				
comp61951_c0_seq1.p1	sp|Q31WY3|HLDE_SHIBS_Bifunctional_protein_HldE_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=hldE_PE=3_SV=1	2.00E-148	[illegible]	[illegible]
comp61964_c0_seq1.p1				
comp61970_c0_seq1.p4				
comp61990_c0_seq1.p1	sp|P37650|BCSC_ECOLI_Cellulose_synthase_operon_protein_C_OS=Escherichia_coli_(strain_K12)_GN=bcsC_PE=1_SV=3	8.00E-85	[illegible]	[illegible]
comp62000_c0_seq1.p1				
comp62001_c0_seq1.p1				
comp62010_c0_seq1.p1	sp|P17078|RL35_RAT_60S_ribosomal_protein_L35_OS=Rattus_norvegicus_GN=Rpl35_PE=1_SV=3	3.00E-30	[illegible]	[illegible]
comp62014_c0_seq1.p2	sp|P76403|YEGQ_ECOLI_Uncharacterized_protease_yegQ_OS=Escherichia_coli_(strain_K12)_GN=yegQ_PE=3_SV=1	2.00E-122	[illegible]	[illegible]
comp62024_c0_seq1.p1				
comp62052_c0_seq1.p1	sp|P16431|HYCE_ECOLI_Formate_hydrogenlyase_subunit_5_OS=Escherichia_coli_(strain_K12)_GN=hycE_PE=1_SV=1	5.00E-116	[illegible]	[illegible]
comp62081_c0_seq1.p2	sp|Q91XQ0|DYH8_MOUSE_Dynein_heavy_chain_8,_axonemal_OS=Mus_musculus_GN=Dnahc8_PE=2_SV=2	1.00E-30	[illegible]	[illegible]
comp62094_c0_seq1.p1				
comp62095_c0_seq1.p1				
comp62096_c0_seq1.p1				
comp62110_c0_seq1.p1	sp|Q9JI39|ABCBA_MOUSE_ATP-binding_cassette_sub-family_B_member_10,_mitochondrial_OS=Mus_musculus_GN=Abcb10_PE=2_SV=1	1.00E-32	[illegible]	[illegible]

comp62128_c0_seq1.p1	sp|P33593|NIKD_ECOLI_Nickel_import_ATP-binding_protein_NikD_OS=Escherichia_coli_(strain_K12)_GN=nikD_PE=3_SV=2	5.00E-150
comp62128_c0_seq1.p3	sp|Q0SZJ3|NIKE_SHIF8_Nickel_import_ATP-binding_protein_NikE_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=nikE_PE=3_SV=1	1.00E-83
comp62132_c0_seq1.p1	sp|Q9AGA7|PTUCB_KLEPN_PTS_system_alpha-glucoside-specific_EIICB_component_OS=Klebsiella_pneumoniae_GN=aglA_PE=4_SV=1	1.00E-170
comp62150_c0_seq1.p1	sp|Q949Y0|UBP6_ARATH_Ubiquitin_carboxyl-terminal_hydrolase_6_OS=Arabidopsis_thaliana_GN=UBP6_PE=1_SV=1	1.00E-14
comp62165_c0_seq1.p1	sp|P0ADP1|YIGB_SHIFL_Uncharacterized_protein_yigB_OS=Shigella_flexneri_GN=yigB_PE=4_SV=1	2.00E-96
comp62178_c0_seq1.p1	sp|P09551|ARGT_ECOLI_Lysine-arginine-ornithine-binding_periplasmic_protein_OS=Escherichia_coli_(strain_K12)_GN=argT_PE=1_SV=3	3.00E-72
comp62182_c0_seq1.p2	sp|P0C0V0|DEGP_ECOLI_Periplasmic_serine_endoprotease_DegP_OS=Escherichia_coli_(strain_K12)_GN=degP_PE=1_SV=1	9.00E-38
comp62187_c0_seq1.p1	sp|P43671|PQIB_ECOLI_Paraquat-inducible_protein_B_OS=Escherichia_coli_(strain_K12)_GN=pqiB_PE=2_SV=2	8.00E-72
comp62238_c0_seq1.p1		
comp62249_c0_seq1.p1		
comp62306_c0_seq1.p1		
comp62311_c0_seq1.p1		
comp62316_c0_seq1.p1		
comp62330_c0_seq1.p1	sp|P33570|TKT2_ECOLI_Transketolase_2_OS=Escherichia_coli_(strain_K12)_GN=tktB_PE=1_SV=1	5.00E-164
comp62331_c0_seq1.p2	sp|Q08112|RS151_ARATH_40S_ribosomal_protein_S15-1_OS=Arabidopsis_thaliana_GN=RPS15A_PE=1_SV=1	1.00E-32
comp62336_c0_seq1.p1	sp|Q8VHE6|DYH5_MOUSE_Dynein_heavy_chain_5,_axonemal_OS=Mus_musculus_GN=Dnah5_PE=1_SV=2	4.00E-16
comp62379_c0_seq1.p1		
comp62393_c0_seq1.p1		
comp62406_c0_seq1.p1	sp|P04825|AMPN_ECOLI_Aminopeptidase_N_OS=Escherichia_coli_(strain_K12)_GN=pepN_PE=1_SV=2	6.00E-62
comp62413_c0_seq1.p2		
comp62417_c0_seq1.p2		
comp62439_c0_seq1.p1	sp|Q2MHE4|HT1_ARATH_Serine/threonine-protein_kinase_HT1_OS=Arabidopsis_thaliana_GN=HT1_PE=1_SV=1	9.00E-14
comp62448_c0_seq1.p1	sp|Q3Z4F1|LPTE_SHISS_LPS-assembly_lipoprotein_lptE_OS=Shigella_sonnei_(strain_Ss046)_GN=lptE_PE=3_SV=1	2.00E-94
comp62450_c0_seq1.p2	sp|P0DJ22|RL35A_TETTS_60S_ribosomal_protein_L35a_OS=Tetrahymena_thermophila_(strain_SB210)_GN=RPL35A_PE=1_SV=1	1.00E-26
comp62454_c0_seq1.p1	sp|Q557E0|HS7C2_DICDI_Heat_shock_cognate_70_kDa_protein_2_OS=Dictyostelium_discoideum_GN=hspE-1_PE=1_SV=1	3.00E-54
comp62479_c0_seq1.p1	sp|Q47153|FHIA_ECOLI_Putative_protein_fhiA_OS=Escherichia_coli_(strain_K12)_GN=fhiA_PE=5_SV=1	3.00E-111
comp62496_c0_seq1.p1	sp|P30143|YAAJ_ECOLI_Uncharacterized_transporter_yaaJ_OS=Escherichia_coli_(strain_K12)_GN=yaaJ_PE=3_SV=1	5.00E-67
comp6251_c0_seq1.p1	sp|P15977|MALQ_ECOLI_4-alpha-glucanotransferase_OS=Escherichia_coli_(strain_K12)_GN=malQ_PE=3_SV=2	6.00E-100
comp62519_c0_seq1.p1	sp|P37672|DLGD_ECOLI_2,3-diketo-L-gulonate_reductase_OS=Escherichia_coli_(strain_K12)_GN=dlgD_PE=1_SV=2	2.00E-162
comp62562_c0_seq1.p1	sp|P0ACU9|YJDC_SHIFL_HTH-type_transcriptional_regulator_yjdC_OS=Shigella_flexneri_GN=yjdC_PE=4_SV=1	3.00E-133
comp62574_c0_seq1.p1	sp|P00547|KHSE_ECOLI_Homoserine_kinase_OS=Escherichia_coli_(strain_K12)_GN=thrB_PE=1_SV=2	8.00E-105
comp62612_c0_seq1.p1		
comp62621_c0_seq1.p1	sp|P42593|FADH_ECOLI_2,4-dienoyl-CoA_reductase_[NADPH]_OS=Escherichia_coli_(strain_K12)_GN=fadH_PE=1_SV=3	5.00E-132
comp62628_c0_seq1.p1	sp|Q8TE73|DYH5_HUMAN_Dynein_heavy_chain_5,_axonemal_OS=Homo_sapiens_GN=DNAH5_PE=1_SV=3	8.00E-25
comp62633_c0_seq1.p1		
comp6265_c0_seq1.p2	sp|P76298|FLHA_ECOLI_Flagellar_biosynthesis_protein_flhA_OS=Escherichia_coli_(strain_K12)_GN=flhA_PE=1_SV=1	5.00E-60
comp62667_c0_seq1.p1	sp|P30011|NADC_ECOLI_Nicotinate-nucleotide_pyrophosphorylase_[carboxylating]_OS=Escherichia_coli_(strain_K12)_GN=nadC_PE=1_SV=3	1.00E-71
comp62671_c0_seq1.p2		
comp6268_c0_seq1.p1	sp|P39314|YTFF_ECOLI_Inner_membrane_protein_ytfF_OS=Escherichia_coli_(strain_K12)_GN=ytfF_PE=1_SV=2	2.00E-87
comp62680_c0_seq1.p2		
comp62696_c0_seq1.p1	sp|P37637|MDTF_ECOLI_Multidrug_resistance_protein_MdtF_OS=Escherichia_coli_(strain_K12)_GN=mdtF_PE=1_SV=1	4.00E-168
comp62733_c0_seq1.p1	sp|P76268|KDGR_ECOLI_Transcriptional_regulator_kdgR_OS=Escherichia_coli_(strain_K12)_GN=kdgR_PE=1_SV=1	6.00E-86
comp62756_c0_seq1.p1	sp|O04630|SYTM_ARATH_Threonine--tRNA_ligase,_mitochondrial_OS=Arabidopsis_thaliana_GN=THRRS_PE=2_SV=3	2.00E-35
comp62849_c0_seq1.p1	sp|P0CX28|RL44B_YEAST_60S_ribosomal_protein_L42-B_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=RPL42B_PE=1_SV=1	1.00E-36
comp62858_c0_seq1.p1		
comp62899_c0_seq1.p1	sp|P49180|RL35A_CAEEL_60S_ribosomal_protein_L35a_OS=Caenorhabditis_elegans_GN=rpl-33_PE=1_SV=3	6.00E-31
comp62912_c0_seq1.p1	sp|P66949|YFGC_SHIFL_TPR_repeat-containing_protein_yfgC_OS=Shigella_flexneri_GN=yfgC_PE=4_SV=1	3.00E-157
comp62923_c0_seq1.p1	sp|Q83M27|SYC_SHIFL_Cysteine--tRNA_ligase_OS=Shigella_flexneri_GN=cysS_PE=3_SV=1	1.00E-70
comp62929_c0_seq1.p1		
comp62949_c0_seq1.p1	sp|Q3Z2R1|CHEB_SHISS_Chemotaxis_response_regulator_protein-glutamate_methylesterase_OS=Shigella_sonnei_(strain_Ss046)_GN=cheB_PE=3_SV=1	1.00E-118
comp62954_c0_seq1.p1		
comp62983_c0_seq1.p1	sp|P16256|PANF_ECOLI_Sodium/pantothenate_symporter_OS=Escherichia_coli_(strain_K12)_GN=panF_PE=1_SV=2	3.00E-168
comp63001_c0_seq1.p1	sp|P0ACP4|FRUR_SHIFL_Fructose_repressor_OS=Shigella_flexneri_GN=fruR_PE=3_SV=1	9.00E-79
comp63026_c0_seq1.p1	sp|P39384|YJIM_ECOLI_Uncharacterized_protein_yjiM_OS=Escherichia_coli_(strain_K12)_GN=yjiM_PE=4_SV=2	2.00E-57
comp63053_c0_seq1.p1		
comp63067_c0_seq1.p1	sp|P07822|FHUD_ECOLI_Iron(3+)-hydroxamate-binding_protein_fhuD_OS=Escherichia_coli_(strain_K12)_GN=fhuD_PE=1_SV=3	7.00E-146
comp63074_c0_seq1.p1		
comp63078_c0_seq1.p2	sp|P34788|RS18_ARATH_40S_ribosomal_protein_S18_OS=Arabidopsis_thaliana_GN=RPS18A_PE=1_SV=1	8.00E-46
comp63087_c0_seq1.p1	sp|P0AB11|YMBA_SHIFL_Uncharacterized_lipoprotein_ymbA_OS=Shigella_flexneri_GN=ymbA_PE=4_SV=2	7.00E-65
comp63118_c0_seq1.p1	sp|P03841|MALM_ECOLI_Maltose_operon_periplasmic_protein_OS=Escherichia_coli_(strain_K12)_GN=malM_PE=4_SV=1	1.00E-41
comp63136_c0_seq1.p1	sp|Q3Z4Y9|DXS_SHISS_1-deoxy-D-xylulose-5-phosphate_synthase_OS=Shigella_sonnei_(strain_Ss046)_GN=dxs_PE=3_SV=1	9.00E-78
comp63146_c0_seq1.p1		
comp63157_c0_seq1.p1	sp|Q0DJ99|COPD2_ORYSJ_Coatomer_subunit_delta-2_OS=Oryza_sativa_subsp._japonica_GN=Os05g0311000_PE=2_SV=1	3.00E-36
comp63159_c0_seq1.p1		
comp63160_c0_seq1.p1	sp|P0ADQ2|YIID_ECOLI_Uncharacterized_protein_yiiD_OS=Escherichia_coli_(strain_K12)_GN=yiiD_PE=4_SV=1	3.00E-178
comp63173_c0_seq1.p1	sp|P0A699|UVRA_SHIFL_UvrABC_system_protein_A_OS=Shigella_flexneri_GN=uvrA_PE=3_SV=1	2.00E-147
comp63175_c0_seq1.p1		
comp63193_c0_seq1.p1		
comp63287_c0_seq1.p1		
comp63291_c0_seq1.p1	sp|P36110|PRY2_YEAST_Protein_PRY2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PRY2_PE=2_SV=1	5.00E-17
comp63296_c0_seq1.p1	sp|Q83LK8|RUTD_SHIFL_Putative_aminoacrylate_hydrolase_RutD_OS=Shigella_flexneri_GN=rutD_PE=3_SV=4	3.00E-67
comp63339_c0_seq1.p1	sp|Q3Z053|GCH1_SHISS_GTP_cyclohydrolase_1_OS=Shigella_sonnei_(strain_Ss046)_GN=folE_PE=3_SV=1	7.00E-85
comp63340_c0_seq1.p1	sp|P77374|YNFE_ECOLI_Putative_dimethyl_sulfoxide_reductase_chain_ynfE_OS=Escherichia_coli_(strain_K12)_GN=ynfE_PE=3_SV=1	3.00E-109
comp63357_c0_seq1.p1	sp|P45552|YHFZ_ECOLI_Uncharacterized_protein_yhfZ_OS=Escherichia_coli_(strain_K12)_GN=yhfZ_PE=4_SV=3	2.00E-106
comp63359_c0_seq1.p1		
comp63396_c0_seq1.p1	sp|Q9LK16|AMT15_ARATH_Putative_ammonium_transporter_1_member_5_OS=Arabidopsis_thaliana_GN=AMT1-5_PE=3_SV=1	3.00E-23
comp63412_c0_seq1.p1	sp|P0AFK0|PMBA_ECOLI_Protein_pmbA_OS=Escherichia_coli_(strain_K12)_GN=pmbA_PE=1_SV=1	0
comp63414_c0_seq1.p2	sp|P0CK95|ACFD_ECOLI_Putative_lipoprotein_AcfD_homolog_OS=Escherichia_coli_(strain_K12)_GN=yghJ_PE=4_SV=1	2.00E-61
comp63432_c0_seq1.p2		
comp63433_c0_seq1.p1		
comp63446_c0_seq1.p1	sp|P42730|CLPB1_ARATH_Chaperone_protein_ClpB1_OS=Arabidopsis_thaliana_GN=CLPB1_PE=1_SV=2	3.00E-36
comp63450_c0_seq1.p1		
comp63470_c0_seq1.p1		
comp63494_c0_seq1.p1		
comp63532_c0_seq1.p2	sp|Q8VYK6|RS43_ARATH_40S_ribosomal_protein_S4-3_OS=Arabidopsis_thaliana_GN=RPS4D_PE=2_SV=2	2.00E-53
comp63541_c0_seq1.p1	sp|P77650|HCAD_ECOLI_3-phenylpropionate/cinnamic_acid_dioxygenase_ferredoxin--NAD(+)_reductase_component_OS=Escherichia_coli_(strain_K12)_GN=hcaD_PE=1_SV=1	5.00E-94
comp63555_c0_seq1.p1	sp|Q3YZE4|GLK_SHISS_Glucokinase_OS=Shigella_sonnei_(strain_Ss046)_GN=glk_PE=3_SV=1	2.00E-111
comp63597_c0_seq1.p1	sp|P31434|XYLS_ECOLI_Alpha-xylosidase_OS=Escherichia_coli_(strain_K12)_GN=yicI_PE=1_SV=2	7.00E-130
comp63611_c0_seq1.p1	sp|B1LMS6|FDHE_ECOSM_Protein_FdhE_OS=Escherichia_coli_(strain_SMS-3-5_/_SECEC)_GN=fdhE_PE=3_SV=1	3.00E-149
comp63612_c0_seq1.p1	sp|Q0DBL6|HFC2B_ORYSJ_Heat_stress_transcription_factor_C-2b_OS=Oryza_sativa_subsp._japonica_GN=HSFC2B_PE=2_SV=1	6.00E-12
comp63627_c0_seq1.p1	sp|O34893|YNGF_BACSU_Putative_enoyl-CoA_hydratase/isomerase_yngF_OS=Bacillus_subtilis_GN=yngF_PE=3_SV=1	3.00E-15
comp63648_c0_seq1.p2	sp|O15883|RL27A_TRYBB_60S_ribosomal_protein_L27a_OS=Trypanosoma_brucei_brucei_GN=RPL27A_PE=2_SV=1	2.00E-60
comp63657_c0_seq1.p1		
comp63662_c0_seq1.p1	sp|P33026|SETB_ECOLI_Sugar_efflux_transporter_B_OS=Escherichia_coli_(strain_K12)_GN=setB_PE=1_SV=1	1.00E-82
comp63675_c0_seq1.p1		
comp63679_c0_seq1.p2	sp|P49691|RL4B_ARATH_60S_ribosomal_protein_L4-2_OS=Arabidopsis_thaliana_GN=RPL4D_PE=1_SV=2	2.00E-14
comp63695_c0_seq1.p1	sp|Q96533|ADHX_ARATH_Alcohol_dehydrogenase_class-3_OS=Arabidopsis_thaliana_GN=ADH2_PE=1_SV=2	4.00E-37
comp63697_c0_seq1.p1	sp|P18200|PGPA_ECOLI_Phosphatidylglycerophosphatase_A_OS=Escherichia_coli_(strain_K12)_GN=pgpA_PE=1_SV=2	4.00E-75
comp63699_c0_seq1.p1	sp|Q31Z86|EFEB_SHIBS_Deferrochelatase/peroxidase_EfeB_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=efeB_PE=3_SV=1	2.00E-134
comp63706_c0_seq1.p1	sp|Q9XGZ9|P2C72_ARATH_Probable_protein_phosphatase_2C_72_OS=Arabidopsis_thaliana_GN=At5g26010_PE=2_SV=2	3.00E-12
comp63743_c0_seq1.p1	sp|O13828|DCP2_SCHPO_mRNA_decapping_complex_subunit_2_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=dcp2_PE=1_SV=1	2.00E-14
comp63779_c0_seq1.p1		
comp63782_c0_seq1.p2	sp|P11874|RL7_DICDI_60S_ribosomal_protein_L7_OS=Dictyostelium_discoideum_GN=rpl7_PE=1_SV=3	4.00E-33
comp63796_c0_seq1.p2		
comp63855_c0_seq1.p1		
comp63868_c0_seq1.p1	sp|P32721|ALSA_ECOLI_D-allose_import_ATP-binding_protein_AlsA_OS=Escherichia_coli_(strain_K12)_GN=alsA_PE=3_SV=2	1.00E-66
comp63890_c0_seq1.p1		
comp63921_c0_seq1.p1	sp|P0A8H7|YIHI_SHIFL_Der_GTPase-activating_protein_YihI_OS=Shigella_flexneri_GN=yihI_PE=3_SV=1	8.00E-81
comp63959_c0_seq1.p1		
comp63968_c0_seq1.p1		
comp64017_c0_seq1.p1	sp|Q3Z4S5|KAD_SHISS_Adenylate_kinase_OS=Shigella_sonnei_(strain_Ss046)_GN=adk_PE=3_SV=1	3.00E-68
comp64070_c0_seq1.p1		
comp64076_c0_seq1.p1	sp|P59393|SELD_SHIFL_Selenide,_water_dikinase_OS=Shigella_flexneri_GN=selD_PE=3_SV=1	0
comp64079_c0_seq1.p1		
comp64086_c0_seq1.p1	sp|Q96MT7|WDR52_HUMAN_WD_repeat-containing_protein_52_OS=Homo_sapiens_GN=WDR52_PE=1_SV=1	2.00E-20
comp64087_c0_seq1.p1		
comp64096_c0_seq1.p1	sp|Q7JQD3|GELS1_LUMTE_Gelsolin-like_protein_1_OS=Lumbricus_terrestris_GN=AM_PE=1_SV=1	9.00E-37
comp64115_c0_seq1.p1		
comp64133_c0_seq1.p1	sp|P04846|NLPA_ECOLI_Lipoprotein_28_OS=Escherichia_coli_(strain_K12)_GN=nlpA_PE=1_SV=1	2.00E-78
comp64144_c0_seq1.p1	sp|P39285|YJEP_ECOLI_Uncharacterized_MscS_family_protein_YjeP_OS=Escherichia_coli_(strain_K12)_GN=yjeP_PE=3_SV=3	8.00E-145
comp64145_c0_seq1.p1		
comp64167_c0_seq1.p1		
comp64179_c0_seq1.p1	sp|Q0T7N0|BETA_SHIF8_Choline_dehydrogenase_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=betA_PE=3_SV=1	3.00E-169
comp64189_c0_seq1.p1	sp|Q329V7|GPPA_SHIDS_Guanosine-5'-triphosphate,3'-diphosphate_pyrophosphatase_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=gppA_PE=3_SV=1	9.00E-85
comp64232_c0_seq1.p1	sp|Q83LP0|MSBA_SHIFL_Lipid_A_export_ATP-binding/permease_protein_MsbA_OS=Shigella_flexneri_GN=msbA_PE=3_SV=1	2.00E-66
comp64246_c0_seq1.p1		
comp64267_c0_seq1.p1	sp|Q7LL04|YQK1_SCHPO_UPF0676_protein_C1494.01_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPCC1494.01_PE=3_SV=2	8.00E-14
comp64270_c0_seq1.p1	sp|P10121|FTSY_ECOLI_Signal_recognition_particle_receptor_FtsY_OS=Escherichia_coli_(strain_K12)_GN=ftsY_PE=1_SV=1	5.00E-169
comp64291_c0_seq1.p1		
comp64307_c0_seq1.p1	sp|P50466|AER_ECOLI_Aerotaxis_receptor_OS=Escherichia_coli_(strain_K12)_GN=aer_PE=1_SV=1	1.00E-94
comp64321_c0_seq1.p1		
comp64341_c0_seq1.p1		
comp64346_c0_seq1.p1	sp|P76540|EUTK_ECOLI_Ethanolamine_utilization_protein_EutK_OS=Escherichia_coli_(strain_K12)_GN=eutK_PE=1_SV=2	1.00E-46
comp64357_c0_seq1.p1		
comp64366_c0_seq1.p1		
comp64375_c0_seq1.p1	sp|Q3Z3S5|RLMC_SHISS_23S_rRNA_(uracil(747)-C(5))-methyltransferase_RlmC_OS=Shigella_sonnei_(strain_Ss046)_GN=rlmC_PE=3_SV=1	2.00E-135
comp64388_c0_seq1.p1	sp|P46837|YHGF_ECOLI_Protein_yhgF_OS=Escherichia_coli_(strain_K12)_GN=yhgF_PE=1_SV=3	0
comp64414_c0_seq1.p1	sp|P09373|PFLB_ECOLI_Formate_acetyltransferase_1_OS=Escherichia_coli_(strain_K12)_GN=pflB_PE=1_SV=2	4.00E-140
comp64423_c0_seq1.p1	sp|P0AB80|ILVE_ECOLI_Branched-chain-amino-acid_aminotransferase_OS=Escherichia_coli_(strain_K12)_GN=ilvE_PE=1_SV=2	3.00E-84
comp64442_c0_seq1.p1		
comp64471_c0_seq1.p1		
comp64498_c0_seq1.p1	sp|P77510|DPIB_ECOLI_Sensor_histidine_kinase_DpiB_OS=Escherichia_coli_(strain_K12)_GN=dpiB_PE=1_SV=1	3.00E-81
comp64508_c0_seq1.p1		
comp64514_c0_seq1.p1		
comp64529_c0_seq1.p1	sp|Q09JW2|RL17_ARGMO_60S_ribosomal_protein_L17_OS=Argas_monolakensis_GN=RpL17_PE=2_SV=1	3.00E-44
comp64540_c0_seq1.p1	sp|P0AC87|PHSG_SHIFL_Glycogen_phosphorylase_OS=Shigella_flexneri_GN=glgP_PE=3_SV=1	4.00E-116
comp64580_c0_seq1.p1		
comp64601_c0_seq1.p1	sp|P0AEJ5|ENVZ_SHIFL_Osmolarity_sensor_protein_EnvZ_OS=Shigella_flexneri_GN=envZ_PE=1_SV=1	5.00E-137
comp64610_c0_seq1.p1		
comp64653_c0_seq1.p1		
comp64654_c0_seq1.p1		
comp64668_c0_seq1.p1	sp|P54609|CD48A_ARATH_Cell_division_control_protein_48_homolog_A_OS=Arabidopsis_thaliana_GN=CDC48A_PE=1_SV=1	1.00E-92
comp6467_c0_seq1.p1		
comp64670_c0_seq1.p1	sp|P23878|FEPC_ECOLI_Ferric_enterobactin_transport_ATP-binding_protein_FepC_OS=Escherichia_coli_(strain_K12)_GN=fepC_PE=3_SV=2	4.00E-107
comp64681_c0_seq1.p2	sp|Q3V384|LACE1_MOUSE_Lactation_elevated_protein_1_OS=Mus_musculus_GN=Lace1_PE=2_SV=1	1.00E-18
comp64683_c0_seq1.p2	sp|Q31YN0|RLMI_SHIBS_Ribosomal_RNA_large_subunit_methyltransferase_I_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=rlmI_PE=3_SV=2	1.00E-81
comp64696_c0_seq1.p1	sp|Q31YW6|END4_SHIBS_Probable_endonuclease_4_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=nfo_PE=3_SV=1	3.00E-84
comp64704_c0_seq1.p1		
comp64710_c0_seq1.p1		
comp64726_c0_seq1.p1	sp|P32703|YJCE_ECOLI_Uncharacterized_Na(+)/H(+)_exchanger_yjcE_OS=Escherichia_coli_(strain_K12)_GN=yjcE_PE=3_SV=1	2.00E-51
comp64728_c0_seq1.p1	sp|Q83IH7|OPGB_SHIFL_Phosphoglycerol_transferase_I_OS=Shigella_flexneri_GN=mdoB_PE=3_SV=1	3.00E-73
comp64740_c0_seq1.p1	sp|P25519|HFLX_ECOLI_GTPase_HflX_OS=Escherichia_coli_(strain_K12)_GN=hflX_PE=1_SV=3	2.00E-103
comp64749_c0_seq1.p2	sp|Q9TV62|MYH4_PIG_Myosin-4_OS=Sus_scrofa_GN=MYH4_PE=2_SV=1	1.00E-12
comp64754_c0_seq1.p1	sp|P41234|ABCA2_MOUSE_ATP-binding_cassette_sub-family_A_member_2_OS=Mus_musculus_GN=Abca2_PE=1_SV=4	2.00E-15
comp64756_c0_seq1.p1	sp|P32710|NRFE_ECOLI_Cytochrome_c-type_biogenesis_protein_NrfE_OS=Escherichia_coli_(strain_K12)_GN=nrfE_PE=3_SV=2	1.00E-122
comp64759_c0_seq1.p1		
comp64768_c0_seq1.p3	sp|Q1R6F4|OBG_ECOUT_GTPase_obg_OS=Escherichia_coli_(strain_UTI89_/_UPEC)_GN=obg_PE=3_SV=1	2.00E-138
comp64770_c0_seq1.p1		
comp64782_c0_seq1.p2	sp|P25743|YCHE_ECOLI_UPF0056_membrane_protein_ychE_OS=Escherichia_coli_(strain_K12)_GN=ychE_PE=3_SV=2	4.00E-60
comp64839_c0_seq1.p1	sp|P69741|MBHT_ECOLI_Hydrogenase-2_small_chain_OS=Escherichia_coli_(strain_K12)_GN=hybO_PE=1_SV=1	2.00E-77
comp64897_c0_seq1.p1		
comp64901_c0_seq1.p1		
comp64918_c0_seq1.p1	sp|P02918|PBPA_ECOLI_Penicillin-binding_protein_1A_OS=Escherichia_coli_(strain_K12)_GN=mrcA_PE=1_SV=1	1.00E-79
comp64926_c0_seq1.p1	sp|Q39757|1433_FUCVE_14-3-3-like_protein_OS=Fucus_vesiculosus_PE=2_SV=1	2.00E-35
comp64946_c0_seq1.p1		
comp64948_c0_seq1.p1		
comp64973_c0_seq1.p1		
comp65007_c0_seq1.p1		
comp65028_c0_seq1.p1	sp|P06720|AGAL_ECOLI_Alpha-galactosidase_OS=Escherichia_coli_(strain_K12)_GN=melA_PE=1_SV=1	1.00E-119
comp65036_c0_seq1.p1	sp|Q3Z503|TGT_SHISS_Queuine_tRNA-ribosyltransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=tgt_PE=3_SV=1	4.00E-98
comp65043_c0_seq1.p1		
comp65053_c0_seq1.p1		
comp65059_c0_seq1.p1		
comp65064_c0_seq1.p1	sp|Q9FEL8|LAX1_MEDTR_Auxin_transporter-like_protein_1_OS=Medicago_truncatula_GN=LAX1_PE=2_SV=1	2.00E-26
comp65085_c0_seq1.p1		
comp65087_c0_seq1.p1	sp|C0LGQ5|GSO1_ARATH_LRR_receptor-like_serine/threonine-protein_kinase_GSO1_OS=Arabidopsis_thaliana_GN=GSO1_PE=2_SV=1	6.00E-22
comp65112_c0_seq1.p2	sp|Q112Z5|ATPD_TRIEI_ATP_synthase_subunit_delta_OS=Trichodesmium_erythraeum_(strain_IMS101)_GN=atpH_PE=3_SV=1	9.00E-13
comp65115_c0_seq1.p1	sp|P0A3B4|TYPA_SHIFL_GTP-binding_protein_TypA/BipA_OS=Shigella_flexneri_GN=typA_PE=3_SV=1	1.00E-60
comp65116_c0_seq1.p1	sp|Q16960|DYI3_ANTCR_Dynein_intermediate_chain_3,_ciliary_OS=Anthocidaris_crassispina_PE=2_SV=1	2.00E-11
comp6513_c0_seq1.p1	sp|Q46812|SSNA_ECOLI_Protein_SsnA_OS=Escherichia_coli_(strain_K12)_GN=ssnA_PE=1_SV=2	3.00E-106
comp65172_c0_seq1.p2	sp|P00452|RIR1_ECOLI_Ribonucleoside-diphosphate_reductase_1_subunit_alpha_OS=Escherichia_coli_(strain_K12)_GN=nrdA_PE=1_SV=2	4.00E-80
comp65180_c0_seq1.p1		
comp65188_c0_seq1.p1	sp|Q9FM01|UGDH2_ARATH_Probable_UDP-glucose_6-dehydrogenase_2_OS=Arabidopsis_thaliana_GN=UGD2_PE=2_SV=1	2.00E-89
comp65200_c0_seq1.p2		
comp65216_c0_seq1.p2	sp|P49211|RL321_ARATH_60S_ribosomal_protein_L32-1_OS=Arabidopsis_thaliana_GN=RPL32A_PE=2_SV=2	3.00E-44
comp65218_c0_seq1.p1		
comp65224_c0_seq1.p1		
comp65247_c0_seq1.p1		
comp65249_c0_seq1.p1	sp|Q3Z3J0|SYN_SHISS_Asparagine--tRNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=asnS_PE=3_SV=1	1.00E-83
comp65298_c0_seq1.p1		
comp65333_c0_seq1.p1		
comp65344_c0_seq1.p2	sp|O22644|RL23A_FRIAG_60S_ribosomal_protein_L23A_OS=Fritillaria_agrestis_GN=RPL23A_PE=2_SV=1	1.00E-56
comp65373_c0_seq1.p1		
comp65375_c0_seq1.p1		
comp65423_c0_seq1.p1		
comp65454_c0_seq1.p1	sp|Q6NW85|ARI1L_DANRE_E3_ubiquitin-protein_ligase_arih1l_OS=Danio_rerio_GN=arih1l_PE=2_SV=1	7.00E-11
comp65478_c0_seq1.p1		
comp65493_c0_seq1.p1	sp|Q83KW2|SUFB_SHIFL_FeS_cluster_assembly_protein_sufB_OS=Shigella_flexneri_GN=sufB_PE=3_SV=1	6.00E-81
comp65506_c0_seq1.p2	sp|P27303|EMRA_ECOLI_Multidrug_resistance_protein_A_OS=Escherichia_coli_(strain_K12)_GN=emrA_PE=3_SV=2	8.00E-64
comp65550_c0_seq1.p1		
comp65572_c0_seq1.p1	sp|B1LLM9|NUON_ECOSM_NADH-quinone_oxidoreductase_subunit_N_OS=Escherichia_coli_(strain_SMS-3-5_/_SECEC)_GN=nuoN_PE=3_SV=1	2.00E-106
comp65595_c0_seq1.p1		
comp65625_c0_seq1.p1	sp|Q3YW11|KGUA_SHISS_Guanylate_kinase_OS=Shigella_sonnei_(strain_Ss046)_GN=gmk_PE=3_SV=1	5.00E-74
comp65627_c0_seq1.p1	sp|A7SLW1|BCAT_NEMVE_Branched-chain-amino-acid_aminotransferase_OS=Nematostella_vectensis_GN=v1g246094_PE=3_SV=1	3.00E-34
comp65631_c0_seq1.p1	sp|P52094|HISQ_ECOLI_Histidine_transport_system_permease_protein_hisQ_OS=Escherichia_coli_(strain_K12)_GN=hisQ_PE=1_SV=2	8.00E-58
comp65640_c0_seq1.p1		
comp65660_c0_seq1.p2		
comp65687_c0_seq1.p1		
comp65700_c0_seq1.p1		
comp65740_c0_seq1.p1		
comp65776_c0_seq1.p1		
comp65819_c0_seq1.p1		
comp65824_c0_seq1.p1	sp|Q3Z5R8|MURC_SHISS_UDP-N-acetylmuramate--L-alanine_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=murC_PE=3_SV=1	7.00E-111
comp65837_c0_seq1.p1	sp|P46825|KLC_LOLPE_Kinesin_light_chain_OS=Loligo_pealeii_PE=2_SV=1	2.00E-19
comp65840_c0_seq1.p1		
comp65892_c0_seq1.p1	sp|P0C0V0|DEGP_ECOLI_Periplasmic_serine_endoprotease_DegP_OS=Escherichia_coli_(strain_K12)_GN=degP_PE=1_SV=1	1.00E-90
comp65894_c0_seq1.p1	sp|Q06034|MDR1_LEIEN_Multidrug_resistance_protein_1_OS=Leishmania_enriettii_GN=MDR1_PE=3_SV=1	5.00E-29
comp65901_c0_seq1.p1	sp|Q83KC1|CINAL_SHIFL_CinA-like_protein_OS=Shigella_flexneri_GN=SF2328_PE=3_SV=1	7.00E-64
comp65935_c0_seq1.p2	sp|Q46834|YGHF_ECOLI_Putative_general_secretion_pathway_protein_C-type_yghF_OS=Escherichia_coli_(strain_K12)_GN=yghF_PE=5_SV=1	8.00E-67
comp65956_c0_seq1.p2		
comp65957_c0_seq1.p1	sp|P77434|ALAC_ECOLI_Glutamate-pyruvate_aminotransferase_AlaC_OS=Escherichia_coli_(strain_K12)_GN=alaC_PE=1_SV=1	5.00E-102
comp65967_c0_seq1.p2		
comp66014_c0_seq1.p2	sp|Q2HFP1|IF4A_CHAGB_ATP-dependent_RNA_helicase_eIF4A_OS=Chaetomium_globosum_(strain_ATCC_6205_/_CBS_148.51_/_DSM_1962_/_NBRC_6347_/_NRRL_1970)_GN=TIF1_PE=3_SV=1	1.00E-72
comp66039_c0_seq1.p1	sp|P0ADX9|RSMD_ECOLI_Ribosomal_RNA_small_subunit_methyltransferase_D_OS=Escherichia_coli_(strain_K12)_GN=rsmD_PE=1_SV=1	2.00E-85
comp66042_c0_seq1.p1	sp|P06612|TOP1_ECOLI_DNA_topoisomerase_1_OS=Escherichia_coli_(strain_K12)_GN=topA_PE=1_SV=2	1.00E-67
comp66061_c0_seq1.p1	sp|P0AE82|CPXA_ECOLI_Sensor_protein_CpxA_OS=Escherichia_coli_(strain_K12)_GN=cpxA_PE=1_SV=1	1.00E-168
comp66097_c0_seq1.p1	sp|P77211|CUSC_ECOLI_Cation_efflux_system_protein_CusC_OS=Escherichia_coli_(strain_K12)_GN=cusC_PE=1_SV=1	5.00E-73
comp66101_c0_seq1.p1	sp|O49627|ISU1_ARATH_Iron-sulfur_cluster_assembly_protein_1_OS=Arabidopsis_thaliana_GN=ISU1_PE=2_SV=1	7.00E-67
comp66103_c0_seq1.p1	sp|P0ADC3|LOLC_ECOLI_Lipoprotein-releasing_system_transmembrane_protein_lolC_OS=Escherichia_coli_(strain_K12)_GN=lolC_PE=1_SV=1	1.00E-43
comp66108_c0_seq1.p2	sp|Q9SRS9|CHIP_ARATH_E3_ubiquitin-protein_ligase_CHIP_OS=Arabidopsis_thaliana_GN=CHIP_PE=1_SV=1	3.00E-13
comp66109_c0_seq1.p1		
comp66166_c0_seq1.p1		
comp66195_c0_seq1.p1		
comp66323_c0_seq1.p1	sp|P0AE21|AMPM_SHIFL_Methionine_aminopeptidase_OS=Shigella_flexneri_GN=map_PE=3_SV=1	5.00E-90
comp66339_c0_seq1.p1		
comp66470_c0_seq1.p1	sp|Q9VZ23|RAN_DROME_GTP-binding_nuclear_protein_Ran_OS=Drosophila_melanogaster_GN=ran_PE=1_SV=1	2.00E-72
comp66505_c0_seq1.p1		
comp66561_c0_seq1.p1		
comp66567_c0_seq1.p1	sp|Q3YUZ0|THIC_SHISS_Phosphomethylpyrimidine_synthase_OS=Shigella_sonnei_(strain_Ss046)_GN=thiC_PE=3_SV=1	2.00E-85
comp66573_c0_seq1.p2		
comp66586_c0_seq1.p1	sp|Q3YUY7|DCUP_SHISS_Uroporphyrinogen_decarboxylase_OS=Shigella_sonnei_(strain_Ss046)_GN=hemE_PE=3_SV=1	2.00E-132
comp66593_c0_seq1.p1		
comp66639_c0_seq1.p1	sp|Q3YXW7|GCSP_SHISS_Glycine_dehydrogenase_[decarboxylating]_OS=Shigella_sonnei_(strain_Ss046)_GN=gcvP_PE=3_SV=1	2.00E-90
comp66648_c0_seq1.p1	sp|P09835|UHPB_ECOLI_Sensor_protein_uhpB_OS=Escherichia_coli_(strain_K12)_GN=uhpB_PE=3_SV=3	6.00E-75
comp66681_c0_seq1.p2		
comp66786_c0_seq1.p1		
comp66800_c0_seq1.p1		
comp6681_c0_seq1.p1		
comp66817_c0_seq1.p1		
comp66823_c0_seq1.p1		
comp66847_c0_seq1.p1	sp|Q3Z5A4|DPO4_SHISS_DNA_polymerase_IV_OS=Shigella_sonnei_(strain_Ss046)_GN=dinB_PE=3_SV=1	1.00E-74
comp66916_c0_seq1.p1		
comp66944_c0_seq1.p1		
comp66951_c0_seq1.p2	sp|B1LPC1|GRPE_ECOSM_Protein_grpE_OS=Escherichia_coli_(strain_SMS-3-5_/_SECEC)_GN=grpE_PE=3_SV=1	2.00E-77
comp67027_c0_seq1.p1		
comp67037_c0_seq1.p1		
comp67052_c0_seq1.p1	sp|P77668|HYFI_ECOLI_Hydrogenase-4_component_I_OS=Escherichia_coli_(strain_K12)_GN=hyfI_PE=3_SV=1	5.00E-109
comp67088_c0_seq1.p1	sp|P04709|ADT1_MAIZE_ADP,ATP_carrier_protein_1,_mitochondrial_OS=Zea_mays_GN=ANT1_PE=2_SV=3	2.00E-59
comp67097_c0_seq1.p2	sp|Q32DK7|PRMB_SHIDS_50S_ribosomal_protein_L3_glutamine_methyltransferase_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=prmB_PE=3_SV=1	2.00E-45
comp67157_c0_seq1.p1	sp|Q9AGA6|AGLB_KLEPN_6-phospho-alpha-glucosidase_OS=Klebsiella_pneumoniae_GN=aglB_PE=1_SV=1	1.00E-73
comp6717_c0_seq1.p2		
comp67201_c0_seq1.p2	sp|O14134|ELF1_SCHPO_mRNA_export_factor_elf1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=elf1_PE=1_SV=1	5.00E-43
comp6731_c0_seq1.p1	sp|Q3Z3Q4|MACB_SHISS_Macrolide_export_ATP-binding/permease_protein_MacB_OS=Shigella_sonnei_(strain_Ss046)_GN=macB_PE=3_SV=1	6.00E-74
comp67403_c0_seq1.p1		
comp67408_c0_seq1.p1		
comp67412_c0_seq1.p1		
comp67414_c0_seq1.p1		
comp67418_c0_seq1.p1	sp|Q8JHJ1|RL35_DANRE_60S_ribosomal_protein_L35_OS=Danio_rerio_GN=rpl35_PE=2_SV=1	3.00E-19
comp67430_c0_seq1.p1	sp|P27253|SCPA_ECOLI_Methylmalonyl-CoA_mutase_OS=Escherichia_coli_(strain_K12)_GN=scpA_PE=1_SV=2	6.00E-72
comp67436_c0_seq1.p1	sp|Q9C0G6|DYH6_HUMAN_Dynein_heavy_chain_6,_axonemal_OS=Homo_sapiens_GN=DNAH6_PE=1_SV=3	5.00E-36
comp67439_c0_seq1.p1		
comp67454_c0_seq1.p1	sp|P63738|CARB_SHIFL_Carbamoyl-phosphate_synthase_large_chain_OS=Shigella_flexneri_GN=carB_PE=3_SV=2	2.00E-85
comp67482_c0_seq1.p1	sp|P31549|THIP_ECOLI_Thiamine_transport_system_permease_protein_thiP_OS=Escherichia_coli_(strain_K12)_GN=thiP_PE=3_SV=2	1.00E-79
comp67494_c0_seq1.p1	sp|P20605|FIC_ECOLI_Probable_adenosine_monophosphate-protein_transferase_fic_OS=Escherichia_coli_(strain_K12)_GN=fic_PE=1_SV=1	3.00E-81
comp67499_c0_seq1.p1	sp|P0AE90|CPXR_SHIFL_Transcriptional_regulatory_protein_CpxR_OS=Shigella_flexneri_GN=cpxR_PE=3_SV=1	3.00E-73
comp67507_c0_seq1.p1		
comp67510_c0_seq1.p1	sp|O22254|RL181_ARATH_Putative_60S_ribosomal_protein_L18-1_OS=Arabidopsis_thaliana_GN=RPL18A_PE=2_SV=3	3.00E-42
comp67530_c0_seq1.p1		
comp67531_c0_seq1.p1	sp|Q3YXI5|UPPP_SHISS_Undecaprenyl-diphosphatase_OS=Shigella_sonnei_(strain_Ss046)_GN=uppP_PE=3_SV=1	7.00E-83
comp67540_c0_seq1.p1	sp|P37680|SGBE_ECOLI_L-ribulose-5-phosphate_4-epimerase_SgbE_OS=Escherichia_coli_(strain_K12)_GN=sgbE_PE=1_SV=1	2.00E-138
comp67557_c0_seq1.p1	sp|Q46839|GLCA_ECOLI_Glycolate_permease_glcA_OS=Escherichia_coli_(strain_K12)_GN=glcA_PE=1_SV=1	1.00E-170
comp67575_c0_seq1.p1	sp|P75749|YBGP_ECOLI_Uncharacterized_fimbrial_chaperone_ybgP_OS=Escherichia_coli_(strain_K12)_GN=ybgP_PE=3_SV=1	5.00E-71
comp67586_c0_seq1.p1		
comp67593_c0_seq1.p1		
comp67599_c0_seq1.p1	sp|Q31YS6|MUKB_SHIBS_Chromosome_partition_protein_MukB_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=mukB_PE=3_SV=1	1.00E-84
comp67600_c0_seq1.p1		
comp67605_c0_seq1.p1		
comp67622_c0_seq1.p2		
comp67626_c0_seq1.p1	sp|P0AFF9|NUSA_SHIFL_Transcription_elongation_protein_nusA_OS=Shigella_flexneri_GN=nusA_PE=3_SV=1	3.00E-170
comp67630_c0_seq1.p1		
comp67633_c0_seq1.p2		
comp67634_c0_seq1.p1	sp|P77562|YAIW_ECOLI_Uncharacterized_protein_yaiW_OS=Escherichia_coli_(strain_K12)_GN=yaiW_PE=4_SV=1	0
comp67637_c0_seq1.p1	sp|Q3YWT2|EFG_SHISS_Elongation_factor_G_OS=Shigella_sonnei_(strain_Ss046)_GN=fusA_PE=3_SV=1	1.00E-71
comp67642_c0_seq1.p1		
comp67645_c0_seq1.p1	sp|Q5UPD4|YL060_MIMIV_Putative_F-box_and_FNIP_repeat-containing_protein_L60_OS=Acanthamoeba_polyphaga_mimivirus_GN=MIMI_L60_PE=4_SV=1	3.00E-25
comp67655_c0_seq1.p1		
comp67656_c0_seq1.p1		
comp67661_c0_seq1.p1		
comp67667_c0_seq1.p1	sp|P51405|RS4_DICDI_40S_ribosomal_protein_S4_OS=Dictyostelium_discoideum_GN=rps4_PE=1_SV=3	1.00E-54
comp67669_c0_seq1.p1		
comp67696_c0_seq1.p1	sp|P36771|LRHA_ECOLI_Probable_HTH-type_transcriptional_regulator_lrhA_OS=Escherichia_coli_(strain_K12)_GN=lrhA_PE=4_SV=2	0
comp67731_c0_seq1.p1	sp|P0AFE3|NUOJ_SHIFL_NADH-quinone_oxidoreductase_subunit_J_OS=Shigella_flexneri_GN=nuoJ_PE=3_SV=1	7.00E-70
comp67743_c0_seq1.p1	sp|P0AG83|PSTS_SHIFL_Phosphate-binding_protein_pstS_OS=Shigella_flexneri_GN=pstS_PE=3_SV=1	5.00E-96
comp67748_c0_seq1.p1		
comp67761_c0_seq1.p1	sp|P32057|WCAI_ECOLI_Putative_colanic_acid_biosynthesis_glycosyl_transferase_wcaI_OS=Escherichia_coli_(strain_K12)_GN=wcaI_PE=4_SV=1	3.00E-89
comp67764_c0_seq1.p1		
comp67767_c0_seq1.p1	sp|Q3Z464|TOLB_SHISS_Protein_TolB_OS=Shigella_sonnei_(strain_Ss046)_GN=tolB_PE=3_SV=1	4.00E-103
comp67768_c0_seq1.p1		
comp67771_c0_seq1.p1	sp|P0A7B1|PPK_ECOLI_Polyphosphate_kinase_OS=Escherichia_coli_(strain_K12)_GN=ppk_PE=1_SV=2	0
comp67783_c0_seq1.p2		

comp67806_c0_seq1.p1	sp|P24207|PHEP_ECOLI_Phenylalanine-specific_permease_OS=Escherichia_coli_(strain_K12)_GN=pheP_PE=1_SV=1	3.00E-86	GO:0003333,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006810,GO:0006865,GO:0006865,GO:0015171,GO:0015823,GO:0015823,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016021,GO:0055085	amino acid transmembrane transport,plasma membrane,plasma membrane,plasma membrane,plasma membrane,transport,transport,amino acid transport,amino acid transport,amino acid transmembrane transporter activity,phenylalanine transport,phenylalanine transport,membrane,membrane,integral component of membrane,integral component of membrane,transmembrane transport
comp67818_c0_seq1.p1				
comp67820_c0_seq1.p2	sp|Q3YZD1|DNLJ_SHISS_DNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=ligA_PE=3_SV=1	2.00E-69	GO:0003677,GO:0003911,GO:0003911,GO:0003911,GO:0006259,GO:0006260,GO:0006260,GO:0006266,GO:0006266,GO:0006281,GO:0006281,GO:0006974,GO:0016874,GO:0046872	DNA binding,DNA ligase (NAD+) activity,DNA ligase (NAD+) activity,DNA ligase (NAD+) activity,DNA metabolic process,DNA replication,DNA replication,DNA ligation,DNA ligation,DNA repair,DNA repair,cellular response to DNA damage stimulus,ligase activity,metal ion binding
comp67865_c0_seq1.p2				
comp67867_c0_seq1.p1				
comp67880_c0_seq1.p1				
comp67896_c0_seq1.p1	sp|P00935|METB_ECOLI_Cystathionine_gamma-synthase_OS=Escherichia_coli_(strain_K12)_GN=metB_PE=1_SV=1	2.00E-69	GO:0003824,GO:0003962,GO:0003962,GO:0005737,GO:0005737,GO:0008652,GO:0009086,GO:0009086,GO:0016740,GO:0030170,GO:0030170	catalytic activity,cystathionine gamma-synthase activity,cystathionine gamma-synthase activity,cytoplasm,cytoplasm,cellular amino acid biosynthetic process,methionine biosynthetic process,methionine biosynthetic process,transferase activity,pyridoxal phosphate binding,pyridoxal phosphate binding
comp67905_c0_seq1.p1	sp|Q3Z360|YCEI_SHISS_Protein_yceI_OS=Shigella_sonnei_(strain_Ss046)_GN=yceI_PE=3_SV=1	9.00E-99	GO:0042597,GO:0042597,GO:0042597	periplasmic space,periplasmic space,periplasmic space
comp67909_c0_seq1.p1	sp|P62278|RS13_RAT_40S_ribosomal_protein_S13_OS=Rattus_norvegicus_GN=Rps13_PE=2_SV=2	3.00E-83	GO:0003674,GO:0003729,GO:0003735,GO:0005622,GO:0005634,GO:0005730,GO:0005840,GO:0005840,GO:0006412,GO:0008150,GO:0016020,GO:0022627,GO:0022627,GO:0022627,GO:0030529,GO:0033119,GO:0044822,GO:0070062	molecular_function,mRNA binding,structural constituent of ribosome,intracellular,nucleus,nucleolus,ribosome,ribosome,translation,biological_process,membrane,cytosolic small ribosomal subunit,cytosolic small ribosomal subunit,cytosolic small ribosomal subunit,ribonucleoprotein complex,negative regulation of RNA splicing,poly(A) RNA binding,extracellular vesicular exosome
comp67936_c0_seq1.p1	sp|P33590|NIKA_ECOLI_Nickel-binding_periplasmic_protein_OS=Escherichia_coli_(strain_K12)_GN=nikA_PE=1_SV=1	2.00E-130	GO:0005215,GO:0006810,GO:0006810,GO:0015675,GO:0016151,GO:0016151,GO:0020037,GO:0020037,GO:0042597,GO:0042597,GO:0042597,GO:0046914,GO:0050919	transporter activity,transport,transport,nickel cation transport,nickel cation binding,nickel cation binding,heme binding,heme binding,periplasmic space,periplasmic space,periplasmic space,transition metal ion binding,negative chemotaxis
comp67950_c0_seq1.p1				
comp67958_c0_seq1.p1	sp|P08997|MASY_ECOLI_Malate_synthase_A_OS=Escherichia_coli_(strain_K12)_GN=aceB_PE=1_SV=1	0	GO:0003824,GO:0004474,GO:0004474,GO:0004474,GO:0005737,GO:0005737,GO:0005737,GO:0006097,GO:0006097,GO:0006097,GO:0006097,GO:0006099,GO:0016740	catalytic activity,malate synthase activity,malate synthase activity,malate synthase activity,cytoplasm,cytoplasm,cytoplasm,glyoxylate cycle,glyoxylate cycle,glyoxylate cycle,glyoxylate cycle,tricarboxylic acid cycle,transferase activity
comp67963_c0_seq1.p1				
comp67967_c0_seq1.p1	sp|P26769|ADCY2_RAT_Adenylate_cyclase_type_2_OS=Rattus_norvegicus_GN=Adcy2_PE=1_SV=1	1.00E-15	GO:0000166,GO:0004016,GO:0004016,GO:0004016,GO:0004016,GO:0004016,GO:0004016,GO:0005515,GO:0005524,GO:0005622,GO:0005737,GO:0005886,GO:0005886,GO:0006171,GO:0006171,GO:0006171,GO:0006171,GO:0007188,GO:0008179,GO:0008294,GO:0009190,GO:0016020,GO:0016020,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016021,GO:0016829,GO:0016849,GO:0030425,GO:0030425,GO:0031683,GO:0035556,GO:0043234,GO:0045121,GO:0046872,GO:0046982	nucleotide binding,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,adenylate cyclase activity,protein binding,ATP binding,intracellular,cytoplasm,plasma membrane,plasma membrane,cAMP biosynthetic process,cAMP biosynthetic process,cAMP biosynthetic process,cAMP biosynthetic process,adenylate cyclase-modulating G-protein coupled receptor signaling pathway,adenylate cyclase binding,calcium- and calmodulin-responsive adenylate cyclase activity,cyclic nucleotide biosynthetic process,membrane,membrane,membrane,membrane,membrane,integral component of membrane,integral component of membrane,lyase activity,phosphorus-oxygen lyase activity,dendrite,dendrite,G-protein beta/gamma-subunit complex binding,intracellular signal transduction,protein complex,membrane raft,metal ion binding,protein heterodimerization activity
comp67975_c0_seq1.p1				
comp67983_c0_seq1.p2	sp|P17959|RS9_TRYBB_Probable_40S_ribosomal_protein_S9_OS=Trypanosoma_brucei_brucei_PE=3_SV=1	1.00E-42	GO:0003723,GO:0003723,GO:0003735,GO:0005622,GO:0005840,GO:0006412,GO:0015935,GO:0019843,GO:0019843,GO:0030529	RNA binding,RNA binding,structural constituent of ribosome,intracellular,ribosome,translation,small ribosomal subunit,rRNA binding,rRNA binding,ribonucleoprotein complex
comp67984_c0_seq1.p1	sp|P33650|FEOB_ECOLI_Ferrous_iron_transport_protein_B_OS=Escherichia_coli_(strain_K12)_GN=feoB_PE=1_SV=1	1.00E-174	GO:0000166,GO:0001882,GO:0005525,GO:0005525,GO:0005525,GO:0005886,GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006811,GO:0006974,GO:0015093,GO:0015093,GO:0015093,GO:0015684,GO:0015684,GO:0015684,GO:0016020,GO:0016021,GO:0016021,GO:0042802,GO:0042802,GO:0055072	nucleotide binding,nucleoside binding,GTP binding,GTP binding,GTP binding,plasma membrane,plasma membrane,plasma membrane,plasma membrane,transport,ion transport,cellular response to DNA damage stimulus,ferrous iron transmembrane transporter activity,ferrous iron transmembrane transporter activity,ferrous iron transmembrane transporter activity,ferrous iron transport,ferrous iron transport,ferrous iron transport,membrane,integral component of membrane,integral component of membrane,identical protein binding,identical protein binding,iron ion homeostasis
comp67991_c0_seq1.p2	sp|P0A6C0|ISCS_SHIFL_Cysteine_desulfurase_OS=Shigella_flexneri_GN=iscS_PE=3_SV=1	7.00E-62	GO:0003824,GO:0005737,GO:0005737,GO:0005737,GO:0006534,GO:0008152,GO:0016740,GO:0030170,GO:0031071,GO:0031071,GO:0031071	catalytic activity,cytoplasm,cytoplasm,cytoplasm,cysteine metabolic process,metabolic process,transferase activity,pyridoxal phosphate binding,cysteine desulfurase activity,cysteine desulfurase activity,cysteine desulfurase activity
comp68003_c0_seq1.p1				
comp68005_c0_seq1.p1				
comp68021_c0_seq1.p1				
comp68028_c0_seq1.p1				
comp68029_c0_seq1.p1	sp|Q3Z5Y4|SYI_SHISS_Isoleucine--tRNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=ileS_PE=3_SV=1	0	GO:0000166,GO:0000166,GO:0002161,GO:0003824,GO:0004812,GO:0004812,GO:0004822,GO:0004822,GO:0004822,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006418,GO:0006428,GO:0006428,GO:0006450,GO:0008270,GO:0016874,GO:0046872	nucleotide binding,nucleotide binding,aminoacyl-tRNA editing activity,catalytic activity,aminoacyl-tRNA ligase activity,aminoacyl-tRNA ligase activity,isoleucine-tRNA ligase activity,isoleucine-tRNA ligase activity,isoleucine-tRNA ligase activity,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,translation,tRNA aminoacylation for protein translation,isoleucyl-tRNA aminoacylation,isoleucyl-tRNA aminoacylation,regulation of translational fidelity,zinc ion binding,ligase activity,metal ion binding
comp68055_c0_seq1.p1				
comp68087_c0_seq1.p1				
comp68088_c0_seq1.p1				
comp68095_c0_seq1.p2	sp|P15034|AMPP_ECOLI_Xaa-Pro_aminopeptidase_OS=Escherichia_coli_(strain_K12)_GN=pepP_PE=1_SV=2	2.00E-99	GO:0004177,GO:0004177,GO:0004177,GO:0005515,GO:0005737,GO:0005737,GO:0005829,GO:0006508,GO:0006508,GO:0008233,GO:0008235,GO:0008237,GO:0016787,GO:0030145,GO:0046872	aminopeptidase activity,aminopeptidase activity,aminopeptidase activity,protein binding,cytoplasm,cytoplasm,cytosol,proteolysis,proteolysis,peptidase activity,metalloexopeptidase activity,metallopeptidase activity,hydrolase activity,manganese ion binding,metal ion binding
comp68098_c0_seq1.p1				

comp73482_c0_seq1.p1	sp|B1IQH4|GLND_ECOLC_[Protein-PII]_uridylyltransferase_OS=Escherichia_coli_(strain_ATCC_8739_/_DSM_1576_/_Crooks)_GN=glnD_PE=3_SV=1	7.00E-102	GO:0003824,GO:0006807,GO:0006808,GO:0008081,GO:0008152,GO:0008152,GO:0008773,GO:0008773,GO:0008773,GO:0016597,GO:0016740,GO:0016779,GO:0016779,GO:0016787	catalytic activity,nitrogen compound metabolic process,regulation of nitrogen utilization,phosphoric diester hydrolase activity,metabolic process,metabolic process,[protein-PII] uridylyltransferase activity,[protein-PII] uridylyltransferase activity,[protein-PII] uridylyltransferase activity,amino acid binding,transferase activity,nucleotidyltransferase activity,nucleotidyltransferase activity,hydrolase activity
comp73501_c0_seq1.p1				
comp73514_c0_seq1.p1				
comp7355_c0_seq1.p1				
comp73584_c0_seq1.p2	sp|Q8XX80|SYV_RALSO_Valine--tRNA_ligase_OS=Ralstonia_solanacearum_(strain_GMI1000)_GN=valS_PE=3_SV=1	2.00E-43	GO:0000166,GO:0000166,GO:0002161,GO:0004812,GO:0004812,GO:0004832,GO:0004832,GO:0004832,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006412,GO:0006418,GO:0006438,GO:0006438,GO:0006450,GO:0016874	nucleotide binding,nucleotide binding,aminoacyl-tRNA editing activity,aminoacyl-tRNA ligase activity,aminoacyl-tRNA ligase activity,aminoacyl-tRNA ligase activity,valine-tRNA ligase activity,valine-tRNA ligase activity,valine-tRNA ligase activity,ATP binding,ATP binding,ATP binding,cytoplasm,cytoplasm,cytoplasm,cytoplasm,translation,tRNA aminoacylation for protein translation,valyl-tRNA aminoacylation,valyl-tRNA aminoacylation,regulation of translational fidelity,ligase activity
comp7361_c0_seq1.p1	sp|Q3YY71|RLMD_SHISS_23S_rRNA_(uracil(1939)-C(5))-methyltransferase_RlmD_OS=Shigella_sonnei_(strain_Ss046)_GN=rlmD_PE=3_SV=1	1.00E-60	GO:0003723,GO:0005506,GO:0006364,GO:0006396,GO:0008168,GO:0008173,GO:0016740,GO:0031167,GO:0032259,GO:0046872,GO:0051536,GO:0051539,GO:0070041	RNA binding,iron ion binding,rRNA processing,RNA processing,methyltransferase activity,RNA methyltransferase activity,transferase activity,rRNA methylation,methylation,metal ion binding,iron-sulfur cluster binding,4 iron, 4 sulfur cluster binding,rRNA (uridine-C5-)-methyltransferase activity
comp73622_c0_seq1.p1				
comp73649_c0_seq1.p1				
comp73714_c0_seq1.p1				
comp73719_c0_seq1.p1				
comp73743_c0_seq1.p1				
comp73790_c0_seq1.p2	sp|P49669|RL4_TRYBB_60S_ribosomal_protein_L4_OS=Trypanosoma_brucei_brucei_GN=RPL4_PE=3_SV=1	2.00E-80	GO:0003735,GO:0005840,GO:0005840,GO:0006412,GO:0030529	structural constituent of ribosome,ribosome,ribosome,translation,ribonucleoprotein complex
comp73793_c0_seq1.p1				
comp73812_c0_seq1.p2	sp|P17197|EF1A_THECE_Elongation_factor_1-alpha_OS=Thermococcus_celer_GN=tuf_PE=3_SV=1	8.00E-14	GO:0000166,GO:0003746,GO:0003746,GO:0003746,GO:0003924,GO:0005525,GO:0005525,GO:0005525,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006184,GO:0006412,GO:0006414,GO:0006414	[illegible]
comp73859_c0_seq1.p1				
comp73870_c0_seq1.p2				
comp73904_c0_seq1.p1	sp|P09980|REP_ECOLI_ATP-dependent_DNA_helicase_rep_OS=Escherichia_coli_(strain_K12)_GN=rep_PE=1_SV=3	5.00E-135	GO:0000166,GO:0003677,GO:0003677,GO:0003677,GO:0004003,GO:0004003,GO:0004386,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0006260,GO:0006268,GO:0006268,GO:0016787,GO:0016787	[illegible]
comp73912_c0_seq1.p1	sp|P76387|WZC_ECOLI_Tyrosine-protein_kinase_wzc_OS=Escherichia_coli_(strain_K12)_GN=wzc_PE=1_SV=2	2.00E-59	GO:0000166,GO:0000271,GO:0004713,GO:0004713,GO:0005524,GO:0005886,GO:0005886,GO:0005886,GO:0005887,GO:0006200,GO:0009103,GO:0009242,GO:0016020,GO:0016020,GO:0016020,GO:0016021,GO:0016301,GO:0016310,GO:0016740,GO:0016887,GO:0018108,GO:0038083,GO:0045226	[illegible]
comp73915_c0_seq1.p2	sp|P0A9M0|LON_ECOLI_Lon_protease_OS=Escherichia_coli_(strain_K12)_GN=lon_PE=1_SV=1	9.00E-50	GO:0000166,GO:0003677,GO:0004176,GO:0004176,GO:0004176,GO:0004176,GO:0004176,GO:0004252,GO:0004252,GO:0004252,GO:0005515,GO:0005524,GO:0005524,GO:0005524,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0005737,GO:0006200,GO:0006200,GO:0006200,GO:0006200,GO:0006200,GO:0006508,GO:0006508,GO:0006508,GO:0006515,GO:0006515,GO:0008233,GO:0008233,GO:0008236,GO:0009408,GO:0016787,GO:0016887,GO:0016887,GO:0030163,GO:0033554,GO:0043565,GO:0043565	[illegible]
comp73931_c0_seq1.p1	sp|A6N6J5|WDR35_RAT_WD_repeat-containing_protein_35_OS=Rattus_norvegicus_GN=Wdr35_PE=1_SV=1	1.00E-12	GO:0005737,GO:0005813,GO:0005813,GO:0005815,GO:0005856,GO:0005929,GO:0005930,GO:0005930,GO:0030030,GO:0030991,GO:0030991,GO:0035721,GO:0036064,GO:0036064,GO:0042384,GO:0042384,GO:0042384,GO:0042995	[illegible]
comp73943_c0_seq1.p1	sp|P33361|YEHY_ECOLI_Putative_osmoprotectant_uptake_system_permease_protein_yehY_OS=Escherichia_coli_(strain_K12)_GN=yehY_PE=1_SV=2	4.00E-28	GO:0005886,GO:0005886,GO:0005886,GO:0006810,GO:0006810,GO:0016020,GO:0016020,GO:0016021	plasma membrane,plasma membrane,plasma membrane,transport,transport,membrane,membrane,integral component of membrane
comp73959_c0_seq1.p2				
comp73971_c0_seq1.p2	sp|Q55G10|PNCB_DICDI_Nicotinate_phosphoribosyltransferase_OS=Dictyostelium_discoideum_GN=naprt_PE=2_SV=1	2.00E-52	GO:0004514,GO:0004516,GO:0009435,GO:0009435,GO:0016740,GO:0016874,GO:0019358,GO:0019363	nicotinate-nucleotide diphosphorylase (carboxylating) activity,nicotinate phosphoribosyltransferase activity,NAD biosynthetic process,NAD biosynthetic process,transferase activity,ligase activity,nicotinate nucleotide salvage,pyridine nucleotide biosynthetic process
comp73980_c0_seq1.p1				
comp74002_c0_seq1.p1	sp|Q3YVD2|UBIE_SHISS_Ubiquinone/menaquinone_biosynthesis_methyltransferase_ubiE_OS=Shigella_sonnei_(strain_Ss046)_GN=ubiE_PE=3_SV=1	1.00E-108	GO:0006744,GO:0006744,GO:0008168,GO:0008168,GO:0008425,GO:0009060,GO:0009234,GO:0009234,GO:0009234,GO:0016740,GO:0032259	[illegible]
comp74011_c0_seq1.p1	sp|P0ADL3|YICN_ECOLI_Uncharacterized_protein_yicN_OS=Escherichia_coli_(strain_K12)_GN=yicN_PE=4_SV=2	7.00E-70	[illegible]	[illegible]
comp74022_c0_seq1.p2	sp|P02919|PBPB_ECOLI_Penicillin-binding_protein_1B_OS=Escherichia_coli_(strain_K12)_GN=mrcB_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp74059_c0_seq1.p1	sp|P0AFG8|ODP1_ECOLI_Pyruvate_dehydrogenase_E1_component_OS=Escherichia_coli_(strain_K12)_GN=aceE_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp74060_c0_seq1.p1	sp|Q3YZS8|NUOH_SHISS_NADH-quinone_oxidoreductase_subunit_H_OS=Shigella_sonnei_(strain_Ss046)_GN=nuoH_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74063_c0_seq1.p1				
comp74064_c0_seq1.p2				
comp74085_c0_seq1.p1				
comp74107_c0_seq1.p2	sp|P0AB83|END3_ECOLI_Endonuclease_III_OS=Escherichia_coli_(strain_K12)_GN=nth_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp74119_c0_seq1.p1	sp|P68186|MALG_SHIFL_Maltose_transport_system_permease_protein_malG_OS=Shigella_flexneri_GN=malG_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74120_c0_seq1.p2				
comp74130_c0_seq1.p2	sp|P24255|RP54_ECOLI_RNA_polymerase_sigma-54_factor_OS=Escherichia_coli_(strain_K12)_GN=rpoN_PE=3_SV=2	[illegible]	[illegible]	[illegible]
comp74193_c0_seq1.p1	sp|P37024|HRPB_ECOLI_ATP-dependent_RNA_helicase_hrpB_OS=Escherichia_coli_(strain_K12)_GN=hrpB_PE=3_SV=3	[illegible]	[illegible]	[illegible]
comp74213_c0_seq1.p1	sp|P36646|HOFC_ECOLI_Protein_transport_protein_hofC_OS=Escherichia_coli_(strain_K12)_GN=hofC_PE=3_SV=3	[illegible]	[illegible]	[illegible]
comp74218_c0_seq1.p1	sp|Q31ZC0|MDTH_SHIBS_Multidrug_resistance_protein_MdtH_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=mdtH_PE=3_SV=2	[illegible]	[illegible]	[illegible]
comp74244_c0_seq1.p1	sp|B1IRU3|LSRF_ECOLC_Uncharacterized_aldolase_lsrF_OS=Escherichia_coli_(strain_ATCC_8739_/_DSM_1576_/_Crooks)_GN=lsrF_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74245_c0_seq1.p1	sp|Q3YXX2|YGFZ_SHISS_tRNA-modifying_protein_ygfZ_OS=Shigella_sonnei_(strain_Ss046)_GN=ygfZ_PE=3_SV=3	[illegible]	[illegible]	[illegible]
comp74249_c0_seq1.p1				
comp74262_c0_seq1.p1	sp|Q0T6G6|YBHG_SHIF8_UPF0194_membrane_protein_ybhG_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=ybhG_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74299_c0_seq1.p1				
comp74305_c0_seq1.p2	sp|P52074|GLCF_ECOLI_Glycolate_oxidase_iron-sulfur_subunit_OS=Escherichia_coli_(strain_K12)_GN=glcF_PE=4_SV=1	[illegible]	[illegible]	[illegible]
comp74344_c0_seq1.p2				
comp74350_c0_seq1.p1	sp|Q3YWK7|MALT_SHISS_HTH-type_transcriptional_regulator_malT_OS=Shigella_sonnei_(strain_Ss046)_GN=malT_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74366_c0_seq1.p1				
comp74387_c0_seq1.p1	sp|P59673|FIXA_SHIFL_Protein_fixA_OS=Shigella_flexneri_GN=fixA_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74409_c0_seq1.p1	sp|P0AGC3|SLT_ECOLI_Soluble_lytic_murein_transglycosylase_OS=Escherichia_coli_(strain_K12)_GN=slt_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp74416_c0_seq1.p1	sp|P75745|YBGK_ECOLI_Uncharacterized_protein_ybgK_OS=Escherichia_coli_(strain_K12)_GN=ybgK_PE=4_SV=1	[illegible]	[illegible]	[illegible]
comp74419_c0_seq1.p1	sp|P76052|ABGB_ECOLI_Aminobenzoyl-glutamate_utilization_protein_B_OS=Escherichia_coli_(strain_K12)_GN=abgB_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp74424_c0_seq1.p1	sp|P45543|FRLD_ECOLI_Fructoselysine_kinase_OS=Escherichia_coli_(strain_K12)_GN=frlD_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74439_c0_seq1.p1				
comp74451_c0_seq1.p1	sp|P13039|FES_ECOLI_Enterochelin_esterase_OS=Escherichia_coli_(strain_K12)_GN=fes_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp74458_c0_seq1.p1				
comp74466_c0_seq1.p1				
comp74485_c0_seq1.p1	sp|Q3Z2Y6|MNMA_SHISS_tRNA-specific_2-thiouridylase_mnmA_OS=Shigella_sonnei_(strain_Ss046)_GN=mnmA_PE=3_SV=2	[illegible]	[illegible]	[illegible]
comp74535_c0_seq1.p1	sp|P41441|GSPF_ECOLI_Putative_general_secretion_pathway_protein_F_OS=Escherichia_coli_(strain_K12)_GN=gspF_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp74564_c0_seq1.p1	sp|Q31UM6|KUP_SHIBS_Low_affinity_potassium_transport_system_protein_kup_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=kup_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74609_c0_seq1.p1	sp|P32718|ALSK_ECOLI_D-allose_kinase_OS=Escherichia_coli_(strain_K12)_GN=alsK_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp74615_c0_seq1.p1	sp|P13035|GLPD_ECOLI_Aerobic_glycerol-3-phosphate_dehydrogenase_OS=Escherichia_coli_(strain_K12)_GN=glpD_PE=1_SV=3	[illegible]	[illegible]	[illegible]
comp74659_c0_seq1.p1				
comp74663_c0_seq1.p2				
comp74714_c0_seq1.p1				
comp74718_c0_seq1.p1	sp|P18956|GGT_ECOLI_Gamma-glutamyltranspeptidase_OS=Escherichia_coli_(strain_K12)_GN=ggt_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp74731_c0_seq1.p1				
comp74745_c0_seq1.p1				
comp74807_c0_seq1.p1	sp|P04816|LIVK_ECOLI_Leucine-specific-binding_protein_OS=Escherichia_coli_(strain_K12)_GN=livK_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp74832_c0_seq1.p1	sp|P75726|CILA_ECOLI_Citrate_lyase_alpha_chain_OS=Escherichia_coli_(strain_K12)_GN=citF_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp74847_c0_seq1.p1	sp|B1IRK5|YHAM_ECOLC_UPF0597_protein_yhaM_OS=Escherichia_coli_(strain_ATCC_8739_/_DSM_1576_/_Crooks)_GN=yhaM_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74853_c0_seq1.p1	sp|Q32HB3|PURT_SHIDS_Phosphoribosylglycinamide_formyltransferase_2_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=purT_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74875_c0_seq1.p1	sp|Q0PXV9|RL17_DIACI_60S_ribosomal_protein_L17_OS=Diaphorina_citri_GN=RpL17_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp74898_c0_seq1.p1				
comp74899_c0_seq1.p1	sp|P0ABC2|ATPZ_SHIFL_ATP_synthase_protein_I_OS=Shigella_flexneri_GN=atpI_PE=3_SV=2	[illegible]	[illegible]	[illegible]
comp74957_c0_seq1.p1	sp|P77554|YAHJ_ECOLI_Uncharacterized_protein_yahJ_OS=Escherichia_coli_(strain_K12)_GN=yahJ_PE=4_SV=1	[illegible]	[illegible]	[illegible]
comp74973_c0_seq1.p1				
comp74975_c0_seq1.p1	sp|B1IUE0|PEPT_ECOLC_Peptidase_T_OS=Escherichia_coli_(strain_ATCC_8739_/_DSM_1576_/_Crooks)_GN=pepT_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74977_c0_seq1.p1	sp|P0ACB1|DNAB_SHIFL_Replicative_DNA_helicase_OS=Shigella_flexneri_GN=dnaB_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp74978_c0_seq1.p1	sp|Q32E34|MSBA_SHIDS_Lipid_A_export_ATP-binding/permease_protein_MsbA_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=msbA_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp75006_c0_seq1.p1				
comp75012_c0_seq1.p2				
comp75034_c0_seq1.p1	sp|P30138|THIF_ECOLI_Sulfur_carrier_protein_ThiS_adenylyltransferase_OS=Escherichia_coli_(strain_K12)_GN=thiF_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp75059_c0_seq1.p1				
comp75073_c0_seq1.p1				
comp75105_c0_seq1.p1				
comp75136_c0_seq1.p1	sp|P45766|YHDW_ECOLI_Putative_amino-acid_ABC_transporter-binding_protein_yhdW_OS=Escherichia_coli_(strain_K12)_GN=yhdW_PE=5_SV=2	[illegible]	[illegible]	[illegible]
comp75160_c0_seq1.p3				
comp7517_c0_seq1.p1	sp|P77589|MHPT_ECOLI_Putative_3-hydroxyphenylpropionic_acid_transporter_OS=Escherichia_coli_(strain_K12)_GN=mhpT_PE=3_SV=2	[illegible]	[illegible]	[illegible]
comp75192_c0_seq1.p1	sp|P15254|PUR4_ECOLI_Phosphoribosylformylglycinamidine_synthase_OS=Escherichia_coli_(strain_K12)_GN=purL_PE=1_SV=3	[illegible]	[illegible]	[illegible]
comp75214_c0_seq1.p1				
comp75217_c0_seq1.p1				
comp7522_c0_seq1.p1	sp|Q3Z2V9|DADA_SHISS_D-amino_acid_dehydrogenase_small_subunit_OS=Shigella_sonnei_(strain_Ss046)_GN=dadA_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp75292_c0_seq1.p1	sp|O96559|APY_CIMLE_Apyrase_OS=Cimex_lectularius_GN=APY_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp75300_c0_seq1.p1	sp|O96552|CHMP1_DICDI_Charged_multivesicular_body_protein_1_OS=Dictyostelium_discoideum_GN=chmp1_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp75347_c0_seq1.p4				
comp75366_c0_seq1.p1	sp|Q3YUB9|F16PA_SHISS_Fructose-1,6-bisphosphatase_class_1_OS=Shigella_sonnei_(strain_Ss046)_GN=fbp_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp75378_c0_seq1.p1				
comp75405_c0_seq1.p1				
comp7545_c0_seq1.p2				
comp75457_c0_seq1.p1				
comp75462_c0_seq1.p1	sp|P77129|YLBE_ECOLI_Uncharacterized_protein_ylbE_OS=Escherichia_coli_(strain_K12)_GN=ylbE_PE=4_SV=1	[illegible]	[illegible]	[illegible]
comp75471_c0_seq1.p1				
comp75479_c0_seq1.p1	sp|P11880|MURF_ECOLI_UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine_ligase_OS=Escherichia_coli_(strain_K12)_GN=murF_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp75483_c0_seq1.p1	sp|P10378|ENTE_ECOLI_Enterobactin_synthase_component_E_OS=Escherichia_coli_(strain_K12)_GN=entE_PE=1_SV=3	[illegible]	[illegible]	[illegible]
comp75508_c0_seq1.p1				
comp75527_c0_seq1.p1				
comp75559_c0_seq1.p1	sp|Q32LL2|STML2_BOVIN_Stomatin-like_protein_2_OS=Bos_taurus_GN=STOML2_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp75581_c0_seq1.p1	sp|Q9S7C0|HSP7O_ARATH_Heat_shock_70_kDa_protein_14_OS=Arabidopsis_thaliana_GN=HSP70-14_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp75582_c0_seq1.p1				
comp75593_c0_seq1.p1	sp|Q3Z476|SUCC_SHISS_Succinyl-CoA_ligase_[ADP-forming]_subunit_beta_OS=Shigella_sonnei_(strain_Ss046)_GN=sucC_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp75668_c0_seq1.p1				
comp75680_c0_seq1.p1	sp|Q38950|2AAB_ARATH_Serine/threonine-protein_phosphatase_2A_65_kDa_regulatory_subunit_A_beta_isoform_OS=Arabidopsis_thaliana_GN=PP2AA2_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp75684_c0_seq1.p1				
comp75697_c0_seq1.p1				
comp75780_c0_seq1.p1				
comp75793_c0_seq1.p2	sp|B1IP46|RTCA_ECOLC_RNA_3'-terminal_phosphate_cyclase_OS=Escherichia_coli_(strain_ATCC_8739_/_DSM_1576_/_Crooks)_GN=rtcA_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp75842_c0_seq1.p1	sp|Q46856|YQHD_ECOLI_Alcohol_dehydrogenase_YqhD_OS=Escherichia_coli_(strain_K12)_GN=yqhD_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp75863_c0_seq1.p1	sp|Q10161|CLH_SCHPO_Probable_clathrin_heavy_chain_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=chc1_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp75872_c0_seq1.p1				
comp75906_c0_seq1.p1				
comp75936_c0_seq1.p1	sp|Q20719|NDUV2_CAEEL_Probable_NADH_dehydrogenase_[ubiquinone]_flavoprotein_2,_mitochondrial_OS=Caenorhabditis_elegans_GN=F53F4.10_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp76040_c0_seq1.p1	sp|P0DJ60|RL19_TETTS_60S_ribosomal_protein_L19_OS=Tetrahymena_thermophila_(strain_SB210)_GN=RPL19_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp76041_c0_seq1.p2				
comp76058_c0_seq1.p1				
comp76066_c0_seq1.p2	sp|Q3YUZ7|RPOB_SHISS_DNA-directed_RNA_polymerase_subunit_beta_OS=Shigella_sonnei_(strain_Ss046)_GN=rpoB_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp76076_c0_seq1.p1				
comp76105_c0_seq1.p1				
comp76119_c0_seq1.p1				
comp76124_c0_seq1.p2				
comp76132_c0_seq1.p1	sp|P0AFR2|YCHM_ECOLI_Putative_sulfate_transporter_ychM_OS=Escherichia_coli_(strain_K12)_GN=ychM_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp76135_c0_seq1.p2				
comp76147_c0_seq1.p3				
comp76178_c0_seq1.p1				
comp76183_c0_seq1.p1	sp|P0A961|ALAA_SHIFL_Glutamate-pyruvate_aminotransferase_AlaA_OS=Shigella_flexneri_GN=alaA_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp76219_c0_seq1.p2				
comp76226_c0_seq1.p1	sp|P02919|PBPB_ECOLI_Penicillin-binding_protein_1B_OS=Escherichia_coli_(strain_K12)_GN=mrcB_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp76300_c0_seq1.p1	sp|P09152|NARG_ECOLI_Respiratory_nitrate_reductase_1_alpha_chain_OS=Escherichia_coli_(strain_K12)_GN=narG_PE=1_SV=4	[illegible]	[illegible]	[illegible]
comp76305_c0_seq1.p1				
comp76307_c0_seq1.p2	sp|P32662|GPH_ECOLI_Phosphoglycolate_phosphatase_OS=Escherichia_coli_(strain_K12)_GN=gph_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp76312_c0_seq1.p2				
comp76322_c0_seq1.p2	sp|Q8FG52|HISX_ECOL6_Histidinol_dehydrogenase_OS=Escherichia_coli_O6_GN=hisD_PE=3_SV=3	[illegible]	[illegible]	[illegible]
comp76374_c0_seq1.p1	sp|P63883|AMIC_ECOLI_N-acetylmuramoyl-L-alanine_amidase_AmiC_OS=Escherichia_coli_(strain_K12)_GN=amiC_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp76389_c0_seq1.p1	sp|Q3Z550|FRMA_SHISS_S-(hydroxymethyl)glutathione_dehydrogenase_OS=Shigella_sonnei_(strain_Ss046)_GN=frmA_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp76406_c0_seq1.p1				
comp76427_c0_seq1.p1				
comp76430_c0_seq1.p2	sp|P93099|RL13A_CYAPA_60S_ribosomal_protein_L13a_OS=Cyanophora_paradoxa_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp76498_c0_seq1.p1				
comp76534_c0_seq1.p1				
comp76547_c0_seq1.p1	sp|P61319|LOLA_SHIFL_Outer-membrane_lipoprotein_carrier_protein_OS=Shigella_flexneri_GN=lolA_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp76566_c0_seq1.p1				
comp76570_c0_seq1.p1				
comp76572_c0_seq1.p1	sp|Q3Z5V5|LPTD_SHISS_LPS-assembly_protein_lptD_OS=Shigella_sonnei_(strain_Ss046)_GN=lptD_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp76579_c0_seq1.p2	sp|P19835|CEL_HUMAN_Bile_salt-activated_lipase_OS=Homo_sapiens_GN=CEL_PE=1_SV=3	[illegible]	[illegible]	[illegible]
comp76587_c0_seq1.p1	sp|Q31XX4|RODZ_SHIBS_Cytoskeleton_protein_rodZ_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=rodZ_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp76597_c0_seq1.p1	sp|P09831|GLTB_ECOLI_Glutamate_synthase_[NADPH]_large_chain_OS=Escherichia_coli_(strain_K12)_GN=gltB_PE=1_SV=3	[illegible]	[illegible]	[illegible]
comp76604_c0_seq1.p1				
comp76619_c0_seq1.p1				
comp76653_c0_seq1.p1	sp|Q3T147|DX39B_BOVIN_Spliceosome_RNA_helicase_DDX39B_OS=Bos_taurus_GN=DDX39B_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp76660_c0_seq1.p1	sp|P0AF78|YJFJ_ECOLI_Uncharacterized_protein_YjfJ_OS=Escherichia_coli_(strain_K12)_GN=yjfJ_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp76664_c0_seq1.p1	sp|Q9SP02|CP20A_ARATH_Peptidyl-prolyl_cis-trans_isomerase_CYP20-1_OS=Arabidopsis_thaliana_GN=CYP20-1_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp76669_c0_seq1.p1				
comp76699_c0_seq1.p1				
comp76717_c0_seq1.p1				
comp76723_c0_seq1.p1				
comp76726_c0_seq1.p1	sp|Q9LZV8|ATL74_ARATH_RING-H2_finger_protein_ATL74_OS=Arabidopsis_thaliana_GN=ATL74_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp76749_c0_seq1.p1				
comp76799_c0_seq1.p1	sp|P38051|MENF_ECOLI_Menaquinone-specific_isochorismate_synthase_OS=Escherichia_coli_(strain_K12)_GN=menF_PE=1_SV=4	[illegible]	[illegible]	[illegible]
comp76804_c0_seq1.p1				
comp76814_c0_seq1.p1				
comp76826_c0_seq1.p1				
comp76838_c0_seq1.p1	sp|P18956|GGT_ECOLI_Gamma-glutamyltranspeptidase_OS=Escherichia_coli_(strain_K12)_GN=ggt_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp76864_c0_seq1.p2				
comp76873_c0_seq1.p1				
comp76878_c0_seq1.p2	sp|P76553|EUTG_ECOLI_Ethanolamine_utilization_protein_EutG_OS=Escherichia_coli_(strain_K12)_GN=eutG_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp76901_c0_seq1.p1	sp|Q3ZBH0|TCPB_BOVIN_T-complex_protein_1_subunit_beta_OS=Bos_taurus_GN=CCT2_PE=1_SV=3	[illegible]	[illegible]	[illegible]
comp76958_c0_seq1.p1				
comp76967_c0_seq1.p1				
comp76982_c0_seq1.p1	sp|P76393|YEGI_ECOLI_Uncharacterized_protein_yegI_OS=Escherichia_coli_(strain_K12)_GN=yegI_PE=4_SV=1	3.00E-78	GO:0003677,GO:0004672,GO:0005524,GO:0006281,GO:0006468,GO:0016772	[illegible]
comp76987_c0_seq1.p1	sp|P03835|INSG_ECOLI_Transposase_insG_for_insertion_sequence_element_IS4_OS=Escherichia_coli_(strain_K12)_GN=insG_PE=3_SV=1	2.00E-65	GO:0003676,GO:0003677,GO:0003677,GO:0004803,GO:0006310,GO:0006313,GO:0032196	[illegible]
comp77005_c0_seq1.p1	sp|P0A6G3|YGAD_ECOLI_Protein_YgaD_OS=Escherichia_coli_(strain_K12)_GN=ygaD_PE=1_SV=1	1.00E-89	GO:0016787,GO:0019159,GO:0019159,GO:0019363	[illegible]
comp77030_c0_seq1.p1				
comp77059_c0_seq1.p1				
comp77088_c0_seq1.p1	sp|P24823|PPBE_MOUSE_Embryonic-type_alkaline_phosphatase_OS=Mus_musculus_GN=Akp5_PE=2_SV=2	2.00E-11	[illegible]	[illegible]
comp77096_c0_seq1.p2	sp|Q7RV88|IF4A_NEUCR_ATP-dependent_RNA_helicase_eIF4A_OS=Neurospora_crassa_(strain_ATCC_24698_/_74-OR23-1A_/_CBS_708.71_/_DSM_1257_/_FGSC_987)_GN=tif-1_PE=3_SV=2	9.00E-92	[illegible]	[illegible]
comp77110_c0_seq1.p1	sp|Q23DE3|RS3A_TETTS_40S_ribosomal_protein_S3a_OS=Tetrahymena_thermophila_(strain_SB210)_GN=TTHERM_00047480_PE=1_SV=2	2.00E-31	[illegible]	[illegible]
comp77131_c0_seq1.p1	sp|Q46888|YGBJ_ECOLI_Uncharacterized_oxidoreductase_ygbJ_OS=Escherichia_coli_(strain_K12)_GN=ygbJ_PE=3_SV=1	4.00E-87	[illegible]	[illegible]
comp77154_c0_seq1.p1	sp|Q8IVF4|DYH10_HUMAN_Dynein_heavy_chain_10,_axonemal_OS=Homo_sapiens_GN=DNAH10_PE=1_SV=4	3.00E-18	[illegible]	[illegible]
comp77156_c0_seq1.p1				
comp77221_c0_seq1.p1	sp|P25524|CODA_ECOLI_Cytosine_deaminase_OS=Escherichia_coli_(strain_K12)_GN=codA_PE=1_SV=3	0	[illegible]	[illegible]
comp77235_c0_seq1.p1	sp|P21499|RNR_ECOLI_Ribonuclease_R_OS=Escherichia_coli_(strain_K12)_GN=rnr_PE=1_SV=2	3.00E-98	[illegible]	[illegible]
comp77251_c0_seq1.p2	sp|P54770|TYDC3_PAPSO_Tyrosine/DOPA_decarboxylase_3_OS=Papaver_somniferum_GN=TYDC3_PE=2_SV=2	1.00E-16	[illegible]	[illegible]
comp77313_c0_seq1.p1	sp|P32714|MDTP_ECOLI_Multidrug_resistance_outer_membrane_protein_MdtP_OS=Escherichia_coli_(strain_K12)_GN=mdtP_PE=1_SV=2	6.00E-70	[illegible]	[illegible]
comp77318_c0_seq1.p1	sp|Q3Z5G3|SYP_SHISS_Proline--tRNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=proS_PE=3_SV=1	7.00E-97	[illegible]	[illegible]
comp77414_c0_seq1.p1	sp|Q9QYJ4|ABCB9_RAT_ATP-binding_cassette_sub-family_B_member_9_OS=Rattus_norvegicus_GN=Abcb9_PE=1_SV=1	5.00E-11	[illegible]	[illegible]
comp77482_c0_seq1.p1				
comp77500_c0_seq1.p1	sp|Q3Z3J0|SYN_SHISS_Asparagine--tRNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=asnS_PE=3_SV=1	3.00E-104	[illegible]	[illegible]
comp77528_c0_seq1.p1	sp|P75863|YCBX_ECOLI_Uncharacterized_protein_ycbX_OS=Escherichia_coli_(strain_K12)_GN=ycbX_PE=1_SV=1	3.00E-71	[illegible]	[illegible]
comp77537_c0_seq1.p1				
comp77538_c0_seq1.p2				
comp77543_c0_seq1.p1	sp|P77439|PTFX1_ECOLI_Multiphosphoryl_transfer_protein_1_OS=Escherichia_coli_(strain_K12)_GN=fryA_PE=1_SV=1	8.00E-146	[illegible]	[illegible]
comp77552_c0_seq1.p1	sp|Q47208|FDRA_ECOLI_Protein_FdrA_OS=Escherichia_coli_(strain_K12)_GN=fdrA_PE=1_SV=1	3.00E-71	[illegible]	[illegible]
comp77567_c0_seq1.p1	sp|P36183|ENPL_HORVU_Endoplasmin_homolog_OS=Hordeum_vulgare_PE=2_SV=1	1.00E-15	[illegible]	[illegible]
comp77651_c0_seq1.p1				
comp77666_c0_seq1.p1	sp|Q32C32|MLTC_SHIDS_Membrane-bound_lytic_murein_transglycosylase_C_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=mltC_PE=3_SV=2	9.00E-120	[illegible]	[illegible]
comp77692_c0_seq1.p3				
comp77712_c0_seq1.p1	sp|P59815|RLUB_SHIFL_Ribosomal_large_subunit_pseudouridine_synthase_B_OS=Shigella_flexneri_GN=rluB_PE=3_SV=1	3.00E-72	[illegible]	[illegible]
comp77730_c0_seq1.p2				
comp77770_c0_seq1.p1				
comp77808_c0_seq1.p1	sp|P0AEJ0|EMRB_ECOLI_Multidrug_resistance_protein_B_OS=Escherichia_coli_(strain_K12)_GN=emrB_PE=1_SV=1	8.00E-111	[illegible]	[illegible]
comp77864_c0_seq1.p1	sp|P31447|YIDJ_ECOLI_Uncharacterized_sulfatase_yidJ_OS=Escherichia_coli_(strain_K12)_GN=yidJ_PE=3_SV=1	4.00E-71	GO:0003824,GO:0008152,GO:0008484,GO:0016787,GO:0046872	[illegible]
comp77918_c0_seq1.p1	sp|P77338|KEFA_ECOLI_Potassium_efflux_system_KefA_OS=Escherichia_coli_(strain_K12)_GN=kefA_PE=1_SV=1	1.00E-86	[illegible]	[illegible]
comp77927_c0_seq1.p2	sp|Q40831|TBA1_PELFA_Tubulin_alpha-1_chain_OS=Pelvetia_fastigiata_GN=TUBA1_PE=2_SV=1	2.00E-47	[illegible]	[illegible]
comp77929_c0_seq1.p2				
comp77969_c0_seq1.p1	sp|Q0T2K1|NUOCD_SHIF8_NADH-quinone_oxidoreductase_subunit_C/D_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=nuoC_PE=3_SV=1	2.00E-73	[illegible]	[illegible]
comp77990_c0_seq1.p1				
comp78007_c0_seq1.p1	sp|Q46833|YGHE_ECOLI_Putative_general_secretion_pathway_protein_L-type_yghE_OS=Escherichia_coli_(strain_K12)_GN=yghE_PE=5_SV=1	8.00E-64	[illegible]	[illegible]
comp78013_c0_seq1.p1	sp|P0AE06|ACRA_ECOLI_Acriflavine_resistance_protein_A_OS=Escherichia_coli_(strain_K12)_GN=acrA_PE=1_SV=1	1.00E-107	[illegible]	[illegible]
comp78062_c0_seq1.p1				
comp78079_c0_seq1.p2	sp|Q3YZN2|AROC_SHISS_Chorismate_synthase_OS=Shigella_sonnei_(strain_Ss046)_GN=aroC_PE=3_SV=1	9.00E-65	[illegible]	[illegible]
comp78097_c0_seq1.p1	sp|P39830|YBAL_ECOLI_Inner_membrane_protein_ybaL_OS=Escherichia_coli_(strain_K12)_GN=ybaL_PE=1_SV=2	9.00E-119	[illegible]	[illegible]
comp78160_c0_seq1.p1	sp|Q3YVX3|GPDA_SHISS_Glycerol-3-phosphate_dehydrogenase_[NAD(P)+]_OS=Shigella_sonnei_(strain_Ss046)_GN=gpsA_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp78179_c0_seq1.p1				
comp7820_c0_seq1.p1				
comp78224_c0_seq1.p1	sp|Q8IWZ3|ANKH1_HUMAN_Ankyrin_repeat_and_KH_domain-containing_protein_1_OS=Homo_sapiens_GN=ANKHD1_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp78232_c0_seq1.p1	sp|Q3YW34|RSMJ_SHISS_Ribosomal_RNA_small_subunit_methyltransferase_J_OS=Shigella_sonnei_(strain_Ss046)_GN=rsmJ_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp78233_c0_seq1.p1	sp|P22106|ASNB_ECOLI_Asparagine_synthetase_B_[glutamine-hydrolyzing]_OS=Escherichia_coli_(strain_K12)_GN=asnB_PE=1_SV=3	[illegible]	[illegible]	[illegible]
comp78263_c0_seq1.p2	sp|P0AEF3|DNAC_SHIFL_DNA_replication_protein_dnaC_OS=Shigella_flexneri_GN=dnaC_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp78268_c0_seq1.p1				
comp78303_c0_seq1.p2				
comp78322_c0_seq1.p1	sp|P97807|FUMH_MOUSE_Fumarate_hydratase,_mitochondrial_OS=Mus_musculus_GN=Fh_PE=1_SV=3	[illegible]	[illegible]	[illegible]
comp78340_c0_seq1.p2				
comp78451_c0_seq1.p1	sp|P46825|KLC_LOLPE_Kinesin_light_chain_OS=Loligo_pealeii_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp78529_c0_seq1.p1	sp|Q6P587|FAHD1_HUMAN_Acylpyruvase_FAHD1,_mitochondrial_OS=Homo_sapiens_GN=FAHD1_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp7854_c0_seq1.p1	sp|P19208|HSP7C_CAEBR_Heat_shock_70_kDa_protein_C_OS=Caenorhabditis_briggsae_GN=hsp-3_PE=3_SV=2	[illegible]	[illegible]	[illegible]
comp78557_c0_seq1.p1	sp|Q83KZ1|MANA_SHIFL_Mannose-6-phosphate_isomerase_OS=Shigella_flexneri_GN=manA_PE=3_SV=4	[illegible]	[illegible]	[illegible]
comp78565_c0_seq1.p1	sp|Q3YY22|LPLT_SHISS_Lysophospholipid_transporter_lplT_OS=Shigella_sonnei_(strain_Ss046)_GN=lplT_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp78568_c0_seq1.p1	sp|P47835|RS3B_XENLA_40S_ribosomal_protein_S3-B_OS=Xenopus_laevis_GN=rps3-b_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp78625_c0_seq1.p1				
comp78647_c0_seq1.p1	sp|P0A880|TRPB_SHIFL_Tryptophan_synthase_beta_chain_OS=Shigella_flexneri_GN=trpB_PE=3_SV=2	[illegible]	[illegible]	[illegible]
comp78679_c0_seq1.p1	sp|Q3Z504|QUEA_SHISS_S-adenosylmethionine:tRNA_ribosyltransferase-isomerase_OS=Shigella_sonnei_(strain_Ss046)_GN=queA_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp78693_c0_seq1.p1	sp|P0AGJ5|YFIF_ECOLI_Uncharacterized_tRNA/rRNA_methyltransferase_YfiF_OS=Escherichia_coli_(strain_K12)_GN=yfiF_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp78713_c0_seq1.p1				
comp78719_c0_seq1.p1	sp|O82204|RL281_ARATH_60S_ribosomal_protein_L28-1_OS=Arabidopsis_thaliana_GN=RPL28A_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp78740_c0_seq1.p2	sp|P28011|AAT1_MEDSA_Aspartate_aminotransferase_1_OS=Medicago_sativa_GN=AAT-1_PE=2_SV=2	[illegible]	[illegible]	[illegible]
comp78744_c0_seq1.p1	sp|P0AB01|YCBC_ECOLI_Uncharacterized_protein_ycbC_OS=Escherichia_coli_(strain_K12)_GN=ycbC_PE=4_SV=1	[illegible]	[illegible]	[illegible]
comp78760_c0_seq1.p2	sp|Q3YWA8|YIDC_SHISS_Membrane_protein_insertase_YidC_OS=Shigella_sonnei_(strain_Ss046)_GN=yidC_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp78787_c0_seq1.p1				
comp78800_c0_seq1.p1				
comp78817_c0_seq1.p1				
comp78869_c0_seq1.p1				
comp78875_c0_seq1.p1	sp|P0AFK3|PNUC_SHIFL_Nicotinamide_riboside_transporter_pnuC_OS=Shigella_flexneri_GN=pnuC_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp78883_c0_seq1.p1	sp|Q9P7P0|YOL4_SCHPO_Uncharacterized_acyltransferase_C1718.04_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPBC1718.04_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp78910_c0_seq1.p1	sp|P45549|YHFW_ECOLI_Uncharacterized_protein_yhfW_OS=Escherichia_coli_(strain_K12)_GN=yhfW_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp78920_c0_seq1.p2				
comp78922_c0_seq1.p1				
comp78939_c0_seq1.p1	sp|Q8VCH0|THIKB_MOUSE_3-ketoacyl-CoA_thiolase_B,_peroxisomal_OS=Mus_musculus_GN=Acaa1b_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp78943_c0_seq1.p1	sp|Q9HBG4|VPP4_HUMAN_V-type_proton_ATPase_116_kDa_subunit_a_isoform_4_OS=Homo_sapiens_GN=ATP6V0A4_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp78952_c0_seq1.p2	sp|P45524|YHET_ECOLI_Putative_esterase_YheT_OS=Escherichia_coli_(strain_K12)_GN=yheT_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp78980_c0_seq1.p1	sp|P35128|UBE2N_DROME_Ubiquitin-conjugating_enzyme_E2_N_OS=Drosophila_melanogaster_GN=ben_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp79045_c0_seq1.p1	sp|P0ABG4|FTSW_ECOLI_Lipid_II_flippase_FtsW_OS=Escherichia_coli_(strain_K12)_GN=ftsW_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp79054_c0_seq1.p1	sp|P69054|DHSC_ECOLI_Succinate_dehydrogenase_cytochrome_b556_subunit_OS=Escherichia_coli_(strain_K12)_GN=sdhC_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp79125_c0_seq1.p1	sp|P40711|ARFB_ECOLI_Peptidyl-tRNA_hydrolase_YaeJ_OS=Escherichia_coli_(strain_K12)_GN=yaeJ_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp79160_c0_seq1.p1				
comp79174_c0_seq1.p1	sp|Q3Z397|EFEO_SHISS_Iron_uptake_system_component_EfeO_OS=Shigella_sonnei_(strain_Ss046)_GN=efeO_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp79196_c0_seq1.p2	sp|Q9T043|RL142_ARATH_60S_ribosomal_protein_L14-2_OS=Arabidopsis_thaliana_GN=RPL14B_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp79207_c0_seq1.p1	sp|P0AFK5|POTB_SHIFL_Spermidine/putrescine_transport_system_permease_protein_PotB_OS=Shigella_flexneri_GN=potB_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp79212_c0_seq1.p1				
comp79250_c0_seq1.p1	sp|P19945|RLA0_RAT_60S_acidic_ribosomal_protein_P0_OS=Rattus_norvegicus_GN=Rplp0_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp79265_c0_seq1.p1	sp|B7LUK4|NFI_ESCF3_Endonuclease_V_OS=Escherichia_fergusonii_(strain_ATCC_35469_/_DSM_13698_/_CDC_0568-73)_GN=nfi_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp79274_c0_seq1.p1	sp|P33235|FLGK_ECOLI_Flagellar_hook-associated_protein_1_OS=Escherichia_coli_(strain_K12)_GN=flgK_PE=3_SV=3	[illegible]	[illegible]	[illegible]
comp79275_c0_seq1.p1				
comp79322_c0_seq1.p1	sp|P0A935|MLTA_ECOLI_Membrane-bound_lytic_murein_transglycosylase_A_OS=Escherichia_coli_(strain_K12)_GN=mltA_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp79401_c0_seq1.p2				
comp79408_c0_seq1.p1	sp|Q0T8C6|LEUC_SHIF8_3-isopropylmalate_dehydratase_large_subunit_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=leuC_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp79409_c0_seq1.p1				
comp79415_c0_seq1.p2				
comp79426_c0_seq1.p1				
comp79436_c0_seq1.p1	sp|P00562|AK2H_ECOLI_Bifunctional_aspartokinase/homoserine_dehydrogenase_2_OS=Escherichia_coli_(strain_K12)_GN=metL_PE=1_SV=3	[illegible]	[illegible]	[illegible]
comp79463_c0_seq1.p2	sp|P0C094|SLMA_SHIFL_Nucleoid_occlusion_factor_SlmA_OS=Shigella_flexneri_GN=slmA_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp79464_c0_seq1.p2				
comp79481_c0_seq1.p1				
comp79502_c0_seq1.p1				
comp79504_c0_seq1.p1				
comp79589_c0_seq1.p2	sp|Q3YUZ4|THIG_SHISS_Thiazole_synthase_OS=Shigella_sonnei_(strain_Ss046)_GN=thiG_PE=3_SV=2	[illegible]	[illegible]	[illegible]
comp79592_c0_seq1.p1				
comp79645_c0_seq1.p1				
comp79702_c0_seq1.p2				
comp79738_c0_seq1.p1				
comp79797_c0_seq1.p1	sp|Q9USI5|STI1_SCHPO_Heat_shock_protein_sti1_homolog_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=sti1_PE=2_SV=1	[illegible]	[illegible]	[illegible]
comp79860_c0_seq1.p1				
comp79903_c0_seq1.p1	sp|Q0T2K1|NUOCD_SHIF8_NADH-quinone_oxidoreductase_subunit_C/D_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=nuoC_PE=3_SV=1	[illegible]	[illegible]	[illegible]
comp79923_c0_seq1.p1				
comp79964_c0_seq1.p1				
comp80030_c0_seq1.p1	sp|Q3YXH0|PAT_SHISS_Putrescine_aminotransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=patA_PE=3_SV=2	[illegible]	[illegible]	[illegible]
comp80031_c0_seq1.p2				
comp80067_c0_seq1.p2	sp|P06999|K6PF2_ECOLI_6-phosphofructokinase_isozyme_2_OS=Escherichia_coli_(strain_K12)_GN=pfkB_PE=1_SV=2	[illegible]	[illegible]	[illegible]
comp80073_c0_seq1.p1	sp|P13466|GELA_DICDI_Gelation_factor_OS=Dictyostelium_discoideum_GN=abpC_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp8013_c0_seq1.p1	sp|O97477|INO1_DROME_Inositol-3-phosphate_synthase_OS=Drosophila_melanogaster_GN=Inos_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp80169_c0_seq1.p1	sp|P0AG93|SECF_ECOLI_Protein_translocase_subunit_SecF_OS=Escherichia_coli_(strain_K12)_GN=secF_PE=1_SV=1	[illegible]	[illegible]	[illegible]
comp80192_c0_seq1.p1	sp|P77610|ANSP_ECOLI_L-asparagine_permease_OS=Escherichia_coli_(strain_K12)_GN=ansP_PE=3_SV=2	[illegible]	[illegible]	[illegible]
comp8023_c0_seq1.p1				

comp80300_c0_seq1.p1	sp|P0AE82|CPXA_ECOLI_Sensor_protein_CpxA_OS=Escherichia_coli_(strain_K12)_GN=cpxA_PE=1_SV=1	3.00E-67	[illegible]	[illegible]
comp80309_c0_seq1.p1	sp|Q0T4K8|UXAB_SHIF8_Altronate_oxidoreductase_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=uxaB_PE=3_SV=1	1.00E-102	[illegible]	[illegible]
comp80326_c0_seq1.p1				
comp80365_c0_seq1.p1				
comp80369_c0_seq1.p1				
comp80400_c0_seq1.p1				
comp80410_c0_seq1.p1				
comp80419_c0_seq1.p1				
comp80423_c0_seq1.p1				
comp80444_c0_seq1.p1				
comp80453_c0_seq1.p2				
comp80494_c0_seq1.p2	sp|Q31XT0|PUR4_SHIBS_Phosphoribosylformylglycinamidine_synthase_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=purL_PE=3_SV=3	5.00E-104	[illegible]	[illegible]
comp80521_c0_seq1.p1	sp|Q3YVU0|SYGB_SHISS_Glycine--tRNA_ligase_beta_subunit_OS=Shigella_sonnei_(strain_Ss046)_GN=glyS_PE=3_SV=1	2.00E-69	[illegible]	[illegible]
comp80523_c0_seq1.p1	sp|P21314|YR75_ECOLX_Putative_uncharacterized_protein_ORF5_in_retron_EC67_OS=Escherichia_coli_PE=3_SV=1	2.00E-109		
comp80555_c0_seq1.p1				
comp80604_c0_seq1.p2				
comp80612_c0_seq1.p1				
comp80637_c0_seq1.p1				
comp80645_c0_seq1.p1	sp|P09645|TBA8_CHICK_Tubulin_alpha-8_chain_(Fragment)_OS=Gallus_gallus_PE=3_SV=1	4.00E-64	[illegible]	[illegible]
comp80670_c0_seq1.p1				
comp80750_c0_seq1.p1	sp|P77499|SUFC_ECOLI_Probable_ATP-dependent_transporter_SufC_OS=Escherichia_coli_(strain_K12)_GN=sufC_PE=1_SV=1	2.00E-73	[illegible]	[illegible]
comp80835_c0_seq1.p1	sp|P10443|DPO3A_ECOLI_DNA_polymerase_III_subunit_alpha_OS=Escherichia_coli_(strain_K12)_GN=dnaE_PE=1_SV=1	2.00E-146	[illegible]	[illegible]
comp80901_c0_seq1.p1	sp|P77445|EUTE_ECOLI_Ethanolamine_utilization_protein_eutE_OS=Escherichia_coli_(strain_K12)_GN=eutE_PE=4_SV=1	6.00E-80	[illegible]	[illegible]
comp80959_c0_seq1.p1	sp|Q31TC4|ULAA_SHIBS_Ascorbate-specific_permease_IIC_component_ulaA_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=ulaA_PE=3_SV=2	5.00E-75	[illegible]	[illegible]
comp80983_c0_seq1.p1				
comp81009_c0_seq1.p1	sp|Q9C0G6|DYH6_HUMAN_Dynein_heavy_chain_6,_axonemal_OS=Homo_sapiens_GN=DNAH6_PE=1_SV=3	3.00E-24	[illegible]	[illegible]
comp81147_c0_seq1.p1				
comp81148_c0_seq1.p1				
comp81150_c0_seq1.p1				
comp81224_c0_seq1.p1				
comp81284_c0_seq1.p1				
comp81300_c0_seq1.p1				
comp81329_c0_seq1.p1	sp|P0ADY1|PPID_ECOLI_Peptidyl-prolyl_cis-trans_isomerase_D_OS=Escherichia_coli_(strain_K12)_GN=ppiD_PE=1_SV=1	8.00E-83	[illegible]	[illegible]
comp81340_c0_seq1.p1	sp|Q3Z556|MHPD_SHISS_2-keto-4-pentenoate_hydratase_OS=Shigella_sonnei_(strain_Ss046)_GN=mhpD_PE=3_SV=2	9.00E-75	[illegible]	[illegible]
comp81385_c0_seq1.p1	sp|P25535|VISC_ECOLI_Protein_visC_OS=Escherichia_coli_(strain_K12)_GN=visC_PE=3_SV=2	3.00E-111	[illegible]	[illegible]
comp81430_c0_seq1.p1	sp|Q9P225|DYH2_HUMAN_Dynein_heavy_chain_2,_axonemal_OS=Homo_sapiens_GN=DNAH2_PE=1_SV=3	3.00E-25	[illegible]	[illegible]
comp81445_c0_seq1.p1	sp|P0AC94|GNTP_ECOLI_High-affinity_gluconate_transporter_OS=Escherichia_coli_(strain_K12)_GN=gntP_PE=1_SV=1	5.00E-144	[illegible]	[illegible]
comp81449_c0_seq1.p1				
comp81492_c0_seq1.p1				
comp81493_c0_seq1.p1				
comp81503_c0_seq1.p1	sp|P16682|PHND_ECOLI_Phosphonates-binding_periplasmic_protein_OS=Escherichia_coli_(strain_K12)_GN=phnD_PE=4_SV=2	8.00E-129	[illegible]	[illegible]
comp81536_c0_seq1.p2	sp|P37167|ACTP_ACACA_Actophorin_OS=Acanthamoeba_castellanii_PE=1_SV=2	1.00E-37	[illegible]	[illegible]
comp81539_c0_seq1.p1	sp|Q27802|DYHC2_TRIGR_Cytoplasmic_dynein_2_heavy_chain_1_OS=Tripneustes_gratilla_GN=DYH1B_PE=2_SV=2	1.00E-30	[illegible]	[illegible]
comp81547_c0_seq1.p1				
comp81557_c0_seq1.p1	sp|P16433|HYCG_ECOLI_Formate_hydrogenlyase_subunit_7_OS=Escherichia_coli_(strain_K12)_GN=hycG_PE=1_SV=2	1.00E-81	[illegible]	[illegible]
comp81559_c0_seq1.p1	sp|Q07949|PSR2_YEAST_Probable_phosphatase_PSR2_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=PSR2_PE=1_SV=1	2.00E-12	[illegible]	[illegible]
comp81595_c0_seq1.p1	sp|C6UMS6|MURR_ECOBR_HTH-type_transcriptional_regulator_murR_OS=Escherichia_coli_(strain_B_/_REL606)_GN=murR_PE=3_SV=1	2.00E-92	[illegible]	[illegible]
comp81611_c0_seq1.p1				
comp81619_c0_seq1.p2	sp|P27894|HSP70_LEIBR_Heat_shock_70_kDa_protein_(Fragment)_OS=Leishmania_braziliensis_GN=HSP70_PE=2_SV=1	2.00E-41	GO:0000166,GO:0005524	[illegible]
comp81625_c0_seq1.p1				
comp81687_c0_seq1.p1	sp|Q9SMH3|DYH1A_CHLRE_Dynein-1-alpha_heavy_chain,_flagellar_inner_arm_I1_complex_OS=Chlamydomonas_reinhardtii_GN=DHC1_PE=1_SV=1	1.00E-42	[illegible]	[illegible]
comp81804_c0_seq1.p2	sp|Q0T3Q1|SYR_SHIF8_Arginine--tRNA_ligase_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=argS_PE=3_SV=1	2.00E-66	[illegible]	[illegible]
comp81829_c0_seq1.p1				
comp81881_c0_seq1.p1	sp|P29610|CY12_SOLTU_Cytochrome_c1-2,_heme_protein,_mitochondrial_(Fragment)_OS=Solanum_tuberosum_GN=CYCL_PE=1_SV=1	8.00E-32	[illegible]	[illegible]
comp81905_c0_seq1.p1	sp|Q9VZE6|BRX1_DROME_Ribosome_biogenesis_protein_BRX1_homolog_OS=Drosophila_melanogaster_GN=CG11583_PE=2_SV=2	3.00E-28	[illegible]	[illegible]
comp81910_c0_seq1.p2				
comp81912_c0_seq1.p1	sp|P59194|YFCJ_SHIFL_UPF0226_protein_yfcJ_OS=Shigella_flexneri_GN=yfcJ_PE=3_SV=1	3.00E-46	[illegible]	[illegible]
comp81931_c0_seq1.p1	sp|Q9H611|PIF1_HUMAN_ATP-dependent_DNA_helicase_PIF1_OS=Homo_sapiens_GN=PIF1_PE=1_SV=2	4.00E-22	[illegible]	[illegible]
comp81945_c0_seq1.p1	sp|P30958|MFD_ECOLI_Transcription-repair-coupling_factor_OS=Escherichia_coli_(strain_K12)_GN=mfd_PE=1_SV=2	2.00E-153	[illegible]	[illegible]
comp81963_c0_seq1.p2	sp|P19318|NARY_ECOLI_Respiratory_nitrate_reductase_2_beta_chain_OS=Escherichia_coli_(strain_K12)_GN=narY_PE=1_SV=2	2.00E-81	[illegible]	[illegible]
comp82080_c0_seq1.p1	sp|O16277|H16_CAEEL_Putative_histone_H1.6_OS=Caenorhabditis_elegans_GN=hil-6_PE=2_SV=3	5.00E-17	[illegible]	[illegible]
comp82135_c0_seq1.p1	sp|P0AC18|FOLB_SHIFL_Dihydroneopterin_aldolase_OS=Shigella_flexneri_GN=folB_PE=3_SV=1	3.00E-63	[illegible]	[illegible]
comp82142_c0_seq1.p1	sp|P63687|CTPF_MYCTU_Probable_cation-transporting_ATPase_F_OS=Mycobacterium_tuberculosis_GN=ctpF_PE=1_SV=1	1.00E-15		
comp822_c0_seq1.p1				
comp82339_c0_seq1.p1				
comp82343_c0_seq1.p1	sp|Q3Z5I6|RRF_SHISS_Ribosome-recycling_factor_OS=Shigella_sonnei_(strain_Ss046)_GN=frr_PE=3_SV=1	6.00E-72	[illegible]	[illegible]
comp82345_c0_seq1.p1	sp|P39321|YTFN_ECOLI_Uncharacterized_protein_ytfN_OS=Escherichia_coli_(strain_K12)_GN=ytfN_PE=4_SV=2	1.00E-67	[illegible]	[illegible]
comp82377_c0_seq1.p1	sp|P13009|METH_ECOLI_Methionine_synthase_OS=Escherichia_coli_(strain_K12)_GN=metH_PE=1_SV=5	2.00E-60	[illegible]	[illegible]
comp82406_c0_seq1.p1				
comp82656_c0_seq1.p1	sp|Q3Z5R1|SECA_SHISS_Protein_translocase_subunit_SecA_OS=Shigella_sonnei_(strain_Ss046)_GN=secA_PE=3_SV=1	1.00E-63	[illegible]	[illegible]
comp82657_c0_seq1.p1	sp|Q9KSB2|MAAI_VIBCH_Probable_maleylacetoacetate_isomerase_OS=Vibrio_cholerae_GN=maiA_PE=3_SV=1	8.00E-12	[illegible]	[illegible]
comp82677_c0_seq1.p2	sp|O34399|GLTB_BACSU_Glutamate_synthase_[NADPH]_small_chain_OS=Bacillus_subtilis_GN=gltB_PE=2_SV=2	1.00E-38	[illegible]	[illegible]
comp82717_c0_seq1.p1	sp|P30847|BAES_ECOLI_Signal_transduction_histidine-protein_kinase_BaeS_OS=Escherichia_coli_(strain_K12)_GN=baeS_PE=1_SV=2	4.00E-91	[illegible]	[illegible]
comp82725_c0_seq1.p1	sp|Q3YYZ8|PUR4_SHISS_Phosphoribosylformylglycinamidine_synthase_OS=Shigella_sonnei_(strain_Ss046)_GN=purL_PE=3_SV=3	7.00E-96	[illegible]	[illegible]
comp82756_c0_seq1.p2				
comp82778_c0_seq1.p1	sp|P08394|EX5B_ECOLI_Exodeoxyribonuclease_V_beta_chain_OS=Escherichia_coli_(strain_K12)_GN=recB_PE=1_SV=1	3.00E-65	[illegible]	[illegible]
comp82791_c0_seq1.p1	sp|Q8XBP8|PTFC_ECO57_Fructose-like_permease_IIC_component_OS=Escherichia_coli_O157:H7_GN=fryC_PE=3_SV=1	9.00E-67	[illegible]	[illegible]
comp82868_c0_seq1.p2				
comp82902_c0_seq1.p1				
comp82973_c0_seq1.p1				
comp83085_c0_seq1.p1	sp|Q3Z1X8|ADD_SHISS_Adenosine_deaminase_OS=Shigella_sonnei_(strain_Ss046)_GN=add_PE=3_SV=1	2.00E-72	[illegible]	[illegible]
comp83124_c0_seq1.p1	sp|P36837|DTPB_ECOLI_Dipeptide_and_tripeptide_permease_B_OS=Escherichia_coli_(strain_K12)_GN=dtpB_PE=1_SV=2	1.00E-85	[illegible]	[illegible]
comp83159_c0_seq1.p1	sp|Q3Z4A6|ATKB_SHISS_Potassium-transporting_ATPase_B_chain_OS=Shigella_sonnei_(strain_Ss046)_GN=kdpB_PE=3_SV=1	1.00E-82	[illegible]	[illegible]
comp83194_c0_seq1.p1				
comp83227_c0_seq1.p1				
comp83282_c0_seq1.p1				
comp83418_c0_seq1.p2				
comp83422_c0_seq1.p2				
comp83437_c0_seq1.p1	sp|P21866|KDPE_ECOLI_KDP_operon_transcriptional_regulatory_protein_KdpE_OS=Escherichia_coli_(strain_K12)_GN=kdpE_PE=1_SV=3	5.00E-139	[illegible]	[illegible]
comp83546_c0_seq1.p1	sp|O82204|RL281_ARATH_60S_ribosomal_protein_L28-1_OS=Arabidopsis_thaliana_GN=RPL28A_PE=1_SV=1	2.00E-19	[illegible]	[illegible]
comp83652_c0_seq1.p1				
comp83673_c0_seq1.p1				
comp83681_c0_seq1.p1				
comp83700_c0_seq1.p1	sp|B7FSL4|LONM_PHATC_Lon_protease_homolog,_mitochondrial_OS=Phaeodactylum_tricornutum_(strain_CCAP_1055/1)_GN=PHATRDRAFT_18202_PE=3_SV=1	4.00E-86	[illegible]	[illegible]
comp83705_c0_seq1.p2				
comp83713_c0_seq1.p1				
comp83754_c0_seq1.p1	sp|P21517|MALZ_ECOLI_Maltodextrin_glucosidase_OS=Escherichia_coli_(strain_K12)_GN=malZ_PE=2_SV=5	9.00E-108	[illegible]	[illegible]
comp83755_c0_seq1.p2				
comp83777_c0_seq1.p1	sp|Q2G350|CTAA_NOVAD_Heme_A_synthase_OS=Novosphingobium_aromaticivorans_(strain_DSM_12444)_GN=ctaA_PE=3_SV=1	1.00E-35	[illegible]	[illegible]
comp83797_c0_seq1.p2	sp|P0AA93|YPDA_ECOLI_Inner_membrane_protein_ypdA_OS=Escherichia_coli_(strain_K12)_GN=ypdA_PE=1_SV=1	8.00E-77	[illegible]	[illegible]
comp83798_c0_seq1.p1				
comp83831_c0_seq1.p1				
comp8393_c0_seq1.p1	sp|P0C0S3|MSCS_SHIFL_Small-conductance_mechanosensitive_channel_OS=Shigella_flexneri_GN=mscS_PE=3_SV=1	1.00E-75	[illegible]	[illegible]
comp83950_c0_seq1.p1	sp|P13035|GLPD_ECOLI_Aerobic_glycerol-3-phosphate_dehydrogenase_OS=Escherichia_coli_(strain_K12)_GN=glpD_PE=1_SV=3	8.00E-156	[illegible]	[illegible]
comp83961_c0_seq1.p1				
comp83967_c0_seq1.p1				
comp83990_c0_seq1.p1				
comp84013_c0_seq1.p1	sp|P0AEC0|YOAE_ECOLI_UPF0053_inner_membrane_protein_yoaE_OS=Escherichia_coli_(strain_K12)_GN=yoaE_PE=1_SV=1	7.00E-91	[illegible]	[illegible]
comp84046_c0_seq1.p1				
comp84121_c0_seq1.p1	sp|P00561|AK1H_ECOLI_Bifunctional_aspartokinase/homoserine_dehydrogenase_1_OS=Escherichia_coli_(strain_K12)_GN=thrA_PE=1_SV=2	8.00E-65	[illegible]	[illegible]
comp84224_c0_seq1.p1	sp|Q3YWC7|YIDE_SHISS_Putative_transport_protein_YidE_OS=Shigella_sonnei_(strain_Ss046)_GN=yidE_PE=3_SV=2	1.00E-46	[illegible]	[illegible]
comp8424_c0_seq1.p1	sp|Q0T7M9|BETB_SHIF8_Betaine_aldehyde_dehydrogenase_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=betB_PE=3_SV=1	1.00E-67	[illegible]	[illegible]
comp84405_c0_seq1.p1	sp|P76594|YFIQ_ECOLI_Uncharacterized_protein_yfiQ_OS=Escherichia_coli_(strain_K12)_GN=yfiQ_PE=4_SV=1	3.00E-54	[illegible]	[illegible]
comp84538_c0_seq1.p1	sp|P32141|YIHT_ECOLI_Uncharacterized_aldolase_yihT_OS=Escherichia_coli_(strain_K12)_GN=yihT_PE=3_SV=1	4.00E-66	[illegible]	[illegible]
comp84737_c0_seq1.p1	sp|P19319|NARZ_ECOLI_Respiratory_nitrate_reductase_2_alpha_chain_OS=Escherichia_coli_(strain_K12)_GN=narZ_PE=1_SV=5	2.00E-74	[illegible]	[illegible]
comp84808_c0_seq1.p1	sp|P0AC72|GLRX4_SHIFL_Glutaredoxin-4_OS=Shigella_flexneri_GN=grxD_PE=3_SV=1	4.00E-76	[illegible]	[illegible]
comp84809_c0_seq1.p1	sp|Q8N0N3|BGBP_PENMO_Beta-1,3-glucan-binding_protein_OS=Penaeus_monodon_PE=2_SV=1	7.00E-11	[illegible]	[illegible]
comp84912_c0_seq1.p1				
comp85005_c0_seq1.p1				
comp85136_c0_seq1.p1	sp|P08371|PPDB_ECOLI_Prepilin_peptidase-dependent_protein_B_OS=Escherichia_coli_(strain_K12)_GN=ppdB_PE=3_SV=2	2.00E-63		
comp85172_c0_seq1.p3				
comp85187_c0_seq1.p1	sp|P37769|KDUD_ECOLI_2-dehydro-3-deoxy-D-gluconate_5-dehydrogenase_OS=Escherichia_coli_(strain_K12)_GN=kduD_PE=3_SV=2	7.00E-61	[illegible]	[illegible]
comp85371_c0_seq1.p1				
comp85385_c0_seq1.p1	sp|Q31YA5|SDHD_SHIBS_D-serine_dehydratase_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=dsdA_PE=3_SV=1	2.00E-69	[illegible]	[illegible]
comp85397_c0_seq1.p1				
comp85456_c0_seq1.p1	sp|P46871|KRP95_STRPU_Kinesin-II_95_kDa_subunit_OS=Strongylocentrotus_purpuratus_GN=KRP95_PE=1_SV=1	7.00E-14	[illegible]	[illegible]
comp85460_c0_seq1.p2	sp|Q8XA23|NADB_ECO57_L-aspartate_oxidase_OS=Escherichia_coli_O157:H7_GN=nadB_PE=3_SV=1	7.00E-67	[illegible]	[illegible]
comp85469_c0_seq1.p2				
comp85471_c0_seq1.p2	sp|B1IRB5|ARAB_ECOLC_Ribulokinase_OS=Escherichia_coli_(strain_ATCC_8739_/_DSM_1576_/_Crooks)_GN=araB_PE=3_SV=1	5.00E-86	[illegible]	[illegible]
comp85489_c0_seq1.p1	sp|P00935|METB_ECOLI_Cystathionine_gamma-synthase_OS=Escherichia_coli_(strain_K12)_GN=metB_PE=1_SV=1	6.00E-85	[illegible]	[illegible]
comp85490_c0_seq1.p1	sp|P0AEJ5|ENVZ_SHIFL_Osmolarity_sensor_protein_EnvZ_OS=Shigella_flexneri_GN=envZ_PE=1_SV=1	2.00E-72	[illegible]	[illegible]
comp85495_c0_seq1.p1	sp|P37665|YIAD_ECOLI_Inner_membrane_lipoprotein_YiaD_OS=Escherichia_coli_(strain_K12)_GN=yiaD_PE=1_SV=2	4.00E-57	[illegible]	[illegible]
comp8550_c0_seq1.p1	sp|Q86CZ2|DHKK_DICDI_Hybrid_signal_transduction_histidine_kinase_K_OS=Dictyostelium_discoideum_GN=dhkK_PE=1_SV=1	2.00E-11	[illegible]	[illegible]
comp85521_c0_seq1.p1	sp|Q46871|YQJH_ECOLI_NADPH-dependent_ferric-chelate_reductase_OS=Escherichia_coli_(strain_K12)_GN=yqjH_PE=1_SV=1	5.00E-77	[illegible]	[illegible]
comp85540_c0_seq1.p2	sp|P0AGG2|TESB_ECOLI_Acyl-CoA_thioesterase_2_OS=Escherichia_coli_(strain_K12)_GN=tesB_PE=1_SV=2	2.00E-74	[illegible]	[illegible]
comp85553_c0_seq1.p1				
comp85565_c0_seq1.p1	sp|P00887|AROH_ECOLI_Phospho-2-dehydro-3-deoxyheptonate_aldolase,_Trp-sensitive_OS=Escherichia_coli_(strain_K12)_GN=aroH_PE=3_SV=4	1.00E-99	[illegible]	[illegible]
comp85568_c0_seq1.p1	sp|P0ABH9|CLPA_ECOLI_ATP-dependent_Clp_protease_ATP-binding_subunit_ClpA_OS=Escherichia_coli_(strain_K12)_GN=clpA_PE=1_SV=1	8.00E-104	[illegible]	[illegible]
comp85570_c0_seq1.p1	sp|O13471|HIS2_KLULA_Histidine_biosynthesis_trifunctional_protein_OS=Kluyveromyces_lactis_(strain_ATCC_8585_/_CBS_2359_/_DSM_70799_/_NBRC_1267_/_NRRL_Y-1140_/_WM37)_GN=HIS4_PE=3_SV=2	9.00E-32	[illegible]	[illegible]
comp85587_c0_seq1.p2	sp|P33286|RS28_KLUMA_40S_ribosomal_protein_S28_OS=Kluyveromyces_marxianus_GN=RPS28_PE=3_SV=1	2.00E-20	[illegible]	[illegible]
comp85600_c0_seq1.p1	sp|Q9LD90|CBF5_ARATH_H/ACA_ribonucleoprotein_complex_subunit_4_OS=Arabidopsis_thaliana_GN=CBF5_PE=1_SV=1	2.00E-26	[illegible]	[illegible]
comp85642_c0_seq1.p2	sp|A4HM77|RS3A_LEIBR_40S_ribosomal_protein_S3a_OS=Leishmania_braziliensis_GN=LbrM34_V2.0430_PE=3_SV=1	1.00E-40	[illegible]	[illegible]
comp8565_c0_seq1.p1				
comp85685_c0_seq1.p1				
comp85704_c0_seq1.p2	sp|Q9D7S7|RL22L_MOUSE_60S_ribosomal_protein_L22-like_1_OS=Mus_musculus_GN=Rpl22l1_PE=1_SV=1	3.00E-27	[illegible]	[illegible]
comp85712_c0_seq1.p1				
comp85724_c0_seq1.p1	sp|P33095|RS15A_STRPU_40S_ribosomal_protein_S15a_OS=Strongylocentrotus_purpuratus_GN=RPS15A_PE=2_SV=3	3.00E-49	[illegible]	[illegible]
comp85735_c0_seq1.p1	sp|D1J722|FTSH_ECTSI_ATP-dependent_zinc_metalloprotease_FtsH_OS=Ectocarpus_siliculosus_GN=ftsH_PE=3_SV=1	0	[illegible]	[illegible]
comp85755_c0_seq1.p1				
comp85761_c0_seq1.p1	sp|P76113|CURA_ECOLI_NADPH-dependent_curcumin_reductase_OS=Escherichia_coli_(strain_K12)_GN=curA_PE=1_SV=3	1.00E-80	[illegible]	[illegible]
comp85769_c0_seq1.p1	sp|P37177|PT1P_ECOLI_Phosphoenolpyruvate-protein_phosphotransferase_ptsP_OS=Escherichia_coli_(strain_K12)_GN=ptsP_PE=3_SV=2	5.00E-61	[illegible]	[illegible]
comp85772_c0_seq1.p1	sp|Q3YYG6|SYA_SHISS_Alanine--tRNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=alaS_PE=3_SV=1	3.00E-66	[illegible]	[illegible]
comp85788_c0_seq1.p1	sp|P0ADV5|YHBW_ECOLI_Uncharacterized_protein_yhbW_OS=Escherichia_coli_(strain_K12)_GN=yhbW_PE=4_SV=1	1.00E-97	GO:0016705,GO:0055114	[illegible]
comp85803_c0_seq1.p1	sp|Q3YV31|KATG_SHISS_Catalase-peroxidase_OS=Shigella_sonnei_(strain_Ss046)_GN=katG_PE=3_SV=1	3.00E-114	[illegible]	[illegible]
comp85843_c0_seq1.p1	sp|Q93ZN9|DAPAT_ARATH_LL-diaminopimelate_aminotransferase,_chloroplastic_OS=Arabidopsis_thaliana_GN=DAP_PE=1_SV=1	5.00E-38	[illegible]	[illegible]
comp85849_c0_seq1.p2	sp|P91924|ARF_DUGJA_ADP-ribosylation_factor_OS=Dugesia_japonica_PE=2_SV=3	3.00E-46	[illegible]	[illegible]
comp85863_c0_seq1.p1	sp|P62083|RS7_RAT_40S_ribosomal_protein_S7_OS=Rattus_norvegicus_GN=Rps7_PE=1_SV=1	5.00E-30	[illegible]	[illegible]
comp85867_c0_seq1.p1	sp|Q7XJ96|GAS8_CHLRE_Growth_arrest-specific_protein_8_homolog_OS=Chlamydomonas_reinhardtii_GN=GAS8_PE=1_SV=1	2.00E-20	[illegible]	[illegible]
comp85879_c0_seq1.p1	sp|P0ABV5|EXBD_SHIFL_Biopolymer_transport_protein_exbD_OS=Shigella_flexneri_GN=exbD_PE=3_SV=1	6.00E-66	[illegible]	[illegible]
comp85882_c0_seq1.p1	sp|P16701|CYST_ECOLI_Sulfate_transport_system_permease_protein_CysT_OS=Escherichia_coli_(strain_K12)_GN=cysU_PE=3_SV=1	1.00E-79	[illegible]	[illegible]
comp85886_c0_seq1.p1	sp|P76102|INSQ_ECOLI_Putative_transposase_InsQ_for_insertion_sequence_element_IS609_OS=Escherichia_coli_(strain_K12)_GN=insQ_PE=3_SV=2	6.00E-77	[illegible]	[illegible]
comp85910_c0_seq1.p1				
comp85915_c0_seq1.p1				
comp85938_c0_seq1.p1				
comp85962_c0_seq1.p1	sp|P33941|YOJI_ECOLI_ABC_transporter_ATP-binding_protein_YojI_OS=Escherichia_coli_(strain_K12)_GN=yojI_PE=1_SV=2	2.00E-58	[illegible]	[illegible]
comp85964_c0_seq1.p1				
comp85975_c0_seq1.p1				
comp86016_c0_seq1.p1				
comp86032_c0_seq1.p1				
comp86037_c0_seq1.p1				
comp86041_c0_seq1.p1				
comp86050_c0_seq1.p1				
comp86090_c0_seq1.p1	sp|Q7ZAM1|MUKB_SHIFL_Chromosome_partition_protein_MukB_OS=Shigella_flexneri_GN=mukB_PE=3_SV=1	3.00E-95	[illegible]	[illegible]
comp86098_c0_seq1.p1	sp|B7LJV2|RLMF_ESCF3_Ribosomal_RNA_large_subunit_methyltransferase_F_OS=Escherichia_fergusonii_(strain_ATCC_35469_/_DSM_13698_/_CDC_0568-73)_GN=rlmF_PE=3_SV=1	6.00E-88	[illegible]	[illegible]
comp86109_c0_seq1.p1	sp|P0A707|IF3_ECOLI_Translation_initiation_factor_IF-3_OS=Escherichia_coli_(strain_K12)_GN=infC_PE=1_SV=1	4.00E-51	[illegible]	[illegible]
comp86128_c0_seq1.p2	sp|Q56FG8|RL18_LYSTE_60S_ribosomal_protein_L18_OS=Lysiphlebus_testaceipes_GN=RpL18_PE=2_SV=1	3.00E-48	[illegible]	[illegible]
comp86132_c0_seq1.p1				
comp86151_c0_seq1.p1				
comp86158_c0_seq1.p1				
comp86167_c0_seq1.p1	sp|P32125|MOBB_ECOLI_Molybdopterin-guanine_dinucleotide_biosynthesis_protein_B_OS=Escherichia_coli_(strain_K12)_GN=mobB_PE=1_SV=3	1.00E-65	[illegible]	[illegible]
comp86183_c0_seq1.p2	sp|P0AAJ7|FDOH_SHIFL_Formate_dehydrogenase-O_iron-sulfur_subunit_OS=Shigella_flexneri_GN=fdoH_PE=3_SV=1	3.00E-52	[illegible]	[illegible]
comp86217_c0_seq1.p1				
comp86224_c0_seq1.p1	sp|P30176|YBIA_ECOLI_Swarming_motility_protein_ybiA_OS=Escherichia_coli_(strain_K12)_GN=ybiA_PE=1_SV=1	1.00E-79	GO:0006928	[illegible]
comp86230_c0_seq1.p1	sp|B1H3B1|FUND1_XENTR_FUN14_domain-containing_protein_1_OS=Xenopus_tropicalis_GN=fundc1_PE=2_SV=1	5.00E-11	[illegible]	[illegible]
comp86271_c0_seq1.p1				
comp86282_c0_seq1.p2				
comp86302_c0_seq1.p1	sp|Q02960|MIF_CHICK_Macrophage_migration_inhibitory_factor_OS=Gallus_gallus_GN=MIF_PE=3_SV=3	2.00E-14	[illegible]	[illegible]
comp86310_c0_seq1.p1				
comp86314_c0_seq1.p1				
comp86352_c0_seq1.p1	sp|P0AEP7|GCL_ECOLI_Glyoxylate_carboligase_OS=Escherichia_coli_(strain_K12)_GN=gcl_PE=1_SV=2	1.00E-55	[illegible]	[illegible]
comp86360_c0_seq1.p2				
comp86369_c0_seq1.p1	sp|P0AA30|THIO_SHIFL_Thioredoxin-1_OS=Shigella_flexneri_GN=trxA_PE=3_SV=2	4.00E-67	[illegible]	[illegible]
comp86396_c0_seq1.p1				
comp86447_c0_seq1.p1				
comp86449_c0_seq1.p2	sp|P0AES8|GYRB_SHIFL_DNA_gyrase_subunit_B_OS=Shigella_flexneri_GN=gyrB_PE=3_SV=2	4.00E-78	[illegible]	[illegible]
comp86465_c0_seq1.p1				
comp86466_c0_seq1.p1				
comp86467_c0_seq1.p1	sp|P16918|RHSC_ECOLI_Protein_rhsC_OS=Escherichia_coli_(strain_K12)_GN=rhsC_PE=3_SV=4	3.00E-54	[illegible]	[illegible]
comp86487_c0_seq1.p1				
comp8649_c0_seq1.p1	sp|Q3Z5I1|YAET_SHISS_Outer_membrane_protein_assembly_factor_yaeT_OS=Shigella_sonnei_(strain_Ss046)_GN=yaeT_PE=3_SV=1	5.00E-81	[illegible]	[illegible]
comp86496_c0_seq1.p1	sp|P76037|PUUP_ECOLI_Putrescine_importer_PuuP_OS=Escherichia_coli_(strain_K12)_GN=puuP_PE=1_SV=2	2.00E-65	[illegible]	[illegible]
comp86523_c0_seq1.p1	sp|Q83PW3|FEOB_SHIFL_Ferrous_iron_transport_protein_B_OS=Shigella_flexneri_GN=feoB_PE=3_SV=4	6.00E-37	[illegible]	[illegible]
comp86538_c0_seq1.p1				
comp86544_c0_seq1.p1				
comp86564_c0_seq1.p1	sp|Q32H69|SYR_SHIDS_Arginine--tRNA_ligase_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=argS_PE=3_SV=1	2.00E-49	[illegible]	[illegible]
comp86589_c0_seq1.p1				
comp86616_c0_seq1.p1				
comp86634_c0_seq1.p1	sp|P24242|ASCG_ECOLI_HTH-type_transcriptional_regulator_AscG_OS=Escherichia_coli_(strain_K12)_GN=ascG_PE=1_SV=4	1.00E-70	[illegible]	[illegible]
comp86688_c0_seq1.p1				
comp86707_c0_seq1.p2				
comp86730_c0_seq1.p1	sp|Q46925|CSDA_ECOLI_Cysteine_sulfinate_desulfinase_OS=Escherichia_coli_(strain_K12)_GN=csdA_PE=1_SV=1	5.00E-82	[illegible]	[illegible]
comp86735_c0_seq1.p1	sp|P30131|HYPF_ECOLI_Carbamoyltransferase_hypF_OS=Escherichia_coli_(strain_K12)_GN=hypF_PE=1_SV=2	3.00E-83	[illegible]	[illegible]
comp86740_c0_seq1.p1				
comp86759_c0_seq1.p2				
comp86774_c0_seq1.p1				
comp86798_c0_seq1.p1	sp|P08660|AK3_ECOLI_Lysine-sensitive_aspartokinase_3_OS=Escherichia_coli_(strain_K12)_GN=lysC_PE=1_SV=2	1.00E-68	[illegible]	[illegible]
comp86823_c0_seq1.p1				
comp86824_c0_seq1.p1				
comp86828_c0_seq1.p1	sp|Q3YXD9|UXAC_SHISS_Uronate_isomerase_OS=Shigella_sonnei_(strain_Ss046)_GN=uxaC_PE=3_SV=1	1.00E-98	[illegible]	[illegible]
comp86856_c0_seq1.p1	sp|Q55C16|UBA1_DICDI_Ubiquitin-like_modifier-activating_enzyme_1_OS=Dictyostelium_discoideum_GN=uba1_PE=3_SV=1	2.00E-58	[illegible]	[illegible]
comp86863_c0_seq1.p1	sp|B7IHU7|RL4_THEAB_50S_ribosomal_protein_L4_OS=Thermosipho_africanus_(strain_TCF52B)_GN=rplD_PE=3_SV=1	6.00E-13	[illegible]	[illegible]
comp86867_c0_seq1.p1				
comp86880_c0_seq1.p1	sp|Q3YVN6|ATPB_SHISS_ATP_synthase_subunit_beta_OS=Shigella_sonnei_(strain_Ss046)_GN=atpD_PE=3_SV=1	4.00E-63	[illegible]	[illegible]
comp86892_c0_seq1.p1	sp|Q9FLF0|RS92_ARATH_40S_ribosomal_protein_S9-2_OS=Arabidopsis_thaliana_GN=RPS9C_PE=2_SV=1	9.00E-23	[illegible]	[illegible]
comp86898_c0_seq1.p1				
comp86900_c0_seq1.p1				
comp86934_c0_seq1.p1	sp|Q83SQ3|KEFC_SHIFL_Glutathione-regulated_potassium-efflux_system_protein_kefC_OS=Shigella_flexneri_GN=kefC_PE=3_SV=1	1.00E-61	[illegible]	[illegible]
comp86965_c0_seq1.p1	sp|Q962R1|RS18_SPOFR_40S_ribosomal_protein_S18_OS=Spodoptera_frugiperda_GN=RpS18_PE=2_SV=1	1.00E-47	[illegible]	[illegible]
comp86972_c0_seq1.p1	sp|P0ADS1|YGDH_SHIFL_LOG_family_protein_ygdH_OS=Shigella_flexneri_GN=ygdH_PE=3_SV=1	3.00E-64		
comp86976_c0_seq1.p1				
comp86981_c0_seq1.p1				
comp86986_c0_seq1.p1				
comp86997_c0_seq1.p1				
comp87001_c0_seq1.p1	sp|Q46840|YGHO_ECOLI_Putative_uncharacterized_protein_yghO_(Fragment)_OS=Escherichia_coli_(strain_K12)_GN=yghO_PE=5_SV=2	2.00E-81	[illegible]	[illegible]
comp87011_c0_seq1.p1	sp|P76347|YEEJ_ECOLI_Uncharacterized_protein_yeeJ_OS=Escherichia_coli_(strain_K12)_GN=yeeJ_PE=3_SV=3	2.00E-104	GO:0007155,GO:0043708	[illegible]
comp87015_c0_seq1.p1	sp|Q9UQ07|MOK_HUMAN_MAPK/MAK/MRK_overlapping_kinase_OS=Homo_sapiens_GN=MOK_PE=2_SV=1	7.00E-50	[illegible]	[illegible]
comp87031_c0_seq1.p1				
comp87042_c0_seq1.p1				
comp87055_c0_seq1.p1				
comp87056_c0_seq1.p1	sp|Q63164|DYH1_RAT_Dynein_heavy_chain_1,_axonemal_OS=Rattus_norvegicus_GN=Dnah1_PE=2_SV=2	8.00E-14	[illegible]	[illegible]
comp87105_c0_seq1.p1	sp|P35016|ENPL_CATRO_Endoplasmin_homolog_OS=Catharanthus_roseus_GN=HSP90_PE=2_SV=1	2.00E-36	[illegible]	[illegible]
comp87117_c0_seq1.p1	sp|P10907|UGPC_ECOLI_sn-glycerol-3-phosphate_import_ATP-binding_protein_UgpC_OS=Escherichia_coli_(strain_K12)_GN=ugpC_PE=1_SV=3	3.00E-111	[illegible]	[illegible]
comp87119_c0_seq1.p1				
comp87124_c0_seq1.p1	sp|Q63164|DYH1_RAT_Dynein_heavy_chain_1,_axonemal_OS=Rattus_norvegicus_GN=Dnah1_PE=2_SV=2	2.00E-52	[illegible]	[illegible]
comp87161_c0_seq1.p1	sp|P24049|RL17_RAT_60S_ribosomal_protein_L17_OS=Rattus_norvegicus_GN=Rpl17_PE=2_SV=3	3.00E-33	[illegible]	[illegible]
comp87188_c0_seq1.p1	sp|P75916|YCDZ_ECOLI_Inner_membrane_protein_ycdZ_OS=Escherichia_coli_(strain_K12)_GN=ycdZ_PE=1_SV=2	5.00E-73	[illegible]	[illegible]
comp87207_c0_seq1.p1				
comp87259_c0_seq1.p3	sp|Q4V8U5|ANO10_DANRE_Anoctamin-10_OS=Danio_rerio_GN=ano10_PE=2_SV=1	2.00E-11	[illegible]	[illegible]
comp87289_c0_seq1.p1	sp|Q0SYT0|RAVA_SHIF8_ATPase_ravA_OS=Shigella_flexneri_serotype_5b_(strain_8401)_GN=ravA_PE=3_SV=2	8.00E-113	[illegible]	[illegible]
comp87313_c0_seq1.p2	sp|P42665|HGLB_SCHJA_Hemoglobinase_OS=Schistosoma_japonicum_GN=HAEM_PE=2_SV=1	1.00E-41	[illegible]	[illegible]
comp87318_c0_seq1.p2	sp|Q3YZ04|GLYA_SHISS_Serine_hydroxymethyltransferase_OS=Shigella_sonnei_(strain_Ss046)_GN=glyA_PE=3_SV=1	1.00E-86	[illegible]	[illegible]
comp87321_c0_seq1.p1	sp|Q42540|UBC7_ARATH_Ubiquitin-conjugating_enzyme_E2_7_OS=Arabidopsis_thaliana_GN=UBC7_PE=2_SV=1	5.00E-66	[illegible]	[illegible]
comp87361_c0_seq1.p1	sp|Q9STD3|CALR_CHLRE_Calreticulin_OS=Chlamydomonas_reinhardtii_PE=2_SV=1	4.00E-42	[illegible]	[illegible]
comp87363_c0_seq1.p1	sp|Q03685|BIP5_TOBAC_Luminal-binding_protein_5_OS=Nicotiana_tabacum_GN=BIP5_PE=2_SV=1	2.00E-45	[illegible]	[illegible]
comp87378_c0_seq1.p2	sp|P75684|YAGP_ECOLI_Uncharacterized_protein_yagP_OS=Escherichia_coli_(strain_K12)_GN=yagP_PE=5_SV=1	3.00E-50		
comp87389_c0_seq1.p1				
comp87396_c0_seq1.p1				
comp87451_c0_seq1.p2	sp|P62907|RL10A_RAT_60S_ribosomal_protein_L10a_OS=Rattus_norvegicus_GN=Rpl10a_PE=1_SV=2	1.00E-51	[illegible]	[illegible]
comp87470_c0_seq1.p1	sp|P76192|YDHV_ECOLI_Uncharacterized_oxidoreductase_YdhV_OS=Escherichia_coli_(strain_K12)_GN=ydhV_PE=2_SV=1	7.00E-89	[illegible]	[illegible]
comp87496_c0_seq1.p1	sp|P0AFR6|YCIO_SHIFL_Uncharacterized_protein_yciO_OS=Shigella_flexneri_GN=yciO_PE=3_SV=1	5.00E-69	GO:0003725	[illegible]
comp87555_c0_seq1.p1	sp|P29018|CYDD_ECOLI_ATP-binding/permease_protein_CydD_OS=Escherichia_coli_(strain_K12)_GN=cydD_PE=1_SV=3	2.00E-68	[illegible]	[illegible]
comp87575_c0_seq1.p1	sp|P0AE06|ACRA_ECOLI_Acriflavine_resistance_protein_A_OS=Escherichia_coli_(strain_K12)_GN=acrA_PE=1_SV=1	9.00E-100	[illegible]	[illegible]
comp87586_c0_seq1.p1	sp|Q9NB33|RL44_AEDTR_60S_ribosomal_protein_L44_OS=Aedes_triseriatus_GN=RpL44_PE=3_SV=3	1.00E-46	[illegible]	[illegible]
comp87602_c0_seq1.p1	sp|P77567|NHOA_ECOLI_N-hydroxyarylamine_O-acetyltransferase_OS=Escherichia_coli_(strain_K12)_GN=nhoA_PE=3_SV=1	7.00E-83	[illegible]	[illegible]
comp87694_c0_seq1.p1	sp|Q3YU91|SYV_SHISS_Valine--tRNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=valS_PE=3_SV=1	1.00E-85	[illegible]	[illegible]
comp87703_c0_seq1.p1	sp|P24182|ACCC_ECOLI_Biotin_carboxylase_OS=Escherichia_coli_(strain_K12)_GN=accC_PE=1_SV=2	4.00E-50	[illegible]	[illegible]
comp87704_c0_seq1.p2	sp|P04395|3MG2_ECOLI_DNA-3-methyladenine_glycosylase_2_OS=Escherichia_coli_(strain_K12)_GN=alkA_PE=1_SV=1	2.00E-67	[illegible]	[illegible]
comp87717_c0_seq1.p1	sp|Q32E44|MUKB_SHIDS_Chromosome_partition_protein_MukB_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=mukB_PE=3_SV=1	2.00E-64	[illegible]	[illegible]
comp87727_c0_seq1.p1				
comp87765_c0_seq1.p1	sp|Q820C8|LNT_SHIFL_Apolipoprotein_N-acyltransferase_OS=Shigella_flexneri_GN=lnt_PE=3_SV=1	4.00E-104	[illegible]	[illegible]
comp87799_c0_seq1.p1	sp|P00561|AK1H_ECOLI_Bifunctional_aspartokinase/homoserine_dehydrogenase_1_OS=Escherichia_coli_(strain_K12)_GN=thrA_PE=1_SV=2	2.00E-100	[illegible]	[illegible]
comp87801_c0_seq1.p2	sp|Q80W93|HYDIN_MOUSE_Hydrocephalus-inducing_protein_OS=Mus_musculus_GN=Hydin_PE=2_SV=2	2.00E-12	[illegible]	[illegible]
comp87838_c0_seq1.p1	sp|P37595|IAAA_ECOLI_Isoaspartyl_peptidase_OS=Escherichia_coli_(strain_K12)_GN=iaaA_PE=1_SV=2	1.00E-117	[illegible]	[illegible]
comp87840_c0_seq1.p1	sp|P38708|YHI0_YEAST_Putative_proline--tRNA_ligase_YHR020W_OS=Saccharomyces_cerevisiae_(strain_ATCC_204508_/_S288c)_GN=YHR020W_PE=1_SV=1	2.00E-20	[illegible]	[illegible]
comp87858_c0_seq1.p1	sp|Q83JC4|EFTU_SHIFL_Elongation_factor_Tu_OS=Shigella_flexneri_GN=tufA_PE=3_SV=3	6.00E-75	[illegible]	[illegible]
comp87862_c0_seq1.p1				
comp87880_c0_seq1.p1				
comp87898_c0_seq1.p1				
comp87938_c0_seq1.p1				
comp87963_c0_seq1.p2				
comp87993_c0_seq1.p1				
comp88033_c0_seq1.p1	sp|Q3YWJ3|TREF_SHISS_Cytoplasmic_trehalase_OS=Shigella_sonnei_(strain_Ss046)_GN=treF_PE=3_SV=1	3.00E-71	[illegible]	[illegible]
comp88035_c0_seq1.p1				
comp88134_c0_seq1.p2				
comp8814_c0_seq1.p1	sp|Q83MG0|MURE_SHIFL_UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate_ligase_OS=Shigella_flexneri_GN=murE_PE=3_SV=1	8.00E-44	[illegible]	[illegible]
comp88159_c0_seq1.p1	sp|P54408|TCPG_TETPY_T-complex_protein_1_subunit_gamma_OS=Tetrahymena_pyriformis_PE=3_SV=1	9.00E-64	[illegible]	[illegible]
comp88161_c0_seq1.p1	sp|P42742|PSB1_ARATH_Proteasome_subunit_beta_type-1_OS=Arabidopsis_thaliana_GN=PBF1_PE=1_SV=2	3.00E-55	[illegible]	[illegible]
comp88173_c0_seq1.p1	sp|P0AEC0|YOAE_ECOLI_UPF0053_inner_membrane_protein_yoaE_OS=Escherichia_coli_(strain_K12)_GN=yoaE_PE=1_SV=1	7.00E-52	[illegible]	[illegible]
comp88183_c0_seq1.p1	sp|Q9FJX2|RL262_ARATH_60S_ribosomal_protein_L26-2_OS=Arabidopsis_thaliana_GN=RPL26B_PE=2_SV=1	1.00E-25	[illegible]	[illegible]
comp88223_c0_seq1.p1	sp|P0A9K8|PHOU_SHIFL_Phosphate_transport_system_protein_phoU_OS=Shigella_flexneri_GN=phoU_PE=3_SV=1	1.00E-67	[illegible]	[illegible]
comp88244_c0_seq1.p2	sp|P15043|RECQ_ECOLI_ATP-dependent_DNA_helicase_recQ_OS=Escherichia_coli_(strain_K12)_GN=recQ_PE=1_SV=5	1.00E-68	[illegible]	[illegible]
comp88248_c0_seq1.p1	sp|P60064|ADIC_SHIFL_Arginine/agmatine_antiporter_OS=Shigella_flexneri_GN=adiC_PE=3_SV=1	1.00E-57	[illegible]	[illegible]
comp88249_c0_seq1.p1	sp|Q6VTH5|RSPH1_CYPCA_Radial_spoke_head_1_homolog_OS=Cyprinus_carpio_GN=rsph1_PE=1_SV=1	1.00E-13	[illegible]	[illegible]
comp88273_c0_seq1.p1				
comp88275_c0_seq1.p1	sp|P09831|GLTB_ECOLI_Glutamate_synthase_[NADPH]_large_chain_OS=Escherichia_coli_(strain_K12)_GN=gltB_PE=1_SV=3	2.00E-77	[illegible]	[illegible]
comp88316_c0_seq1.p1	sp|Q32BV3|SYK_SHIDS_Lysine--tRNA_ligase_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=lysS_PE=3_SV=1	3.00E-70	[illegible]	[illegible]
comp88321_c0_seq1.p1				
comp88346_c0_seq1.p1	sp|P0ABB8|ATMA_ECOLI_Magnesium-transporting_ATPase,_P-type_1_OS=Escherichia_coli_(strain_K12)_GN=mgtA_PE=1_SV=1	1.00E-99	[illegible]	[illegible]
comp88387_c0_seq1.p2				
comp88416_c0_seq1.p2				
comp88433_c0_seq1.p1				
comp88447_c0_seq1.p1				
comp88450_c0_seq1.p1				

comp88487_c0_seq1.p1		
comp88491_c0_seq1.p1	sp|P42911|PTPD_ECOLI_N-acetylgalactosamine_permease_IID_component_OS=Escherichia_coli_(strain_K12)_GN=agaD_PE=4_SV=1	4.00E-74
comp88500_c0_seq1.p1	sp|Q8GXI9|PV42B_ARATH_SNF1-related_protein_kinase_regulatory_subunit_gamma-like_PV42b_OS=Arabidopsis_thaliana_GN=PV42B_PE=2_SV=1	4.00E-13
comp88528_c0_seq1.p1		
comp88554_c0_seq1.p1	sp|B2TYP0|RNFH_SHIB3_Protein_RnfH_OS=Shigella_boydii_serotype_18_(strain_CDC_3083-94_/_BS512)_GN=rnfH_PE=3_SV=1	2.00E-60
comp88555_c0_seq1.p1		
comp88592_c0_seq1.p1		
comp88606_c0_seq1.p3		
comp88630_c0_seq1.p1		
comp88653_c0_seq1.p2	sp|P27250|YJGB_ECOLI_Uncharacterized_zinc-type_alcohol_dehydrogenase-like_protein_YjgB_OS=Escherichia_coli_(strain_K12)_GN=yjgB_PE=3_SV=2	3.00E-116
comp88670_c0_seq1.p1		
comp88675_c0_seq1.p1		
comp88688_c0_seq1.p1	sp|P33225|TORA_ECOLI_Trimethylamine-N-oxide_reductase_1_OS=Escherichia_coli_(strain_K12)_GN=torA_PE=1_SV=2	9.00E-75
comp88710_c0_seq1.p1		
comp88730_c0_seq1.p1		
comp88735_c0_seq1.p1	sp|Q3YX23|NANA_SHISS_N-acetylneuraminate_lyase_OS=Shigella_sonnei_(strain_Ss046)_GN=nanA_PE=3_SV=1	2.00E-71
comp88762_c0_seq1.p1	sp|Q3YU89|AMPA_SHISS_Probable_cytosol_aminopeptidase_OS=Shigella_sonnei_(strain_Ss046)_GN=pepA_PE=3_SV=1	3.00E-104
comp88788_c0_seq1.p1	sp|O65082|RL15B_PICMA_60S_ribosomal_protein_L15-2_OS=Picea_mariana_GN=SB62_PE=2_SV=1	3.00E-62
comp88793_c0_seq1.p1		
comp88798_c0_seq1.p1	sp|P76577|PBPC_ECOLI_Penicillin-binding_protein_1C_OS=Escherichia_coli_(strain_K12)_GN=pbpC_PE=3_SV=1	6.00E-77
comp88829_c0_seq1.p1		
comp88883_c0_seq1.p1	sp|Q9SIV2|RPN1A_ARATH_26S_proteasome_non-ATPase_regulatory_subunit_2_1A_OS=Arabidopsis_thaliana_GN=RPN1A_PE=1_SV=2	2.00E-35
comp88889_c0_seq1.p2	sp|B8ELE2|KAD_METSB_Adenylate_kinase_OS=Methylocella_silvestris_(strain_BL2_/_DSM_15510_/_NCIMB_13906)_GN=adk_PE=3_SV=1	3.00E-38
comp88958_c0_seq1.p2	sp|Q1R270|RF3_ECOUT_Peptide_chain_release_factor_3_OS=Escherichia_coli_(strain_UTI89_/_UPEC)_GN=prfC_PE=3_SV=1	2.00E-78
comp88959_c0_seq1.p1	sp|Q6RUV5|RAC1_RAT_Ras-related_C3_botulinum_toxin_substrate_1_OS=Rattus_norvegicus_GN=Rac1_PE=1_SV=1	3.00E-72
comp88966_c0_seq1.p1		
comp88983_c0_seq1.p2		
comp88996_c0_seq1.p1	sp|Q3YW05|RNPH_SHISS_Ribonuclease_PH_OS=Shigella_sonnei_(strain_Ss046)_GN=rph_PE=3_SV=1	2.00E-70
comp89036_c0_seq1.p1		
comp89046_c0_seq1.p1		
comp89139_c0_seq1.p1	sp|O00295|TULP2_HUMAN_Tubby-related_protein_2_OS=Homo_sapiens_GN=TULP2_PE=2_SV=2	3.00E-12
comp89150_c0_seq1.p1	sp|P50528|PLO1_SCHPO_Serine/threonine-protein_kinase_plo1_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=plo1_PE=1_SV=1	1.00E-13
comp8920_c0_seq1.p1		
comp89211_c0_seq1.p1		
comp89243_c0_seq1.p2	sp|P63236|GADC_SHIFL_Probable_glutamate/gamma-aminobutyrate_antiporter_OS=Shigella_flexneri_GN=gadC_PE=3_SV=1	4.00E-60
comp89286_c0_seq1.p2	sp|P08394|EX5B_ECOLI_Exodeoxyribonuclease_V_beta_chain_OS=Escherichia_coli_(strain_K12)_GN=recB_PE=1_SV=1	2.00E-67
comp89305_c0_seq1.p1	sp|A9ILH7|DNAK_BART1_Chaperone_protein_DnaK_OS=Bartonella_tribocorum_(strain_CIP_105476_/_IBS_506)_GN=dnaK_PE=3_SV=1	7.00E-62
comp89309_c0_seq1.p1	sp|Q3YY94|CYSJ_SHISS_Sulfite_reductase_[NADPH]_flavoprotein_alpha-component_OS=Shigella_sonnei_(strain_Ss046)_GN=cysJ_PE=3_SV=1	8.00E-51
comp89428_c0_seq1.p1	sp|Q9FRS6|PXL1_ARATH_Leucine-rich_repeat_receptor-like_protein_kinase_PXL1_OS=Arabidopsis_thaliana_GN=PXL1_PE=2_SV=1	1.00E-12
comp89474_c0_seq1.p1		
comp89475_c0_seq1.p1	sp|P15029|FECD_ECOLI_Fe(3+)_dicitrate_transport_system_permease_protein_fecD_OS=Escherichia_coli_(strain_K12)_GN=fecD_PE=1_SV=2	1.00E-92
comp8949_c0_seq1.p1		
comp89602_c0_seq1.p1		
comp89643_c0_seq1.p1		
comp89661_c0_seq1.p1		
comp89668_c0_seq1.p1	sp|Q869Q0|Y4527_DICDI_COBW_domain-containing_protein_DDB_G0274527_OS=Dictyostelium_discoideum_GN=DDB_G0274527_PE=3_SV=1	1.00E-13
comp89699_c0_seq1.p1		
comp89704_c0_seq1.p1		
comp89771_c0_seq1.p1	sp|P77187|YAHF_ECOLI_Uncharacterized_protein_yahF_OS=Escherichia_coli_(strain_K12)_GN=yahF_PE=4_SV=1	7.00E-37
comp89782_c0_seq1.p1		
comp89809_c0_seq1.p1	sp|P0A988|DPO3B_ECOLI_DNA_polymerase_III_subunit_beta_OS=Escherichia_coli_(strain_K12)_GN=dnaN_PE=1_SV=1	9.00E-77
comp89827_c0_seq1.p1		
comp89848_c0_seq1.p1		
comp89855_c0_seq1.p1	sp|Q4PM12|RL36_IXOSC_60S_ribosomal_protein_L36_OS=Ixodes_scapularis_GN=RpL36_PE=3_SV=1	6.00E-18
comp89862_c0_seq1.p1	sp|P61082|UBC12_MOUSE_NEDD8-conjugating_enzyme_Ubc12_OS=Mus_musculus_GN=Ube2m_PE=2_SV=1	1.00E-60
comp89906_c0_seq1.p2	sp|P0A9G6|ACEA_ECOLI_Isocitrate_lyase_OS=Escherichia_coli_(strain_K12)_GN=aceA_PE=1_SV=1	1.00E-71
comp8991_c0_seq1.p1	sp|P42592|YGJK_ECOLI_Uncharacterized_protein_ygjK_OS=Escherichia_coli_(strain_K12)_GN=ygjK_PE=1_SV=1	1.00E-69
comp90068_c0_seq1.p1	sp|Q3YY94|CYSJ_SHISS_Sulfite_reductase_[NADPH]_flavoprotein_alpha-component_OS=Shigella_sonnei_(strain_Ss046)_GN=cysJ_PE=3_SV=1	4.00E-60
comp90069_c0_seq1.p1		
comp90103_c0_seq1.p1		
comp90106_c0_seq1.p1	sp|Q3Z5K2|CLCA_SHISS_H(+)/Cl(-)_exchange_transporter_ClcA_OS=Shigella_sonnei_(strain_Ss046)_GN=clcA_PE=3_SV=1	2.00E-75
comp90121_c0_seq1.p2	sp|Q3YUF1|ULAE_SHISS_L-ribulose-5-phosphate_3-epimerase_UlaE_OS=Shigella_sonnei_(strain_Ss046)_GN=ulaE_PE=3_SV=1	8.00E-66
comp90149_c0_seq1.p1	sp|Q3Z515|RDGC_SHISS_Recombination-associated_protein_rdgC_OS=Shigella_sonnei_(strain_Ss046)_GN=rdgC_PE=3_SV=1	1.00E-83
comp90173_c0_seq1.p1		
comp90197_c0_seq1.p1	sp|Q8BH16|FBXL2_MOUSE_F-box/LRR-repeat_protein_2_OS=Mus_musculus_GN=Fbxl2_PE=2_SV=1	2.00E-14
comp90218_c0_seq1.p1	sp|P77489|YAGR_ECOLI_Putative_xanthine_dehydrogenase_YagR_molybdenum-binding_subunit_OS=Escherichia_coli_(strain_K12)_GN=yagR_PE=3_SV=1	8.00E-57
comp90246_c0_seq1.p1	sp|P27133|COROA_DICDI_Coronin-A_OS=Dictyostelium_discoideum_GN=corA_PE=1_SV=2	2.00E-50
comp90301_c0_seq1.p1	sp|Q3YZ29|PEPB_SHISS_Peptidase_B_OS=Shigella_sonnei_(strain_Ss046)_GN=pepB_PE=3_SV=2	1.00E-76
comp90307_c0_seq1.p1		
comp90309_c0_seq1.p1	sp|Q9NQT8|KI13B_HUMAN_Kinesin-like_protein_KIF13B_OS=Homo_sapiens_GN=KIF13B_PE=1_SV=1	5.00E-26
comp90345_c0_seq1.p1	sp|P0ACL1|GLPR_SHIFL_Glycerol-3-phosphate_regulon_repressor_OS=Shigella_flexneri_GN=glpR_PE=4_SV=1	8.00E-71
comp90350_c0_seq1.p1		
comp90374_c0_seq1.p1		
comp90432_c0_seq1.p1	sp|Q8FAG0|IPYR_ECOL6_Inorganic_pyrophosphatase_OS=Escherichia_coli_O6_GN=ppa_PE=3_SV=3	4.00E-98
comp90478_c0_seq1.p1	sp|P0AA21|OMPR_SHIFL_Transcriptional_regulatory_protein_OmpR_OS=Shigella_flexneri_GN=ompR_PE=3_SV=1	1.00E-167
comp90483_c0_seq1.p1	sp|P24230|RECG_ECOLI_ATP-dependent_DNA_helicase_recG_OS=Escherichia_coli_(strain_K12)_GN=recG_PE=1_SV=1	1.00E-58
comp90503_c0_seq1.p1	sp|P77802|YAGX_ECOLI_Uncharacterized_protein_yagX_OS=Escherichia_coli_(strain_K12)_GN=yagX_PE=4_SV=1	3.00E-131
comp90513_c0_seq1.p1		
comp90519_c0_seq1.p1	sp|P24182|ACCC_ECOLI_Biotin_carboxylase_OS=Escherichia_coli_(strain_K12)_GN=accC_PE=1_SV=2	3.00E-68
comp90607_c0_seq1.p1		
comp90657_c0_seq1.p1	sp|Q4R7Y5|DNJB6_MACFA_DnaJ_homolog_subfamily_B_member_6_OS=Macaca_fascicularis_GN=DNAJB6_PE=2_SV=1	4.00E-18
comp90730_c0_seq1.p1	sp|Q5I0K3|CLYBL_RAT_Citrate_lyase_subunit_beta-like_protein,_mitochondrial_OS=Rattus_norvegicus_GN=Clybl_PE=2_SV=2	6.00E-13
comp90735_c0_seq1.p1	sp|Q3YVC1|FADB_SHISS_Fatty_acid_oxidation_complex_subunit_alpha_OS=Shigella_sonnei_(strain_Ss046)_GN=fadB_PE=3_SV=1	1.00E-69
comp90775_c0_seq1.p1		
comp90823_c0_seq1.p1		
comp90870_c0_seq1.p2	sp|B8D757|DNAJ_BUCAT_Chaperone_protein_DnaJ_OS=Buchnera_aphidicola_subsp._Acyrthosiphon_pisum_(strain_Tuc7)_GN=dnaJ_PE=3_SV=1	1.00E-16
comp90901_c0_seq1.p1	sp|P29217|YCEH_ECOLI_UPF0502_protein_YceH_OS=Escherichia_coli_(strain_K12)_GN=yceH_PE=1_SV=3	7.00E-97
comp90914_c0_seq1.p1		
comp90934_c0_seq1.p1	sp|Q46855|YQHC_ECOLI_Uncharacterized_HTH-type_transcriptional_regulator_yqhC_OS=Escherichia_coli_(strain_K12)_GN=yqhC_PE=4_SV=2	2.00E-79
comp90976_c0_seq1.p1		
comp90991_c0_seq1.p1		
comp91182_c0_seq1.p1		
comp91218_c0_seq1.p1	sp|B1IP46|RTCA_ECOLC_RNA_3'-terminal_phosphate_cyclase_OS=Escherichia_coli_(strain_ATCC_8739_/_DSM_1576_/_Crooks)_GN=rtcA_PE=3_SV=1	1.00E-96
comp91220_c0_seq1.p1		
comp91248_c0_seq1.p1		
comp91256_c0_seq1.p1		
comp91286_c0_seq1.p2	sp|P21345|GLTP_ECOLI_Proton_glutamate_symport_protein_OS=Escherichia_coli_(strain_K12)_GN=gltP_PE=1_SV=2	4.00E-60
comp91327_c0_seq1.p1		
comp91365_c0_seq1.p1	sp|P77804|YDGA_ECOLI_Protein_ydgA_OS=Escherichia_coli_(strain_K12)_GN=ydgA_PE=1_SV=1	8.00E-106
comp91377_c0_seq1.p1		
comp91445_c0_seq1.p1	sp|P10443|DPO3A_ECOLI_DNA_polymerase_III_subunit_alpha_OS=Escherichia_coli_(strain_K12)_GN=dnaE_PE=1_SV=1	3.00E-86
comp91482_c0_seq1.p2		
comp91530_c0_seq1.p1		
comp91571_c0_seq1.p2		
comp91579_c0_seq1.p1		
comp91634_c0_seq1.p2	sp|P17315|CIRA_ECOLI_Colicin_I_receptor_OS=Escherichia_coli_(strain_K12)_GN=cirA_PE=1_SV=2	8.00E-115
comp91666_c0_seq1.p1		
comp91671_c0_seq1.p1	sp|P16095|SDHL_ECOLI_L-serine_dehydratase_1_OS=Escherichia_coli_(strain_K12)_GN=sdaA_PE=1_SV=3	2.00E-105
comp91685_c0_seq1.p1	sp|P06972|FHUB_ECOLI_Iron(3+)-hydroxamate_import_system_permease_protein_fhuB_OS=Escherichia_coli_(strain_K12)_GN=fhuB_PE=1_SV=2	2.00E-46
comp91712_c0_seq1.p2	sp|P0ADV8|MLAC_SHIFL_Probable_phospholipid-binding_protein_mlaC_OS=Shigella_flexneri_GN=mlaC_PE=3_SV=1	4.00E-86
comp91798_c0_seq1.p1		
comp91846_c0_seq1.p1		
comp91952_c0_seq1.p1	sp|Q96M98|PACRG_HUMAN_Parkin_coregulated_gene_protein_OS=Homo_sapiens_GN=PACRG_PE=1_SV=2	5.00E-12
comp91995_c0_seq1.p2	sp|Q9AKR8|ARGC_RHIET_N-acetyl-gamma-glutamyl-phosphate_reductase_OS=Rhizobium_etli_GN=argC_PE=3_SV=1	6.00E-29
comp92009_c0_seq1.p1	sp|Q3YXB3|TDCC_SHISS_Threonine/serine_transporter_TdcC_OS=Shigella_sonnei_(strain_Ss046)_GN=tdcC_PE=3_SV=1	3.00E-98
comp92133_c0_seq1.p1		
comp92143_c0_seq1.p2	sp|P0AF72|YJEI_SHIFL_Uncharacterized_protein_yjeI_OS=Shigella_flexneri_GN=yjeI_PE=4_SV=1	6.00E-79
comp92217_c0_seq1.p2		
comp92298_c0_seq1.p2		
comp92311_c0_seq1.p1	sp|P76128|DDPA_ECOLI_Probable_D,D-dipeptide-binding_periplasmic_protein_ddpA_OS=Escherichia_coli_(strain_K12)_GN=ddpA_PE=2_SV=1	6.00E-104
comp92326_c0_seq1.p1		
comp92385_c0_seq1.p2		
comp92402_c0_seq1.p1		
comp92493_c0_seq1.p1	sp|P09373|PFLB_ECOLI_Formate_acetyltransferase_1_OS=Escherichia_coli_(strain_K12)_GN=pflB_PE=1_SV=2	3.00E-95
comp92580_c0_seq1.p1	sp|P69804|PTNC_SHIFL_Mannose_permease_IIC_component_OS=Shigella_flexneri_GN=manY_PE=3_SV=1	3.00E-62
comp92589_c0_seq1.p1		
comp92871_c0_seq1.p1	sp|P76389|YEGH_ECOLI_UPF0053_protein_yegH_OS=Escherichia_coli_(strain_K12)_GN=yegH_PE=3_SV=2	7.00E-93
comp92891_c0_seq1.p1	sp|Q3Z2M4|SYD_SHISS_Aspartate--tRNA_ligase_OS=Shigella_sonnei_(strain_Ss046)_GN=aspS_PE=3_SV=1	8.00E-78
comp92963_c0_seq1.p2	sp|P00968|CARB_ECOLI_Carbamoyl-phosphate_synthase_large_chain_OS=Escherichia_coli_(strain_K12)_GN=carB_PE=1_SV=2	2.00E-107
comp92969_c0_seq1.p1		
comp92980_c0_seq1.p1	sp|P0AEC4|ARCB_SHIFL_Aerobic_respiration_control_sensor_protein_ArcB_OS=Shigella_flexneri_GN=arcB_PE=3_SV=1	1.00E-51
comp93059_c0_seq1.p1	sp|P0A9S1|FUCO_ECOLI_Lactaldehyde_reductase_OS=Escherichia_coli_(strain_K12)_GN=fucO_PE=1_SV=2	1.00E-93
comp93068_c0_seq1.p1		
comp93111_c0_seq1.p1		
comp93125_c0_seq1.p1	sp|P09373|PFLB_ECOLI_Formate_acetyltransferase_1_OS=Escherichia_coli_(strain_K12)_GN=pflB_PE=1_SV=2	5.00E-71
comp93141_c0_seq1.p1		
comp93247_c0_seq1.p1	sp|P04994|EX7L_ECOLI_Exodeoxyribonuclease_7_large_subunit_OS=Escherichia_coli_(strain_K12)_GN=xseA_PE=1_SV=2	5.00E-155
comp93266_c0_seq1.p1		
comp93309_c0_seq1.p1	sp|P27828|WECB_ECOLI_UDP-N-acetylglucosamine_2-epimerase_OS=Escherichia_coli_(strain_K12)_GN=wecB_PE=1_SV=2	2.00E-84
comp93354_c0_seq1.p1		
comp93367_c0_seq1.p1		
comp93467_c0_seq1.p1	sp|P30958|MFD_ECOLI_Transcription-repair-coupling_factor_OS=Escherichia_coli_(strain_K12)_GN=mfd_PE=1_SV=2	3.00E-98
comp93471_c0_seq1.p1		
comp93475_c0_seq1.p1		
comp93572_c0_seq1.p1	sp|Q26626|KIFA3_STRPU_Kinesin-associated_protein_3_OS=Strongylocentrotus_purpuratus_GN=KAP115_PE=1_SV=1	2.00E-13
comp93855_c0_seq1.p1	sp|Q54QB1|ERK2_DICDI_Extracellular_signal-regulated_kinase_2_OS=Dictyostelium_discoideum_GN=erkB_PE=1_SV=1	6.00E-60
comp93881_c0_seq1.p1	sp|O29441|Y817_ARCFU_Uncharacterized_protein_AF_0817_OS=Archaeoglobus_fulgidus_(strain_ATCC_49558_/_VC-16_/_DSM_4304_/_JCM_9628_/_NBRC_100126)_GN=AF_0817_PE=4_SV=1	3.00E-13
comp94006_c0_seq1.p1		
comp94014_c0_seq1.p1		
comp94022_c0_seq1.p1	sp|Q55C16|UBA1_DICDI_Ubiquitin-like_modifier-activating_enzyme_1_OS=Dictyostelium_discoideum_GN=uba1_PE=3_SV=1	3.00E-36
comp94038_c0_seq1.p1		
comp94075_c0_seq1.p1	sp|Q6UR05|MRP1_CANFA_Multidrug_resistance-associated_protein_1_OS=Canis_familiaris_GN=ABCC1_PE=2_SV=1	3.00E-21
comp94159_c0_seq1.p1		
comp94305_c0_seq1.p1		
comp94368_c0_seq1.p1		
comp94372_c0_seq1.p1		
comp9449_c0_seq1.p1		
comp94499_c0_seq1.p1		
comp9450_c1_seq1.p1		
comp94519_c0_seq1.p2		
comp9454_c0_seq2.p1		
comp94559_c0_seq1.p1		
comp94609_c0_seq1.p1		
comp9461_c0_seq1.p1		
comp9470_c0_seq1.p1		
comp9472_c0_seq2.p1		
comp9475_c0_seq2.p1		
comp9493_c0_seq1.p1	sp|Q8PUD6|MSRA_METMA_Peptide_methionine_sulfoxide_reductase_MsrA_OS=Methanosarcina_mazei_(strain_ATCC_BAA-159_/_DSM_3647_/_Goe1_/_Go1_/_JCM_11833_/_OCM_88)_GN=msrA_PE=3_SV=1	2.00E-18
comp94933_c0_seq1.p1		
comp94958_c0_seq1.p1	sp|Q38872|CDPK6_ARATH_Calcium-dependent_protein_kinase_6_OS=Arabidopsis_thaliana_GN=CPK6_PE=1_SV=1	7.00E-15
comp94968_c0_seq1.p2		
comp9497_c0_seq1.p1		
comp94979_c0_seq1.p1		
comp9498_c0_seq1.p2	sp|Q8F641|HPPA_LEPIN_Putative_K(+)-stimulated_pyrophosphate-energized_sodium_pump_OS=Leptospira_interrogans_serogroup_Icterohaemorrhagiae_serovar_Lai_(strain_56601)_GN=hppA_PE=3_SV=1	2.00E-65
comp9505_c0_seq1.p2		
comp9516_c0_seq1.p2		
comp9516_c0_seq1.p3		
comp9524_c0_seq1.p1		
comp9524_c0_seq2.p1		
comp9525_c0_seq1.p1		
comp9529_c0_seq1.p2		
comp95317_c0_seq1.p1	sp|P11442|CLH_RAT_Clathrin_heavy_chain_1_OS=Rattus_norvegicus_GN=Cltc_PE=1_SV=3	4.00E-37
comp9537_c0_seq1.p1	sp|O76756|RS8_APIME_40S_ribosomal_protein_S8_OS=Apis_mellifera_GN=RpS8_PE=2_SV=2	2.00E-53
comp9542_c0_seq1.p1		
comp9548_c0_seq1.p1	sp|Q8XWB1|MUTL_RALSO_DNA_mismatch_repair_protein_mutL_OS=Ralstonia_solanacearum_(strain_GMI1000)_GN=mutL_PE=3_SV=1	7.00E-12
comp9550_c0_seq1.p2		
comp9554_c0_seq1.p1	sp|Q7CEG6|CLPB_BRUSU_Chaperone_protein_ClpB_OS=Brucella_suis_biovar_1_(strain_1330)_GN=clpB_PE=2_SV=1	6.00E-106
comp9556_c0_seq1.p1		
comp95580_c0_seq1.p1		
comp9567_c0_seq1.p1		
comp9570_c0_seq2.p2		
comp95731_c0_seq1.p1		
comp9574_c0_seq1.p3	sp|P46293|RS16_GOSHI_40S_ribosomal_protein_S16_OS=Gossypium_hirsutum_GN=RPS16_PE=2_SV=1	7.00E-56
comp95879_c0_seq1.p1	sp|Q55G10|PNCB_DICDI_Nicotinate_phosphoribosyltransferase_OS=Dictyostelium_discoideum_GN=naprt_PE=2_SV=1	5.00E-19
comp9588_c0_seq1.p1		
comp95886_c0_seq1.p1		
comp9600_c0_seq2.p2		
comp96047_c0_seq1.p1		
comp9622_c0_seq2.p1	sp|Q63164|DYH1_RAT_Dynein_heavy_chain_1,_axonemal_OS=Rattus_norvegicus_GN=Dnah1_PE=2_SV=2	7.00E-59
comp96232_c0_seq1.p1		
comp96250_c0_seq1.p2		
comp9637_c0_seq1.p1		
comp96405_c0_seq1.p1		
comp96425_c0_seq1.p1	sp|P32715|MDTO_ECOLI_Multidrug_resistance_protein_MdtO_OS=Escherichia_coli_(strain_K12)_GN=mdtO_PE=2_SV=2	1.00E-61
comp9647_c0_seq1.p1		
comp96472_c0_seq1.p1	sp|B1LKE8|FOLD_ECOSM_Bifunctional_protein_FolD_OS=Escherichia_coli_(strain_SMS-3-5_/_SECEC)_GN=folD_PE=3_SV=1	7.00E-63
comp96500_c0_seq1.p1		
comp96524_c0_seq1.p1		
comp9653_c0_seq2.p2		
comp9654_c0_seq1.p1	sp|O23255|SAHH1_ARATH_Adenosylhomocysteinase_1_OS=Arabidopsis_thaliana_GN=SAHH1_PE=1_SV=1	2.00E-160
comp9654_c0_seq1.p3	sp|P50246|SAHH_MEDSA_Adenosylhomocysteinase_OS=Medicago_sativa_GN=SAHH_PE=2_SV=1	2.00E-39
comp9662_c0_seq2.p1		
comp96666_c0_seq1.p1	sp|Q3Z397|EFEO_SHISS_Iron_uptake_system_component_EfeO_OS=Shigella_sonnei_(strain_Ss046)_GN=efeO_PE=3_SV=1	9.00E-65
comp9667_c0_seq1.p1		
comp96706_c0_seq1.p1	sp|P0AFP6|YBGI_ECOLI_UPF0135_protein_ybgI_OS=Escherichia_coli_(strain_K12)_GN=ybgI_PE=1_SV=1	7.00E-102
comp9671_c0_seq1.p1		
comp9682_c0_seq1.p1		
comp96832_c0_seq1.p1		
comp96834_c0_seq1.p1		
comp9687_c0_seq1.p1	sp|P17704|RS17_DROME_40S_ribosomal_protein_S17_OS=Drosophila_melanogaster_GN=RpS17_PE=2_SV=2	1.00E-63
comp96874_c0_seq1.p1	sp|Q3YUZ7|RPOB_SHISS_DNA-directed_RNA_polymerase_subunit_beta_OS=Shigella_sonnei_(strain_Ss046)_GN=rpoB_PE=3_SV=1	3.00E-98
comp9689_c0_seq1.p1	sp|Q0MQF0|NDUB9_PANTR_NADH_dehydrogenase_[ubiquinone]_1_beta_subcomplex_subunit_9_OS=Pan_troglodytes_GN=NDUFB9_PE=2_SV=3	2.00E-15
comp96893_c0_seq1.p1		
comp96904_c0_seq1.p1	sp|P76220|YDJY_ECOLI_Uncharacterized_protein_ydjY_OS=Escherichia_coli_(strain_K12)_GN=ydjY_PE=4_SV=2	1.00E-85
comp9693_c0_seq1.p2	sp|Q31V17|LLDD_SHIBS_L-lactate_dehydrogenase_[cytochrome]_OS=Shigella_boydii_serotype_4_(strain_Sb227)_GN=lldD_PE=3_SV=1	2.00E-57
comp96933_c0_seq1.p1		
comp96934_c0_seq1.p1	sp|Q3YYF4|NORV_SHISS_Anaerobic_nitric_oxide_reductase_flavorubredoxin_OS=Shigella_sonnei_(strain_Ss046)_GN=norV_PE=3_SV=1	1.00E-81
comp96945_c0_seq1.p1	sp|Q9U6Z1|KM11_TRYCR_Kinetoplastid_membrane_protein_11_OS=Trypanosoma_cruzi_GN=KMP-11_PE=2_SV=2	5.00E-55
comp9696_c0_seq1.p1	sp|P0AF18|NAGA_ECOLI_N-acetylglucosamine-6-phosphate_deacetylase_OS=Escherichia_coli_(strain_K12)_GN=nagA_PE=1_SV=1	5.00E-134
comp9700_c0_seq1.p2		
comp9701_c0_seq1.p1		
comp9703_c0_seq1.p1	sp|Q63HN8|RN213_HUMAN_E3_ubiquitin-protein_ligase_RNF213_OS=Homo_sapiens_GN=RNF213_PE=1_SV=3	2.00E-28
comp9706_c0_seq2.p1		
comp97066_c0_seq1.p1		
comp97067_c0_seq1.p1		
comp9707_c0_seq1.p1	sp|Q22000|PDE4_CAEEL_Probable_3',5'-cyclic_phosphodiesterase_pde-4_OS=Caenorhabditis_elegans_GN=pde-4_PE=2_SV=2	2.00E-13
comp97135_c0_seq1.p1	sp|P13669|MNGR_ECOLI_Mannosyl-D-glycerate_transport/metabolism_system_repressor_mngR_OS=Escherichia_coli_(strain_K12)_GN=mngR_PE=1_SV=1	4.00E-69
comp97167_c0_seq1.p1		
comp9719_c0_seq1.p1		
comp97246_c0_seq1.p1		
comp97279_c0_seq1.p1		
comp97320_c0_seq1.p2	sp|P0AAJ4|FDNH_SHIFL_Formate_dehydrogenase,_nitrate-inducible,_iron-sulfur_subunit_OS=Shigella_flexneri_GN=fdnH_PE=3_SV=1	2.00E-66
comp97388_c0_seq1.p2	sp|P0ABI8|CYOB_ECOLI_Ubiquinol_oxidase_subunit_1_OS=Escherichia_coli_(strain_K12)_GN=cyoB_PE=1_SV=1	9.00E-75
comp97398_c0_seq1.p1		
comp97416_c0_seq1.p1	sp|Q9M1Q9|AB21B_ARATH_ABC_transporter_B_family_member_21_OS=Arabidopsis_thaliana_GN=ABCB21_PE=1_SV=2	3.00E-13
comp97418_c0_seq1.p1	sp|P43672|UUP_ECOLI_ABC_transporter_ATP-binding_protein_uup_OS=Escherichia_coli_(strain_K12)_GN=uup_PE=3_SV=2	3.00E-55
comp97470_c0_seq1.p1		
comp97559_c0_seq1.p1	sp|P37675|YIAN_ECOLI_2,3-diketo-L-gulonate_TRAP_transporter_large_permease_protein_yiaN_OS=Escherichia_coli_(strain_K12)_GN=yiaN_PE=3_SV=2	2.00E-42
comp97611_c0_seq1.p2		
comp97662_c0_seq1.p1		
comp97687_c0_seq1.p1	sp|P33570|TKT2_ECOLI_Transketolase_2_OS=Escherichia_coli_(strain_K12)_GN=tktB_PE=1_SV=1	1.00E-65
comp97698_c0_seq1.p1		
comp9773_c0_seq1.p1		
comp9777_c0_seq1.p1		
comp9777_c0_seq2.p1		
comp9783_c0_seq1.p1	sp|P37330|MASZ_ECOLI_Malate_synthase_G_OS=Escherichia_coli_(strain_K12)_GN=glcB_PE=1_SV=3	0
comp9783_c0_seq1.p2	sp|P0AEQ1|GLCG_ECOLI_Protein_glcG_OS=Escherichia_coli_(strain_K12)_GN=glcG_PE=3_SV=1	3.00E-76
comp97851_c0_seq1.p1		
comp97878_c0_seq1.p1		
comp9790_c0_seq1.p1	sp|Q6PBI5|RS25_DANRE_40S_ribosomal_protein_S25_OS=Danio_rerio_GN=rps25_PE=2_SV=1	2.00E-16
comp9791_c0_seq1.p1		
comp97943_c0_seq1.p1		
comp97945_c0_seq1.p1		
comp97992_c0_seq1.p1		
comp98007_c0_seq1.p1	sp|Q47537|TAUA_ECOLI_Taurine-binding_periplasmic_protein_OS=Escherichia_coli_(strain_K12)_GN=tauA_PE=1_SV=1	9.00E-146
comp9811_c0_seq1.p1		
comp9813_c0_seq1.p1	sp|Q5EB52|MEST_HUMAN_Mesoderm-specific_transcript_homolog_protein_OS=Homo_sapiens_GN=MEST_PE=2_SV=2	2.00E-11
comp9814_c0_seq1.p1	sp|Q3YVC0|PEPQ_SHISS_Xaa-Pro_dipeptidase_OS=Shigella_sonnei_(strain_Ss046)_GN=pepQ_PE=3_SV=1	2.00E-77
comp98181_c0_seq1.p1	sp|P0AEQ3|GLNH_ECOLI_Glutamine-binding_periplasmic_protein_OS=Escherichia_coli_(strain_K12)_GN=glnH_PE=1_SV=1	4.00E-95
comp98191_c0_seq1.p1	sp|P50456|MLC_ECOLI_Protein_mlc_OS=Escherichia_coli_(strain_K12)_GN=mlc_PE=1_SV=2	2.00E-79
comp9820_c0_seq1.p1		
comp9831_c0_seq2.p1	sp|P49534|YCF39_ODOSI_Uncharacterized_protein_ycf39_OS=Odontella_sinensis_GN=ycf39_PE=3_SV=1	2.00E-99
comp98391_c0_seq1.p1	sp|Q03253|RS12_TRYBB_40S_ribosomal_protein_S12_OS=Trypanosoma_brucei_brucei_GN=RPS12_PE=2_SV=2	1.00E-29
comp9843_c0_seq1.p1		
comp98437_c0_seq1.p1		
comp9856_c0_seq1.p1		
comp98565_c0_seq1.p2		
comp9857_c0_seq1.p1		
comp98702_c0_seq1.p1	sp|Q5R705|SURF4_PONAB_Surfeit_locus_protein_4_OS=Pongo_abelii_GN=SURF4_PE=2_SV=1	5.00E-70
comp9871_c0_seq1.p1	sp|Q9NZJ4|SACS_HUMAN_Sacsin_OS=Homo_sapiens_GN=SACS_PE=1_SV=2	3.00E-48
comp98725_c0_seq1.p1		
comp98768_c0_seq1.p1	sp|P52048|YGGP_ECOLI_Uncharacterized_protein_yggP_OS=Escherichia_coli_(strain_K12)_GN=yggP_PE=4_SV=1	2.00E-66
comp98779_c0_seq1.p1		
comp98939_c0_seq1.p1	sp|P77790|DDPX_ECOLI_D-alanyl-D-alanine_dipeptidase_OS=Escherichia_coli_(strain_K12)_GN=ddpX_PE=1_SV=1	3.00E-81
comp9897_c0_seq1.p1		
comp9899_c0_seq1.p1		
comp98995_c0_seq1.p1	sp|Q3Z4C2|NAGB_SHISS_Glucosamine-6-phosphate_deaminase_OS=Shigella_sonnei_(strain_Ss046)_GN=nagB_PE=3_SV=1	3.00E-68
comp99002_c0_seq1.p1	sp|P77694|YAGW_ECOLI_Uncharacterized_protein_yagW_OS=Escherichia_coli_(strain_K12)_GN=yagW_PE=1_SV=1	4.00E-64
comp99063_c0_seq1.p1		
comp99094_c0_seq1.p1		
comp9910_c0_seq1.p1		
comp9917_c0_seq1.p1		
comp9919_c0_seq1.p1		
comp9923_c0_seq2.p1		
comp99260_c0_seq1.p1		
comp99265_c0_seq1.p1	sp|Q32EH3|DCD_SHIDS_Deoxycytidine_triphosphate_deaminase_OS=Shigella_dysenteriae_serotype_1_(strain_Sd197)_GN=dcd_PE=3_SV=1	2.00E-76
comp99307_c0_seq1.p2	sp|P0A9C8|GLNA_SHIFL_Glutamine_synthetase_OS=Shigella_flexneri_GN=glnA_PE=3_SV=2	6.00E-78
comp99313_c0_seq1.p1	sp|Q46812|SSNA_ECOLI_Protein_SsnA_OS=Escherichia_coli_(strain_K12)_GN=ssnA_PE=1_SV=2	9.00E-84
comp9932_c0_seq1.p2		
comp9937_c0_seq1.p1		
comp99371_c0_seq1.p1		
comp99383_c0_seq1.p1	sp|Q7DLR9|PSB4_ARATH_Proteasome_subunit_beta_type-4_OS=Arabidopsis_thaliana_GN=PBG1_PE=1_SV=2	1.00E-26
comp99399_c0_seq1.p1		
comp99418_c0_seq1.p1	sp|P0A714|KDGT_SHIFL_2-keto-3-deoxygluconate_permease_OS=Shigella_flexneri_GN=kdgT_PE=3_SV=1	4.00E-54
comp99452_c0_seq1.p1	sp|Q11176|WDR1_CAEEL_Actin-interacting_protein_1_OS=Caenorhabditis_elegans_GN=unc-78_PE=1_SV=1	7.00E-18
comp99457_c0_seq1.p1		
comp99461_c0_seq1.p1	sp|P20083|PARE_ECOLI_DNA_topoisomerase_4_subunit_B_OS=Escherichia_coli_(strain_K12)_GN=parE_PE=1_SV=3	4.00E-77
comp99538_c0_seq1.p1		
comp99602_c0_seq1.p1		
comp99693_c0_seq1.p1	sp|P0AE45|YTFL_ECOLI_UPF0053_inner_membrane_protein_ytfL_OS=Escherichia_coli_(strain_K12)_GN=ytfL_PE=1_SV=1	5.00E-64
comp99729_c0_seq1.p1		
comp9978_c0_seq1.p1		
comp9979_c0_seq1.p1	sp|P98179|RBM3_HUMAN_Putative_RNA-binding_protein_3_OS=Homo_sapiens_GN=RBM3_PE=1_SV=1	7.00E-19
comp9985_c0_seq2.p1		
comp9986_c0_seq1.p1		
comp9986_c0_seq1.p2	sp|Q9LIE5|FHY3_ARATH_Protein_FAR-RED_ELONGATED_HYPOCOTYL_3_OS=Arabidopsis_thaliana_GN=FHY3_PE=1_SV=1	5.00E-11
comp9986_c0_seq2.p2	sp|Q9LIE5|FHY3_ARATH_Protein_FAR-RED_ELONGATED_HYPOCOTYL_3_OS=Arabidopsis_thaliana_GN=FHY3_PE=1_SV=1	5.00E-11
comp9986_c0_seq2.p4		
comp9988_c0_seq1.p1		
comp99880_c0_seq1.p2	sp|Q3Z4A6|ATKB_SHISS_Potassium-transporting_ATPase_B_chain_OS=Shigella_sonnei_(strain_Ss046)_GN=kdpB_PE=3_SV=1	2.00E-60

comp9994_c0_seq1.p1	sp|P02350|RS31_XENLA_40S_ribosomal_protein_S3-A_OS=Xenopus_laevis_GN=rps3-a_PE=2_SV=2	1.00E-108	GO:0000737,GO:0003677,GO:0003723,GO:0003723,GO:0003735,GO:0003906,GO:0005622,GO:0005634,GO:0005634,GO:0005730,GO:0005737,GO:0005737,GO:0005739,GO:0005743,GO:0005743,GO:0005819,GO:0005840,GO:0005840,GO:0005856,GO:0006281,GO:0006351,GO:0006355,GO:0006412,GO:0006417,GO:0006915,GO:0006974,GO:0007049,GO:0007067,GO:0015935,GO:0016020,GO:0016829,GO:0030529,GO:0051301	DNA catabolic process, endonucleolytic,DNA binding,RNA binding,RNA binding,structural constituent of ribosome,DNA-(apurinic or apyrimidinic site) lyase activity,intracellular,nucleus,nucleus,nucleolus,cytoplasm,cytoplasm,mitochondrion,mitochondrial inner membrane,mitochondrial inner membrane,spindle,ribosome,ribosome,cytoskeleton,DNA repair,transcription, DNA-templated,regulation of transcription, DNA-templated,translation,regulation of translation,apoptotic process,cellular response to DNA damage stimulus,cell cycle,mitotic nuclear division,small ribosomal subunit,membrane,lyase activity,ribonucleoprotein complex,cell division
comp9995_c0_seq1.p1				
comp99953_c0_seq1.p1	sp|Q9C102|GLT1_SCHPO_Putative_glutamate_synthase_[NADPH]_OS=Schizosaccharomyces_pombe_(strain_972_/_ATCC_24843)_GN=SPAPB1E7.07_PE=2_SV=1	2.00E-22	GO:0003824,GO:0004355,GO:0005506,GO:0005737,GO:0005737,GO:0005739,GO:0005829,GO:0006537,GO:0006537,GO:0006537,GO:0006537,GO:0006541,GO:0006807,GO:0006807,GO:0008152,GO:0008652,GO:0010181,GO:0015930,GO:0016040,GO:0016040,GO:0016040,GO:0016491,GO:0016491,GO:0016638,GO:0016639,GO:0019676,GO:0045181,GO:0046872,GO:0050660,GO:0051536,GO:0051536,GO:0051538,GO:0055114,GO:0055114,GO:0097054	catalytic activity,glutamate synthase (NADPH) activity,iron ion binding,cytoplasm,cytoplasm,mitochondrion,cytosol,glutamate biosynthetic process,glutamate biosynthetic process,glutamate biosynthetic process,glutamate biosynthetic process,glutamine metabolic process,nitrogen compound metabolic process,nitrogen compound metabolic process,metabolic process,cellular amino acid biosynthetic process,FMN binding,glutamate synthase activity,glutamate synthase (NADH) activity,glutamate synthase (NADH) activity,glutamate synthase (NADH) activity,oxidoreductase activity,oxidoreductase activity,oxidoreductase activity, acting on the CH-NH2 group of donors,oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor,ammonia assimilation cycle,glutamate synthase activity, NAD(P)H as acceptor,metal ion binding,flavin adenine dinucleotide binding,iron-sulfur cluster binding,iron-sulfur cluster binding,3 iron, 4 sulfur cluster binding,oxidation-reduction process,oxidation-reduction process,L-glutamate biosynthetic process
comp9997_c0_seq1.p1				
comp9997_c0_seq2.p1				

Table S5. DEGs in 3 h AF vs 10 h AF.

Contig name	a.value	m.value	p.value	q.value	rank	description	Uniprot ID	Organism
comp29434_c0_seq1.p1	-20.930567	29.4887419	2.24E-11	5.79E-07	1			
comp19835_c0_seq1.p1	8.96585572	5.73341624	2.95E-09	3.82E-05	2			
comp30946_c0_seq1.p2	8.53524858	5.61613952	9.71E-09	8.38E-05	3			
comp12763_c0_seq1.p1	8.70953592	5.44809022	1.73E-08	9.80E-05	4			
comp24437_c0_seq1.p2	0.43698535	16.5285844	1.89E-08	9.80E-05	5			
comp29637_c0_seq2.p1	9.13713605	5.27887814	2.36E-08	0.00010193	6			
comp32255_c0_seq10.p1	10.000636	5.06276241	3.35E-08	0.00012401	7			
comp31851_c1_seq1.p1	8.30736012	5.42324803	3.88E-08	0.00012572	8			
comp32609_c0_seq16.p2	9.59980386	5.04536514	4.83E-08	0.00013903	9			
comp30740_c1_seq24.p1	-20.930567	28.3983891	6.72E-08	0.00017396	10	RNA polymerase sigma factor rpoD3	Q31QG5	*Synechococcus elongatus* (strain PCC 7942)
comp12039_c0_seq1.p1	8.66935901	5.14042282	8.37E-08	0.00019711	11			
comp31426_c1_seq11.p1	10.3919691	4.76603864	1.14E-07	0.00024694	12	DnAJ-like protein slr0093	P50027	*Synechocystis* sp. (strain PCC 6803 / Kazusa)
comp31851_c1_seq2.p1	7.84172355	5.255871	2.08E-07	0.00041477	13			
comp30049_c0_seq1.p1	-20.930567	28.1904431	2.73E-07	0.00050481	14	Mitogen-activated protein kinase kinase 2	Q9S7U9	*Arabidopsis thaliana*
comp29471_c0_seq2.p1	9.05994903	4.779644	2.97E-07	0.00051243	15	Probable E3 ubiquitin-protein ligase HERC1	Q15751	*Homo sapiens*
comp31851_c1_seq4.p1	7.05961882	5.47305219	4.61E-07	0.00074586	16			
comp27441_c0_seq5.p2	9.22841575	4.58849889	6.33E-07	0.00096461	17	Probable urea active transporter 1	O94469	*Schizosaccharomyces pombe* (strain 972 / ATCC 24843)
comp32647_c0_seq22.p1	7.98304027	4.93098519	6.96E-07	0.0010013	18			
comp28285_c0_seq1.p1	6.76278211	5.41605726	1.51E-06	0.00206085	19			
comp32897_c0_seq8.p1	-1.1325332	18.3337062	1.64E-06	0.00212398	20			
comp31948_c0_seq11.p1	5.02012245	7.01401068	2.18E-06	0.00266857	21	Calcium/calmodulin-dependent protein kinas	P11730	*Rattus norvegicus*
comp27441_c0_seq8.p1	9.49036547	4.25884701	2.33E-06	0.00266857	22	Probable urea active transporter 1	O94469	*Schizosaccharomyces pombe* (strain 972 / ATCC 24843)
comp30731_c0_seq2.p1	-20.930567	27.8543449	2.37E-06	0.00266857	23			
comp30809_c0_seq1.p1	10.0791373	4.14718641	2.63E-06	0.00283177	24			
comp32125_c0_seq11.p2	6.82734466	5.20533236	3.17E-06	0.00328411	25	NEDD4-like E3 ubiquitin-protein ligase WW	Q8BZZ3	*Mus musculus*
comp32537_c0_seq3.p1	11.7401026	3.93774902	3.97E-06	0.00395107	26	Catalase-peroxidase	B4RW28	*Alteromonas macleodii* (strain DSM 17117 / Deep ecotype)
comp25257_c0_seq2.p1	9.72257003	4.07691987	4.60E-06	0.00441185	27			
comp22476_c0_seq1.p1	9.9065544	4.02519426	5.18E-06	0.00479209	28			
comp13072_c0_seq1.p3	6.65403197	5.19855699	5.38E-06	0.00480094	29			
comp31731_c2_seq2.p1	7.33688222	4.7504763	6.17E-06	0.00532781	30	Putative RNA (cytidine(34)-2'-O)-methyltra	Q042B4	*Lactobacillus gasseri* (strain ATCC 33323 / DSM 20243)
comp24503_c0_seq3.p1	11.0032373	3.86107918	6.77E-06	0.00565312	31			
comp32527_c0_seq69.p1	8.23908367	4.33697804	7.07E-06	0.00572291	32			
comp19956_c0_seq1.p1	7.23365678	-4.7590348	7.31E-06	0.00573881	33			
comp21979_c1_seq1.p1	9.49374701	3.99210007	8.03E-06	0.00594971	34			
comp32615_c1_seq31.p1	6.49897777	5.18436999	8.04E-06	0.00594971	35			
comp29480_c0_seq3.p1	7.66554891	4.50648685	8.89E-06	0.00639563	36	Short transient receptor potential channel 4	Q9QUQ5	*Mus musculus*
comp31297_c0_seq1.p1	7.55473228	4.50410258	1.12E-05	0.00785173	37			
comp27949_c0_seq1.p1	8.88952567	4.00376435	1.32E-05	0.0090242	38			
comp30780_c0_seq2.p1	-20.930567	27.5540865	1.39E-05	0.00920385	39	Serine/threonine-protein kinase/endoribonucl	P32361	*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)
comp12509_c0_seq1.p1	8.19367957	4.18906395	1.42E-05	0.00921778	40	Alcohol dehydrogenase	P42327	*Geobacillus stearothermophilus*
comp32240_c0_seq4.p1	10.7586465	3.7105402	1.47E-05	0.00927716	41			
comp19957_c0_seq2.p1	8.54265768	4.05694517	1.57E-05	0.0096543	42			
comp12933_c0_seq1.p1	10.8451805	3.68411959	1.61E-05	0.00968632	43	Probable serine/threonine-protein kinase CC	P0C8M8	*Zea mays*
comp29173_c0_seq1.p1	9.13413819	3.9002034	1.65E-05	0.00968652	44			
comp32905_c0_seq22.p1	9.94727995	3.75143637	1.76E-05	0.00998157	45			
comp34050_c0_seq1.p1	9.6870957	3.78175048	1.81E-05	0.00998157	46			
comp32812_c1_seq1.p1	8.34223185	4.07910172	1.85E-05	0.00998157	47	Probable glutamine amidotransferase DUG3	P53871	*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)
comp31368_c0_seq3.p1	11.3892808	3.61801302	1.87E-05	0.00998157	48			
comp26119_c0_seq1.p1	7.89820952	4.23438524	1.89E-05	0.00998157	49			
comp29838_c1_seq2.p1	5.54327787	5.80141012	2.04E-05	0.01038078	50	D-xylose-proton symporter-like 3, chloropla	Q0WWW9	*Arabidopsis thaliana*
comp29139_c1_seq2.p1	-5.1362789	25.4810724	2.04E-05	0.01038078	51			
comp32858_c2_seq18.p1	6.8342241	4.640078	3.31E-05	0.01530986	52			
comp32024_c0_seq4.p1	7.39019174	4.32413227	3.32E-05	0.01530986	53			
comp24321_c0_seq2.p2	9.15214655	3.73714877	3.32E-05	0.01530986	54	Xylosyltransferase sqv-6	Q5QQ52	*Caenorhabditis briggsae*
comp29876_c0_seq1.p1	8.23397561	3.97879515	3.33E-05	0.01530986	55			
comp29543_c0_seq1.p1	9.80376259	3.62474235	3.37E-05	0.01530986	56	UPF0187 protein alr2987	Q8YSU5	*Nostoc* sp. (strain PCC 7120 / UTEX 2576)
comp30494_c2_seq3.p1	8.26644278	3.96574123	3.37E-05	0.01530986	57			
comp32035_c0_seq4.p2	9.31964611	-3.6820317	3.64E-05	0.0162595	58			
comp30844_c0_seq1.p1	6.87837043	4.56853717	3.80E-05	0.01669139	59			
comp26636_c0_seq4.p1	-20.930567	27.345344	4.23E-05	0.01807683	60			
comp13145_c0_seq1.p1	8.67735908	3.7893703	4.26E-05	0.01807683	61	Putative ankyrin repeat protein R873	Q5UP39	*Acanthamoeba polyphaga mimivirus*
comp11702_c0_seq1.p1	7.94653696	4.01828088	4.35E-05	0.01815779	62	ABC transporter G family member 14	Q9C6W5	*Arabidopsis thaliana*
comp20554_c0_seq1.p1	10.5558558	3.47355809	4.57E-05	0.01879232	63	Nephrocystin-3	Q7TNH6	*Mus musculus*
comp30565_c0_seq11.p1	-20.930567	-27.398652	4.73E-05	0.01914779	64	Protein MOS2	Q9C801	*Arabidopsis thaliana*
comp29535_c0_seq4.p1	-20.930567	27.3170485	4.99E-05	0.0196056	65			
comp29976_c0_seq1.p1	9.18474477	3.63421667	5.04E-05	0.0196056	66			
comp26873_c0_seq1.p1	7.27955346	4.27467428	5.18E-05	0.0196056	67			
comp29899_c0_seq3.p1	1.14342956	12.5748825	5.21E-05	0.0196056	68			
comp25714_c0_seq1.p1	8.61962479	3.75674156	5.23E-05	0.0196056	69			
comp29273_c0_seq1.p1	7.33088761	4.21241826	5.99E-05	0.02214294	70	2-epi-5-epi-valiolone synthase	Q9ZAE9	*Actinoplanes* sp. (strain ATCC 31044 / CBS 674.73 / SE50/110)
comp32597_c0_seq13.p1	4.106583	7.07724558	6.16E-05	0.02245206	71	Ubiquitin carboxyl-terminal hydrolase 22	A6H8I0	*Danio rerio*
comp31985_c0_seq1.p1	7.58402381	4.07483447	6.41E-05	0.02266689	72	Uncharacterized protein PB7E8.02	Q9C0V4	*Schizosaccharomyces pombe* (strain 972 / ATCC 24843)
comp32686_c0_seq5.p1	9.88827885	-3.4631534	6.46E-05	0.02266689	73			
comp32858_c2_seq8.p1	6.99600718	4.3727324	6.48E-05	0.02266689	74	Zinc transporter ZIP10	Q6PEH9	*Danio rerio*
comp31436_c0_seq2.p1	9.76177964	-3.4713061	6.65E-05	0.02276527	75			
comp14128_c0_seq1.p1	12.0102387	-3.3050771	6.75E-05	0.02276527	76	La-related protein 7	Q05CL8	*Mus musculus*
comp26937_c0_seq4.p1	4.66124105	-6.4553116	6.77E-05	0.02276527	77	Exportin-7	Q5ZLT0	*Gallus gallus*
comp32374_c8_seq4.p1	4.02651674	-7.1237729	6.90E-05	0.02276767	78	Uncharacterized acyltransferase C1718.04	Q9P7P0	*Schizosaccharomyces pombe* (strain 972 / ATCC 24843)
comp34646_c0_seq1.p1	8.79576087	3.64428831	6.95E-05	0.02276767	79			
comp32920_c1_seq24.p1	9.8959518	3.43415402	7.32E-05	0.02368625	80	Probable cysteine desulfurase	Q9K7A0	*Bacillus halodurans* (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125)
comp29976_c0_seq2.p1	7.42527806	4.10201488	7.78E-05	0.02485944	81			
comp25609_c0_seq3.p1	7.20094529	4.19905613	8.20E-05	0.02560483	82	Guanine nucleotide-binding protein G(o) sul	O15976	*Mizuhopecten yessoensis*
comp33138_c0_seq13.p1	8.55972122	3.66508481	8.23E-05	0.02560483	83	Kinesin-like protein KIF11	B2GU58	*Xenopus tropicalis*
comp30350_c0_seq4.p1	-20.930567	27.2129637	8.32E-05	0.02560483	84			
comp30402_c0_seq2.p1	6.88498988	4.37276042	8.41E-05	0.02560483	85	ATP-dependent DNA helicase PIF1	Q9H611	*Homo sapiens*
comp30731_c0_seq3.p1	9.88995729	3.38109115	9.21E-05	0.02751647	86			
comp24536_c0_seq2.p1	3.88255004	7.36664925	9.25E-05	0.02751647	87	Splicing factor U2AF 65 kDa subunit	P90978	*Caenorhabditis elegans*
comp31844_c0_seq1.p1	-20.930567	27.1923122	9.48E-05	0.02785175	88			
comp32255_c0_seq1.p1	10.9196171	3.27208977	9.75E-05	0.02785175	89			
comp31723_c0_seq9.p1	-20.930567	27.1818969	9.90E-05	0.02785175	90.5	HBS1-like protein	Q2KHZ2	*Bos taurus*
comp31941_c0_seq2.p1	-20.930567	27.1816159	9.90E-05	0.02785175	90.5	Major facilitator superfamily domain-contain	Q8CBH5	*Mus musculus*
comp26299_c0_seq1.p2*	3.80466629	7.49982562	9.97E-05	0.02785175	92	Poly(beta-D-mannuronate) C5 epimerase	Q88NC9	*Pseudomonas putida* (strain KT2440)
comp25123_c0_seq2.p1	6.82247824	4.36552452	0.00010005	0.02785175	93	Heat shock factor protein	P22813	*Drosophila melanogaster*
comp29163_c0_seq6.p1	3.52460409	-7.9694569	0.00010447	0.02870992	94	Dynein heavy chain 1, axonemal	Q63164	*Rattus norvegicus*
comp30593_c0_seq1.p1	9.32665313	3.43462161	0.00010535	0.02870992	95	Probable outer membrane protein pmp6	Q9Z899	*Chlamydia pneumoniae*
comp11912_c0_seq2.p1	5.98659327	4.94481634	0.00010826	0.02919519	96			
comp24770_c0_seq1.p1	9.38403747	3.41446435	0.00010995	0.02934518	97			
comp33218_c0_seq21.p2	-20.930567	27.1463968	0.0001181	0.03119968	98	Putative serine protease K12H4.7	P34528	*Caenorhabditis elegans*
comp33217_c0_seq37.p1	5.77130733	5.09325771	0.00012293	0.03214729	99			
comp32683_c0_seq3.p1	-20.930567	27.1227012	0.00013496	0.03494077	100			
comp32398_c1_seq13.p1	8.07591437	3.66267268	0.00015333	0.03930498	101			
comp32002_c0_seq2.p2*	10.498789	3.17858492	0.00016635	0.04222316	102	GDP-mannose 6-dehydrogenase	P11759	*Pseudomonas aeruginosa* (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)
comp31142_c0_seq4.p1	5.1675788	5.58179446	0.0001697	0.04265446	103	Peptidyl-Asp metalloendopeptidase	B2FQP3	*Stenotrophomonas maltophilia* (strain K279a)
comp32647_c0_seq2.p2	7.71612848	3.75384082	0.00018163	0.04521636	104			
comp31338_c0_seq10.p1	8.2178986	3.56251235	0.00018428	0.04543759	105			
comp32035_c0_seq2.p1	9.01631449	-3.3534966	0.00018756	0.04581135	106			
comp32887_c0_seq19.p1	9.92588693	3.19001809	0.00020239	0.04896971	107			

* confirmation of expression level by RT-qPCR

Table S6. DEGs in 3 h AF vs 24 h AF.

Contig name	a.value	m.value	p.value	q.value	rank	description	Uniprot ID	Organism
comp30946_c0_seq1.p2	10.18803	8.600961466	2.92E-09	7.28E-05	1			
comp24437_c0_seq1.p2	1.408872	18.15161611	5.62E-09	7.28E-05	2			
comp32408 c2 seq24.p1*	-20.9176	29.3619053	1.69E-07	0.001455497	3	Poly(beta-D-mannuronate) C5 epimerase	Q88NC9	*Pseudomonas putida* (strain KT2440)
comp31851_c1_seq4.p1	7.979959	6.99299002	8.03E-07	0.003855527	4			
comp32647_c0_seq22.p1	9.016417	6.676996719	9.74E-07	0.003855527	5			
comp32167 c4 seq1.p1	-20.9176	28.94082432	9.77E-07	0.003855527	6	RNA-binding protein Musashi homolog 2	Q96DH6	*Homo sapiens*
comp31608_c0_seq3.p1	7.55588	7.06680202	1.07E-06	0.003855527	7			
comp32096_c0_seq7.p1	6.734351	7.423743109	1.32E-06	0.003855527	8			
comp31851_c1_seq1.p1	9.042802	6.57338988	1.34E-06	0.003855527	9			
comp32647_c0_seq14.p1	8.548829	6.604782698	1.63E-06	0.00400072	10			
comp28285_c0_seq1.p1	7.646199	6.862147978	1.70E-06	0.00400072	11			
comp24510_c0_seq2.p1	6.069545	7.708841048	2.31E-06	0.004980454	12			
comp30049 c0 seq1.p1	-20.9176	28.63170418	3.53E-06	0.007034909	13	Mitogen-activated protein kinase kinase 2	Q9S7U9	*Arabidopsis thaliana*
comp30350_c0_seq4.p1	-20.9176	28.57674473	4.46E-06	0.008164305	14			
comp30892_c1_seq2.p1	7.931916	6.386459168	4.73E-06	0.008164305	15			
comp33139_c0_seq6.p1	5.537691	7.952891519	6.10E-06	0.009729369	16			
comp32096_c0_seq8.p1	5.268865	8.107480382	6.41E-06	0.009729369	17			
comp29434_c0_seq1.p1	-20.9176	28.47178845	6.87E-06	0.009729369	18			
comp30844_c0_seq1.p1	7.876202	6.24345778	7.14E-06	0.009729369	19			
comp29637_c0_seq2.p1	9.558728	5.801320592	8.87E-06	0.011487304	20			
comp31948 c0 seq11.p1	5.533306	7.71963485	9.69E-06	0.011949093	21	Calcium/calmodulin-dependent protein kinase type II subunit gamma	P11730	*Rattus norvegicus*
comp32609 c0 seq16.p2	10.06715	5.659315433	1.12E-05	0.012664883	22	HBS1-like protein	Q2KHZ2	*Bos taurus*
comp19835_c0_seq1.p1	9.14727	5.775502396	1.13E-05	0.012664883	23			
comp33139_c0_seq7.p1	6.135426	6.964730927	1.18E-05	0.012750062	24			
comp32588_c0_seq12.p1	5.849862	7.090472891	1.68E-05	0.017420108	25			
comp32647_c0_seq17.p2	4.529311	8.628372514	1.76E-05	0.017518176	26			
comp31142 c0 seq4.p1	6.01292	6.951734315	1.91E-05	0.018073631	27	Peptidyl-Asp metalloendopeptidase	B2FQP3	*Stenotrophomonas maltophilia* (strain K279a)
comp31844_c0_seq1.p1	-20.9176	28.21435993	1.95E-05	0.018073631	28			
comp33139_c0_seq25.p1	-20.9176	28.12553854	2.81E-05	0.025095404	29			
comp32255_c0_seq10.p1	10.26248	5.26571539	3.18E-05	0.02740893	30			
comp32814_c0_seq23.p1	-20.9176	-28.27220615	4.17E-05	0.033844999	31			
comp36711_c0_seq1.p1	7.740805	5.650482408	4.24E-05	0.033844999	32			
comp32158_c1_seq28.p1	7.140679	-5.871064106	4.31E-05	0.033844999	33			
comp26636_c0_seq4.p1	-20.9176	27.98698195	4.84E-05	0.036854067	34			
comp32954_c2_seq3.p1	7.139718	5.849187788	4.99E-05	0.03691921	35			
comp32125 c0 seq11.p2	7.267426	5.764753075	5.31E-05	0.037566611	36	NEDD4-like E3 ubiquitin-protein ligase WWP1	Q8BZZ3	*Mus musculus*
comp31851_c1_seq2.p1	8.099755	5.451192047	5.37E-05	0.037566611	37			
comp26119_c0_seq1.p1	8.587502	5.292228907	5.68E-05	0.038712552	38			
comp30838_c0_seq2.p1	4.980823	7.531396032	5.94E-05	0.03880784	39			
comp29663 c0 seq7.p1	5.581634	6.944639201	6.00E-05	0.03880784	40	Carboxypeptidase N subunit 2	Q9DBB9	*Mus musculus*
comp32686_c0_seq5.p1	9.225519	-5.109415706	6.55E-05	0.041384858	41			
comp12763_c0_seq1.p1	8.734975	5.178226535	7.05E-05	0.042428858	42			
comp25093_c0_seq1.p1	9.2034	5.090663564	7.06E-05	0.042428858	43			
comp31723_c0_seq9.p1	-20.9176	27.88580389	7.21E-05	0.042428858	44			
comp32780_c1_seq6.p1	4.409353	8.119487104	7.62E-05	0.043573102	45			
comp25257_c0_seq2.p1	10.30884	4.928712766	7.74E-05	0.043573102	46			
comp24681_c0_seq1.p1	10.44553	4.859020302	9.07E-05	0.049985551	47			

* confirmation of expression level by RT-qPCR

Table S7. DEGs in 10 h AF vs 24 h AF.

Contig name	a.value	m.value	p.value	q.value	rank	description	Uniprot ID	Organism
comp31608_c0_seq3.p1	7.226321857	7.9163	3.83E-26	9.92E-22	1			
comp30892_c1_seq2.p1	7.659291447	7.1221	5.00E-24	6.48E-20	2			
comp32408_c2_seq24.p1*	2.572456685	14.336	5.67E-19	4.89E-15	3	Poly(beta-D-mannuronate) C5 epimerase	Q88NC9	*Pseudomonas putida* (strain KT2440)
comp32096_c0_seq7.p1	7.273275199	6.5363	1.85E-18	1.20E-14	4			
comp32948_c1_seq5.p1	10.16825089	4.74	3.23E-18	1.67E-14	5			
comp33139_c0_seq6.p1	-20.928435	29.443	6.58E-18	2.84E-14	6			
comp32954_c2_seq3.p1	6.858590588	6.6018	1.62E-16	5.99E-13	7			
comp27318_c0_seq1.p1	7.71102096	5.7158	3.69E-16	1.20E-12	8			
comp30557_c0_seq3.p1	6.654272361	6.6793	7.29E-16	2.10E-12	9			
comp32167_c4_seq1.p1	-20.928435	29.153	1.14E-15	2.95E-12	10	RNA-binding protein Musashi homolog 2	Q96DH6	*Homo sapiens*
comp31977_c0_seq7.p1	7.018510284	6.2393	1.61E-15	3.80E-12	11	Peptidyl-Asp metalloendopeptidase	B2FQP3	*Stenotrophomonas maltophilia* (strain K279a)
comp33151_c0_seq1.p1	10.29681246	4.1404	7.53E-15	1.62E-11	12	Vanadium-dependent bromoperoxidase	P81701	*Ascophyllum nodosum*
comp32070_c1_seq1.p1	11.36377414	3.7123	1.31E-13	2.61E-10	13			
comp32096_c0_seq8.p1	6.050502326	6.7346	9.95E-13	1.84E-09	14			
comp32647_c0_seq20.p2	6.574400453	6.1117	1.25E-12	2.16E-09	15			
comp27008_c0_seq1.p1	12.28053642	3.2059	2.54E-11	4.11E-08	16	Dual oxidase 2	Q8HZK2	*Sus scrofa*
comp26937_c0_seq4.p1	5.289985454	7.4108	2.89E-11	4.40E-08	17	Exportin-7	Q5ZLT0	*Gallus gallus*
comp31866_c0_seq20.p1	-20.928435	28.473	3.47E-11	4.99E-08	18			
comp32647_c0_seq14.p1	10.20844931	3.4759	4.43E-11	6.04E-08	19			
comp30946_c0_seq1.p2	13.03900907	3.0894	6.20E-11	8.03E-08	20			
comp33139_c0_seq7.p1	7.198170442	5.0296	1.08E-10	1.33E-07	21			
comp33139_c0_seq25.p1	-20.928435	28.338	2.00E-10	2.35E-07	22			
comp28157_c0_seq3.p1	8.499248706	4.0174	2.35E-10	2.64E-07	23			
comp32737_c2_seq1.p1	6.569624383	5.5419	2.59E-10	2.80E-07	24			
comp33151_c0_seq7.p1	10.4574249	3.2608	2.77E-10	2.86E-07	25	Vanadium-dependent bromoperoxidase	P81701	*Ascophyllum nodosum*
comp29719_c0_seq3.p1	7.856570421	4.4075	2.88E-10	2.87E-07	26	Ankyrin-3	Q12955	*Homo sapiens*
comp31490_c1_seq1.p1	8.231663668	4.0919	5.64E-10	5.41E-07	27	Vanadium-dependent bromoperoxidase	P81701	*Ascophyllum nodosum*
comp32174_c0_seq1.p1	10.66692086	2.9518	5.75E-09	5.31E-06	28			
comp33134_c0_seq9.p1	6.686089724	5.0007	1.01E-08	8.98E-06	29			
comp32814_c0_seq23.p1	-20.928435	-28.12	1.22E-08	1.05E-05	30			
comp32647_c0_seq26.p1	5.397260669	6.3606	1.63E-08	1.36E-05	31			
comp28953_c0_seq2.p1	7.261352941	4.4178	1.83E-08	1.48E-05	32	Flavohemoprotein	Q8ETH0	*Oceanobacillus iheyensis* (strain DSM 14371 / JCM 11309 / KCTC 3954 / HTE831)
comp32647_c0_seq17.p2	6.368687001	5.14	4.07E-08	3.20E-05	33			
comp24510_c0_seq2.p1	8.182665166	3.673	4.29E-08	3.27E-05	34			
comp32647_c0_seq4.p1	9.29479604	3.1333	4.47E-08	3.31E-05	35			
comp24681_c0_seq1.p1	11.67578516	2.5889	6.52E-08	4.69E-05	36			
comp33037_c0_seq5.p1	12.71910868	-2.507	6.97E-08	4.88E-05	37	WSC domain-containing protein 1	Q505J3	*Rattus norvegicus*
comp21513_c0_seq2.p1	10.4030795	2.766	7.40E-08	5.04E-05	38	Probable transketolase	Q9URM2	*Schizosaccharomyces pombe* (strain 972 / ATCC 24843)
comp26164_c0_seq1.p1	6.082122799	5.3239	9.78E-08	6.49E-05	39	HHIP-like protein 1	Q96JK4	*Homo sapiens*
comp12523_c0_seq1.p1	9.756099424	2.8677	1.35E-07	8.76E-05	40			
comp31476_c0_seq6.p1	-20.928435	27.737	1.53E-07	9.65E-05	41	Fanconi anemia group D2 protein	Q9BXW9	*Homo sapiens*
comp33139_c0_seq12.p1	-20.928435	27.689	2.36E-07	0.000145283	42			
comp33287_c0_seq7.p1	10.72238388	2.5822	2.61E-07	0.000157002	43	Retrovirus-related Pol polyprotein from transposon TNT 1-94	P10978	*Nicotiana tabacum*
comp31346_c0_seq7.p1	7.704189935	3.756	2.89E-07	0.000169928	44			
comp33955_c0_seq1.p2	10.6881279	-2.573	3.01E-07	0.000173139	45			
comp17843_c1_seq1.p1	5.678326945	5.5454	4.70E-07	0.000264298	46			
comp12401_c0_seq1.p1	9.57787814	-2.75	6.72E-07	0.000369925	47			
comp32717_c0_seq6.p2	9.829906008	2.6615	7.99E-07	0.000427027	48			
comp33037_c0_seq9.p1	15.73153814	-2.217	8.08E-07	0.000427027	49	WSC domain-containing protein 2	A2BGL3	*Danio rerio*
comp13093_c0_seq1.p1	9.305649034	2.813	8.83E-07	0.000457346	50	Probable transketolase	Q9URM2	*Schizosaccharomyces pombe* (strain 972 / ATCC 24843)
comp32276_c1_seq7.p1	6.592465999	4.4926	9.05E-07	0.000459518	51			
comp30413_c0_seq1.p1	5.869217287	5.2021	1.04E-06	0.000518801	52			
comp25475_c0_seq1.p1	7.523278434	3.6801	1.38E-06	0.000673869	53			
comp30103_c0_seq2.p1	4.51431748	6.8321	1.88E-06	0.000903099	54			
comp30740_c1_seq21.p1	2.561050234	10.112	1.94E-06	0.000915279	55	RNA polymerase sigma factor rpoD4	Q31QR8	*Synechococcus elongatus* (strain PCC 7942)
comp32588_c0_seq12.p1	7.779065762	3.4224	2.73E-06	0.001259943	56			
comp26763_c0_seq1.p1	8.98087907	2.7976	2.88E-06	0.001307962	57	L-aspartate oxidase	Q51363	*Pseudomonas aeruginosa* (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)
comp32306_c0_seq15.p1	-20.928435	27.389	3.07E-06	0.001369192	58			
comp32794_c0_seq2.p1	-20.928435	27.379	3.44E-06	0.001509442	59			
comp32944_c0_seq11.p1	8.89243574	2.7643	4.99E-06	0.002154316	60			
comp30557_c0_seq5.p1	-20.928435	27.327	5.15E-06	0.002185009	61			
comp32302_c1_seq10.p1	7.675601495	3.3805	5.70E-06	0.002381323	62			
comp32456_c0_seq12.p1	12.92949282	2.0662	6.14E-06	0.002523254	63			
comp29766_c0_seq1.p1	9.878686556	2.406	7.10E-06	0.002873776	64			
comp29137_c0_seq1.p1	11.62634144	2.1067	8.85E-06	0.003523699	65	CBL-interacting serine/threonine-protein kinase 26	Q84VQ3	*Arabidopsis thaliana*
comp27786_c0_seq3.p1	7.927053752	3.1617	9.16E-06	0.003547728	66			
comp31977_c0_seq8.p1	5.512621691	5.2275	9.18E-06	0.003547728	67	Peptidyl-Asp metalloendopeptidase	B2FQP3	*Stenotrophomonas maltophilia* (strain K279a)
comp24972_c0_seq1.p1	6.357890904	4.3443	9.38E-06	0.003569845	68			
comp32439_c0_seq5.p1	-20.928435	27.232	1.04E-05	0.003885283	69			
comp32609_c0_seq10.p1	5.003133574	5.8098	1.09E-05	0.004031459	70			
comp36711_c0_seq1.p1	9.423473369	2.4755	1.15E-05	0.004178534	71			
comp32736_c0_seq17.p1	8.720537264	2.7298	1.17E-05	0.004195725	72			
comp32374_c8_seq2.p1	3.089622006	-8.449	1.25E-05	0.00442232	73	Uncharacterized acyltransferase C1718.04	Q9P7P0	*Schizosaccharomyces pombe* (strain 972 / ATCC 24843)
comp33068_c1_seq5.p1	5.494273876	5.1773	1.32E-05	0.00462933	74			
comp31266_c0_seq2.p3	13.30885469	1.9714	1.35E-05	0.004665712	75			
comp34620_c0_seq1.p1	9.149689757	2.5401	1.40E-05	0.004727197	76			
comp32858_c2_seq16.p1	9.307502828	2.4869	1.41E-05	0.004727197	77	S-type anion channel SLAH2	Q9ASQ7	*Arabidopsis thaliana*
comp27266_c0_seq1.p1	6.748934877	3.9005	1.69E-05	0.00560557	78	CBL-interacting serine/threonine-protein kinase 24	Q9LDI3	*Arabidopsis thaliana*
comp20142_c0_seq2.p1	12.4003803	1.9796	1.75E-05	0.005750344	79	6-phosphogluconate dehydrogenase, decarboxylating	P21577	*Synechococcus elongatus* (strain PCC 7942)
comp12356_c0_seq1.p1	8.700524005	2.671	1.94E-05	0.006283862	80			
comp32439_c0_seq22.p1	10.97405337	2.0706	2.32E-05	0.007408884	81			
comp33287_c0_seq9.p1	8.439939738	2.7288	2.95E-05	0.009329296	82			
comp32523_c0_seq13.p3	9.224342121	-2.405	3.23E-05	0.010090463	83			
comp23261_c1_seq1.p1	9.356605822	2.3524	3.59E-05	0.010853128	84			
comp24915_c0_seq2.p1	-20.928435	27.056	3.60E-05	0.010853128	85	DNA-binding protein SMUBP-2	P38935	*Homo sapiens*
comp33109_c0_seq7.p1	11.22900544	-1.989	3.61E-05	0.010853128	86			
comp36129_c0_seq1.p1	3.753056517	7.3096	4.00E-05	0.011901657	87	Niemann-Pick C1 protein	O35604	*Mus musculus*
comp32284_c0_seq33.p1	-2.456021205	-19.19	4.16E-05	0.012233704	88	Centrosomal protein of 76 kDa	A7E2V1	*Danio rerio*
comp28201_c0_seq9.p1	-20.928435	27.011	4.87E-05	0.014004234	89.5	DGAT2 DICDI Diacylglycerol O-acyltransferase 2	Q54GC1	*Dictyostelium discoideum*
comp33139_c0_seq3.p1	-20.928435	27.011	4.87E-05	0.014004234	89.5			
comp27817_c0_seq2.p1	7.784478383	2.9928	5.04E-05	0.014342625	91	Ras-related protein Rab-8B	Q2HJI8	*Bos taurus*
comp31407_c0_seq1.p1	9.86096043	2.1665	5.34E-05	0.014903323	92	Superoxide dismutase [Fe]	O15905	*Babesia bovis*
comp11755_c0_seq1.p1	10.1648534	2.0996	5.41E-05	0.014903323	93	Ankyrin repeat, PH and SEC7 domain containing protein secG	Q54KA7	*Dictyostelium discoideum*
comp20554_c0_seq1.p1	11.48494305	-1.917	5.41E-05	0.014903323	94	Nephrocystin-3	Q7TNH6	*Mus musculus*
comp32374_c8_seq4.p1	3.988360376	6.7454	5.56E-05	0.015164978	95	Uncharacterized acyltransferase C1718.04	Q9P7P0	*Schizosaccharomyces pombe* (strain 972 / ATCC 24843)
comp31627_c1_seq3.p1	7.572009403	3.086	6.28E-05	0.016944222	96	Serine acetyltransferase	Q9ZK14	*Helicobacter pylori* (strain J99)
comp29898_c0_seq1.p1	11.14021571	-1.931	6.46E-05	0.017240233	97	Probable outer membrane protein pmp6	Q9Z899	*Chlamydia pneumoniae*
comp33287_c0_seq1.p1	8.200289554	2.7211	6.85E-05	0.018088545	98	Retrovirus-related Pol polyprotein from transposon TNT 1-94	P10978	*Nicotiana tabacum*
comp30996_c0_seq7.p1	-20.928435	26.95	7.01E-05	0.018319988	99	MOUSE Importin-7	Q9EPL8	*Mus musculus*
comp31004_c0_seq2.p1	5.38390919	4.9566	7.14E-05	0.018490689	100			
comp20707_c0_seq3.p1	9.174847808	2.3165	7.24E-05	0.018568726	101			
comp25093_c0_seq1.p1	10.87072523	1.9464	7.46E-05	0.018945067	102			
comp28107_c0_seq3.p1	11.51468942	1.8724	7.77E-05	0.019540396	103	Pheophorbide a oxygenase, chloroplastic	Q9FYC2	*Arabidopsis thaliana*
comp13049_c0_seq1.p1	8.209655341	2.6919	8.17E-05	0.020251721	104	60S ribosomal protein L6	P34091	*Mesembryanthemum crystallinum*
comp27073_c0_seq1.p1	7.897984974	-2.85	8.21E-05	0.020251721	105			
comp33151_c0_seq10.p1	7.852844926	2.8777	8.37E-05	0.020448913	106	Vanadium-dependent bromoperoxidase	P81701	*Ascophyllum nodosum*
comp32647_c0_seq22.p1	11.52481838	1.8506	9.28E-05	0.022447103	107			
comp31602_c0_seq5.p1	8.950114771	-2.343	0.00010082	0.024168725	108	Abhydrolase domain-containing protein FAM108A	Q5XIJ5	*Rattus norvegicus*
comp20385_c0_seq1.p1	11.01487269	-1.889	0.000103013	0.024467873	109	[Pyruvate dehydrogenase [lipoamide]] kinase, mitochondrial	P91622	*Drosophila melanogaster*
comp32927_c0_seq11.p1	7.839567212	2.8388	0.000108496	0.025536017	110			
comp32516_c0_seq9.p1	7.139010977	3.229	0.000144233	0.033641331	111	Probable outer membrane protein pmp6	Q9Z899	*Chlamydia pneumoniae*
comp33109_c0_seq1.p1*	15.30305253	-1.672	0.000155485	0.035942043	112	Poly(beta-D-mannuronate) C5 epimerase	Q88NC9	*Pseudomonas putida* (strain KT2440)
comp32948_c1_seq4.p1	14.02475974	1.6837	0.000158449	0.036303046	113			
comp32924_c0_seq5.p1	6.882559253	3.3887	0.000164298	0.037286375	114			
comp32733_c0_seq1.p1	12.00972628	1.7465	0.000165621	0.037286375	115			
comp26625_c0_seq1.p1	11.43466099	-1.784	0.000172172	0.038427036	116			
comp32116_c0_seq13.p1	7.284365851	-3.077	0.000181946	0.040261348	117			
comp33061_c0_seq20.p1	6.017964062	4.1184	0.000185998	0.040809266	118	CAP-Gly domain-containing linker protein 2	Q9Z0H8	*Mus musculus*
comp28121_c0_seq1.p1	6.628504838	3.5507	0.000197977	0.043072534	119	Heat shock 70 kDa protein	P41753	*Achlya klebsiana*
comp31208_c0_seq3.p1	8.064001502	2.6151	0.00020534	0.044302016	120	Phosphatidylinositol 4-phosphate 5-kinase 3	O48709	*Arabidopsis thaliana*
comp33777_c0_seq1.p1	10.67147184	1.8443	0.000209415	0.044807857	121	3-oxoacyl-[acyl-carrier-protein] reductase 1	P73574	*Synechocystis* sp. (strain PCC 6803 / Kazusa)
comp32728_c0_seq18.p3	-20.928435	26.768	0.000212027	0.044994876	122	Probable methyltransferase TARBP1	Q13395	*Homo sapiens*
comp26942_c0_seq1.p1	9.517956492	-2.059	0.000222853	0.046907841	123	Serine/threonine-protein kinase Nek1	Q96PY6	*Homo sapiens*
comp32243_c2_seq21.p1	-20.928435	26.751	0.000225639	0.047111194	124			
comp32794_c0_seq7.p1	9.50206588	2.0575	0.000233243	0.048309288	125			

* confirmation of expression level by RT-qPCR

Table S8. GO enrichment analysis of DEGs on each timepoint.

	Category	GO.ID	Term	Annotated	Significant	Expected	p value
Up-regulated on the late timepoint							
10h AF vs 24h AF	MF	GO:0004144	diacylglycerol O-acyltransferase activity	10	1	0.01	0.0059
	CC	GO:0000793	condensed chromosome	5	1	0	0.0046
		GO:0005694	chromosome	104	1	0.1	0.0937
Down-regulated on the late timepoint							
3 h AF vs 10h AF	MF	GO:0005215	transporter activity	286	5	0.98	0.0024
10h AF vs 24h AF	BP	GO:0006508	proteolysis	46	2	0.1	0.0037
		GO:0008219	cell death	4	1	0.01	0.0089
	MF	GO:0008146	sulfotransferase activity	10	2	0.05	0.001
		GO:0004366	glycerol-3-phosphate O-acyltransferase activity	11	2	0.05	0.0012
		GO:0016782	transferase activity, transferring sulfur-containing groups	11	2	0.05	0.0012
	CC	GO:0005576	extracellular region	82	3	0.27	0.0016

p value,0.01 was considered significant.

Table S9. The list of longest ORF contigs in *S. babingtonii* annotated by blastp for Ectocarpus gene model.

Contig name	Ectocarpus Gene.ID	description	GO.labels	protein.domains	KOGid
comp31498_c0_seq2.p1	Ec-00_000030.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; PF13637: Ankyrin repeats (many copies); PTHR24133: ; IPR002110: Ankyrin repeat	NA
comp32529_c0_seq13.p1	Ec-00_000140.1	BRCT domain	GO:0005622	IPR001357: BRCT domain	NA
comp26638_c0_seq1.p1	Ec-00_000160.1	Methylthiotransferase, N-terminal	GO:0003824;GO:0009451;GO:0051539	SSF102114: ; IPR020612: Methylthiotransferase, conserved site; IPR023970: Methylthiotransferase/radical SAM-type protein; IPR023404: Radical SAM, alpha/beta horseshoe; IPR013848: Methylthiotransferase, N-terminal	NA
comp32831_c2_seq3.p1	Ec-00_000210.1	Cyclin-like	n/a;n/a;n/a	PTHR14248: ; IPR013763: Cyclin-like; IPR006671: Cyclin, N-terminal	NA
comp20076_c0_seq1.p1	Ec-00_000410.1	RNA-binding protein Lupus La	GO:0006396;GO:0005634;GO:0003723;GO:0030529	IPR006630: RNA-binding protein Lupus La; IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; IPR002344: Lupus La protein; PTHR22792:	NA
comp30473_c0_seq1.p1	Ec-00_000550.1	N-acetylglucosaminyl transferase component	GO:0006506;GO:0017176;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR21329: ; IPR007720: N-acetylglucosaminyl transferase component; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29248_c0_seq12.p2	Ec-00_000630.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	IPR000719: Protein kinase domain; PTHR26392: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site	NA
comp31862_c0_seq1.p1	Ec-00_000640.1	conserved unknown protein	GO:0005524;GO:0006298;GO:0030983	NA	NA
comp30191_c0_seq3.p1	Ec-00_000650.1	Zinc finger, RING-type	GO:0005515;GO:0008270	IPR001841: Zinc finger, RING-type; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type	NA
comp26813_c0_seq2.p1	Ec-00_000680.1	F-box domain	GO:0005515	IPR001810: F-box domain; Coil:	NA
comp27320_c0_seq1.p1	Ec-00_000790.1	Glycosyltransferase, DXD sugar-binding motif	n/a;n/a;n/a	IPR029044: Nucleotide-diphospho-sugar transferases; PTHR32385: ; IPR007577: Glycosyltransferase, DXD sugar-binding motif	NA
comp32397_c0_seq3.p1	Ec-00_000900.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20465_c0_seq1.p1	Ec-00_000940.1	Purple acid phosphatase, N-terminal	GO:0003993;GO:0046872	IPR029052: Metallo-dependent phosphatase-like; IPR015914: Purple acid phosphatase, N-terminal; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; IPR025733: Iron/zinc purple acid phosphatase-like C-terminal domain; PTHR22953: ; IPR008963: Purple acid phosphatase-like, N-terminal	NA
comp31161_c1_seq1.p2	Ec-00_000950.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR002291: Phosphorylase kinase, gamma catalytic subunit; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; PTHR24351:	KOG0032
comp31161_c1_seq1.p1	Ec-00_000970.1	SEN1 protein	GO:0005525;GO:0005874;GO:0007017	PTHR10887: ; PF13086: AAA domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PF13087: AAA domain	NA
comp28560_c0_seq1.p1	Ec-00_000980.1	CDC50/LEM3 family	GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005045: CDC50/LEM3 family; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33608_c0_seq1.p1	Ec-00_001020.1	Zinc finger, TFIIS-type	GO:0003676;GO:0006351;GO:0008270	PTHR11239: ; IPR001222: Zinc finger, TFIIS-type; IPR001529: DNA-directed RNA polymerase, M/15kDa subunit; IPR019761: DNA-directed RNA polymerase M, 15kDa subunit, conserved site; SSF57783: ; G3DSA:2.20.25.10:	NA
comp29091_c0_seq3.p1	Ec-00_001040.1	Ankyrin repeat-containing domain	GO:0005515	PF13637: Ankyrin repeats (many copies); IPR020683: Ankyrin repeat-containing domain; PTHR10489:SF584: ; PTHR10489: ; IPR002110: Ankyrin repeat	NA
comp28676_c0_seq3.p1	Ec-00_001070.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp11816_c0_seq2.p1	Ec-00_001080.1	GPI inositol-deacylase PGAP1-like	GO:0016788;GO:0006505;GO:0006886	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR15495: ; IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR012908: GPI inositol-deacylase PGAP1-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12218_c0_seq1.p1	Ec-00_001090.1	Dimeric alpha-beta barrel	n/a;n/a;n/a	G3DSA:3.30.70.900: ; IPR011008: Dimeric alpha-beta barrel	NA
comp19895_c0_seq1.p1	Ec-00_001100.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp19296_c0_seq1.p1	Ec-00_001110.1	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PF13540: Regulator of chromosome condensation (RCC1) repeat; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25209_c0_seq1.p1	Ec-00_001130.1	Mak16 protein	n/a;n/a;n/a	IPR006958: Mak16 protein; Coil: ; PTHR23405: ; IPR029004: Ribosomal L28e/Mak16	NA
comp31135_c0_seq3.p1	Ec-00_001140.2	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR10292:SF1: ; IPR016025: Clathrin, heavy chain, linker/propeller domain; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR10292: ; IPR001473: Clathrin, heavy chain, propeller, N-terminal	NA
comp27875_c0_seq1.p1	Ec-00_001150.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0006470	IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C	NA
comp29787_c0_seq6.p1	Ec-00_001160.1	Forkhead-associated (FHA) domain	GO:0005515	IPR008984: SMAD/FHA domain; PTHR23308: ; Coil: ; IPR000253: Forkhead-associated (FHA) domain	NA
comp29787_c0_seq6.p2	Ec-00_001170.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31004_c0_seq2.p1	Ec-00_001180.3	Leucine rich repeat protein	GO:0003779;GO:0007010	SM00364: Leucine-rich repeats, bacterial type; IPR003591: Leucine-rich repeat, typical subtype; IPR001611: Leucine-rich repeat; IPR032675: Leucine-rich repeat domain, L domain-like; Coil: ; PTHR23155:	NA
comp12109_c0_seq1.p1	Ec-00_001190.1	expressed unknown protein	GO:0004871;GO:0007165;n/a	NA	NA
comp28737_c1_seq1.p1	Ec-00_001220.1	Pleckstrin homology-like domain	n/a;GO:0005515	SSF50729: ; IPR011993: Pleckstrin homology-like domain; IPR020683: Ankyrin repeat-containing domain; PF13637: Ankyrin repeats (many copies); PTHR24198: ; IPR002110: Ankyrin repeat	NA
comp32178_c0_seq5.p1	Ec-00_001230.1	Kynurenine/Oxoglutarate Transaminase	GO:0003824;GO:0009058;GO:0030170	IPR004839: Aminotransferase, class I/classII; IPR015424: Pyridoxal phosphate-dependent transferase; PTHR11751: ; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	KOG0257
comp12358_c0_seq1.p1	Ec-00_001240.1	Ribosomal protein L41	GO:0003735;GO:0005840;GO:0006412	PTHR10666: ; G3DSA:3.10.20.90: ; IPR029071: Ubiquitin-related domain; IPR000626: Ubiquitin domain; IPR007836: Ribosomal protein L41	NA
comp20474_c0_seq2.p1	Ec-00_001280.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR010655: Pre-mRNA cleavage complex II Clp1; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR12755: ; IPR029007: MobB-type P-loop domain	NA
comp12333_c0_seq1.p1	Ec-00_001290.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31505_c0_seq9.p1	Ec-00_001300.1	Dolichol kinase	GO:0004168;GO:0043048;GO:0030176	PTHR13205: ; IPR026566: Dolichol kinase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30201_c0_seq5.p1	Ec-00_001310.1	SET domain protein	GO:0005515	NA	NA
comp30490_c0_seq2.p1	Ec-00_001320.1	Flavoprotein Monooxygenase	GO:0008152;GO:0016491	IPR002938: Monooxygenase, FAD-binding; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; G3DSA:3.50.50.60: ; PTHR13789: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF51905: ; PR00420: Aromatic-ring hydroxylase (flavoprotein monooxygenase) signature	KOG2614
comp24798_c0_seq2.p2	Ec-00_001340.1	Ankyrin repeat	GO:0005515	PF13637: Ankyrin repeats (many copies); IPR020683: Ankyrin repeat-containing domain; PF13857: Ankyrin repeats (many copies); PTHR24188: ; IPR002110: Ankyrin repeat	NA
comp30963_c0_seq8.p1	Ec-00_001350.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR15863: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp21448_c0_seq2.p1	Ec-00_001360.1	aureochrome 2	GO:0004871;GO:0007165	IPR004827: Basic-leucine zipper domain; IPR001610: PAC motif; IPR000014: PAS domain; SSF57959: ; G3DSA:1.20.5.170: ; G3DSA:3.30.450.20: ; Coil: ; PTHR24351:	NA
comp25586_c0_seq2.p1	Ec-00_001370.1	Mannosyl-oligosaccharide glucosidase, family GH63	GO:0003824	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR004888: Glycoside hydrolase, family 63; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR008928: Six-hairpin glycosidase-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10412:	KOG2161
comp12955_c0_seq1.p1	Ec-00_001380.1	G-patch domain	GO:0003676	PTHR23149: ; IPR000467: G-patch domain; Coil:	NA
comp12955_c0_seq1.p3	Ec-00_001390.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp32485_c0_seq5.p3	Ec-00_001400.1	Tyrosyl-DNA phosphodiesterase	GO:0005634;GO:0006281;GO:0008081	IPR010347: Tyrosyl-DNA phosphodiesterase I; IPR027415: Tyrosyl-DNA phosphodiesterase C-terminal domain; G3DSA:3.30.870.10: ; SSF56024:	KOG2031
comp32485_c0_seq5.p1	Ec-00_001410.1	ubiquitin domain-containing protein	GO:0004221;GO:0006511	SSF63748: ; SSF54001: ; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; SSF47473: ; PTHR24006: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018200: Ubiquitin specific protease, conserved site; IPR028889: Ubiquitin specific protease domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1863
comp12825_c0_seq1.p1	Ec-00_001420.2	D123	n/a;n/a;n/a	PTHR15323: ; IPR009772: Cell division cycle protein 123	NA
comp12973_c0_seq1.p1	Ec-00_001430.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR012562: GUCT; IPR000629: ATP-dependent RNA helicase DEAD-box, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24031: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR014014: RNA helicase, DEAD-box type, Q motif; SignalP-noTM: ; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0331
comp33818_c0_seq1.p1	Ec-00_001440.1	ATP-dependent Clp protease adaptor protein ClpS	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR014719: Ribosomal protein L7/L12, C-terminal/adaptor protein ClpS-like; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003769: Adaptor protein ClpS, core; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21380_c0_seq1.p1	Ec-00_001450.1	Thioredoxin-like fold	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30766_c0_seq4.p1	Ec-00_001460.1	Ubiquitin-conjugating enzyme E2	GO:0019787;GO:0043687;GO:0051246	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; SM00212: Ubiquitin-conjugating enzyme E2, catalytic domain homologues; IPR000608: Ubiquitin-conjugating enzyme E2; Coil: ; PTHR24068:	NA
comp20802_c1_seq1.p1	Ec-00_001490.1	DNA glycosylase	GO:0003824;GO:0006281	IPR005759: Endonuclease III; IPR011257: DNA glycosylase; PTHR10359:SF18: ; PTHR10359: ; IPR004036: Endonuclease III-like, conserved site-2; IPR023170: Helix-turn-helix, base-excision DNA repair, C-terminal; IPR003265: HhH-GPD domain; IPR000445: Helix-hairpin-helix motif	NA
comp27421_c0_seq1.p1	Ec-00_001500.1	Integral membrane protein TerC, riboswitch-linked	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR30238: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR005496: Integral membrane protein TerC; IPR022369: Integral membrane protein TerC, riboswitch-linked; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20771_c0_seq1.p1	Ec-00_001510.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp31812_c0_seq5.p1	Ec-00_001530.1	HIT-like domain	GO:0003824	IPR011146: HIT-like domain; IPR026963: Aprataxin; IPR001310: Histidine triad (HIT) protein; PF11969: Scavenger mRNA decapping enzyme C-term binding	NA
comp28311_c0_seq1.p1	Ec-00_001540.1	hypothetical protein	n/a;n/a;n/a	SSF81995: ; Coil:	NA
comp11705_c0_seq1.p1	Ec-00_001550.1	FYVE zinc finger	GO:0046872	IPR000306: FYVE zinc finger; IPR017455: Zinc finger, FYVE-related; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; IPR007461: Ysc84 actin-binding domain; PTHR15629:	NA
comp26700_c0_seq2.p1	Ec-00_001570.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp32292_c1_seq8.p1	Ec-00_001580.1	WD40 repeat	GO:0005515	IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR013934: Small-subunit processome, Utp13; IPR020472: G-protein beta WD-40 repeat; IPR017986: WD40-repeat-containing domain; PTHR19854: ; IPR015943: WD40/YVTN repeat-like-containing domain; Coil: ; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily	NA
comp27275_c0_seq1.p1	Ec-00_001600.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp26417_c0_seq4.p1	Ec-00_001610.1	F-box domain	GO:0005515	IPR001810: F-box domain; G3DSA:1.20.1280.50:	NA
comp29543_c0_seq1.p1	Ec-00_001620.1	Bestrophin/UPF0187	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR021134: Bestrophin/UPF0187; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33060_c0_seq12.p1	Ec-00_001630.1	Potassium channel, inwardly rectifying, Kir	GO:0005242;GO:0006813;GO:0016021	IPR016449: Potassium channel, inwardly rectifying, Kir; G3DSA:1.10.287.70: ; IPR014756: Immunoglobulin E-set; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013518: Potassium channel, inwardly rectifying, Kir, cytoplasmic; SSF81324: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20941_c0_seq3.p1	Ec-00_001640.1	putative decarboxylase family protein, lysine decarboxylase?	NA	PTHR31223: ; IPR005269: Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG; G3DSA:3.40.50.450: ; SSF102405: ; IPR031100: LOG family; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29555_c0_seq1.p1	Ec-00_001700.2	Putative NIN-like transcription factor	n/a;n/a;n/a	IPR003035: RWP-RK domain; PTHR32002:	NA
comp34150_c0_seq1.p1	Ec-00_001710.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31397_c1_seq1.p1	Ec-00_001720.1	Winged helix-turn-helix DNA-binding domain	n/a;GO:0005515	IPR000717: Proteasome component (PCI) domain; IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; PTHR10855:	NA
comp24400_c0_seq2.p1	Ec-00_001730.1	WD40 repeat	GO:0005515	IPR013890: Transcriptional repressor Tup1, N-terminal; PTHR22847: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; Coil: ; IPR020472: G-protein beta WD-40 repeat	NA
comp31397_c4_seq1.p1	Ec-00_001750.1	porphobilinogen synthase, putative chloroplast precursor	GO:0004655;GO:0033014;GO:0046872	IPR013785: Aldolase-type TIM barrel; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001731: Delta-aminolevulinic acid dehydratase; SignalP-noTM: ; SSF51569: ; IPR030656: Delta-aminolevulinic acid dehydratase, active site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2794
comp11681_c0_seq1.p1	Ec-00_001760.1	WD40/YVTN repeat-like-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp29793_c0_seq2.p1	Ec-00_001810.1	PR1-like metalloprotease	GO:0016020;GO:0004222;GO:0007155;GO:0006508	G3DSA:2.10.25.10: ; IPR024079: Metallopeptidase, catalytic domain; G3DSA:3.90.132.10: ; IPR000742: Epidermal growth factor-like domain; SSF55486: ; IPR001577: Peptidase M8, leishmanolysin; SSF57196:	NA
comp31317_c0_seq8.p1	Ec-00_001930.1	Domain of unknown function DUF2431	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; PTHR11538: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR019446: Domain of unknown function DUF2431; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32682_c0_seq15.p1	Ec-00_001940.1	NADH:ubiquinone oxidoreductase complex I	NA	SSF51735: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR13194: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; IPR013857: NADH:ubiquinone oxidoreductase intermediate-associated protein 30; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PF13460: NADH(P)-binding; IPR008979: Galactose-binding domain-like	NA
comp31131_c0_seq4.p1	Ec-00_001950.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR002885: Pentatricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; IPR005158: Bacterial transcriptional activator domain; PTHR24015:	NA
comp29031_c0_seq1.p1	Ec-00_001960.1	Armadillo-like helical	GO:0005488	PF13513: HEAT-like repeat; IPR001494: Importin-beta, N-terminal domain; IPR027140: Importin subunit beta-1; IPR011989: Armadillo-like helical; IPR000225: Armadillo; PTHR10527: ; IPR016024: Armadillo-type fold	NA
comp29031_c1_seq1.p3	Ec-00_001990.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp32347_c0_seq7.p1	Ec-00_002000.1	Leucine rich repeat protein	GO:0005515	G3DSA:3.80.10.10: ; IPR003591: Leucine-rich repeat, typical subtype; SSF52058: ; PTHR24420: ; IPR001611: Leucine-rich repeat; IPR025875: Leucine rich repeat 4	NA
comp32940_c0_seq13.p1	Ec-00_002010.1	3-Dehydroquinate Synthase	GO:0003856;GO:0005737;GO:0009073	IPR016037: 3-dehydroquinate synthase AroB; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; G3DSA:3.40.50.1970: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:1.20.1090.10: ; SSF56796: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR030960: 3-dehydroquinate synthase domain; PTHR21090: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0692
comp24200_c0_seq1.p1	Ec-00_002030.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR000629: ATP-dependent RNA helicase DEAD-box, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR24031: ; IPR014014: RNA helicase, DEAD-box type, Q motif; IPR014001: Helicase superfamily 1/2, ATP-binding domain; Coil: ; IPR001650: Helicase, C-terminal	KOG0331
comp31392_c0_seq3.p2	Ec-00_002040.1	Thioredoxin-like fold	n/a;n/a;n/a	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013766: Thioredoxin domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10984: ; PF13850: Endoplasmic Reticulum-Golgi Intermediate Compartment (ERGIC); IPR012336: Thioredoxin-like fold; IPR012936: Endoplasmic reticulum vesicle transporter, C-terminal; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32518_c0_seq4.p1	Ec-00_002050.1	Myosin light chain kinase (MLCK)	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000719: Protein kinase domain; IPR008266: Tyrosine-protein kinase, active site; G3DSA:1.10.510.10: ; IPR020635: Tyrosine-protein kinase, catalytic domain; PTHR24351: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0032
comp32047_c0_seq1.p1	Ec-00_002060.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32342_c0_seq12.p1	Ec-00_002070.1	MIF4-like, type 1/2/3	GO:0005515;GO:0016070	PTHR12839: ; IPR003890: MIF4G-like, type 3; IPR016024: Armadillo-type fold; Coil: ; IPR016021: MIF4-like, type 1/2/3; IPR007193: Up-frameshift suppressor 2	NA
comp31708_c0_seq3.p1	Ec-00_002080.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31216_c1_seq4.p1	Ec-00_002090.1	Exo-1,3-beta-glucanase, family GH5	GO:0003824;GO:0043169;GO:0005975	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR017853: Glycoside hydrolase superfamily; IPR001547: Glycoside hydrolase, family 5; PTHR31297: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013781: Glycoside hydrolase, catalytic domain	NA
comp34221_c0_seq1.p1	Ec-00_002100.1	WD40 repeat	GO:0005515	PTHR22847: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp32367_c0_seq8.p1	Ec-00_002140.1	Ribonuclease H-like domain	GO:0003676	IPR012337: Ribonuclease H-like domain	NA
comp30666_c0_seq5.p3	Ec-00_002190.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp27202_c0_seq2.p1	Ec-00_002570.1	2Fe-2S ferredoxin-type domain	GO:0009055;GO:0051536	PTHR11908: ; IPR001041: 2Fe-2S ferredoxin-type domain; IPR006058: 2Fe-2S ferredoxin, iron-sulphur binding site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR012675: Beta-grasp domain	NA
comp28472_c0_seq1.p1	Ec-00_002700.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28794_c0_seq2.p1	Ec-00_003260.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp19390_c0_seq1.p1	Ec-00_003270.1	Cytochrome b5-like heme/steroid binding domain	GO:0020037	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10281:SF26: ; PTHR10281: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001199: Cytochrome b5-like heme/steroid binding domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34126_c0_seq1.p1	Ec-00_003280.1	EF-hand domain pair	n/a;n/a;n/a	IPR011992: EF-hand domain pair	NA
comp31391_c0_seq4.p1	Ec-00_003320.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp30331_c0_seq1.p1	Ec-00_003330.1	Similar to Iron-containing Alcohol Dehydrogenase	GO:0055114;GO:0046872;GO:0016491	SSF56796: ; PTHR11496: ; IPR001670: Alcohol dehydrogenase, iron-type; G3DSA:3.40.50.1970:	NA
comp20679_c0_seq1.p1	Ec-00_003340.1	Transthyretin/hydroxyisourate hydrolase, superfamily	GO:0005496;GO:0006810	IPR023416: Transthyretin/hydroxyisourate hydrolase, superfamily; IPR023419: Transthyretin, conserved site; PTHR10395:	NA
comp21218_c2_seq1.p2	Ec-00_003350.1	pyruvate dehydrogenase E1 component subunit beta	NA	G3DSA:2.40.50.100: ; PTHR23151: ; IPR011053: Single hybrid motif; IPR000089: Biotin/lipoyl attachment	KOG0557
comp24204_c0_seq1.p1	Ec-00_003360.1	General transcription factor II H, polypeptide 2	GO:0000439;GO:0006289;GO:0006351	SSF57889: ; IPR007198: Ssl1-like; IPR012170: TFIIH subunit Ssl1/p44; G3DSA:3.10.370.10: ; IPR007087: Zinc finger, C2H2; PTHR12695: ; IPR004595: TFIIH C1-like domain; IPR002035: von Willebrand factor, type A	KOG2807
comp31138_c0_seq2.p1	Ec-00_003390.1	Zinc finger, RING-type	GO:0005515;GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR22763:	NA
comp20486_c0_seq1.p1	Ec-00_003410.1	Beta-grasp domain	n/a;n/a;n/a	IPR001041: 2Fe-2S ferredoxin-type domain; IPR012675: Beta-grasp domain; PTHR23426:	NA
comp21488_c0_seq1.p1	Ec-00_003420.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28975_c0_seq1.p2	Ec-00_003430.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR21236: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28975_c0_seq1.p1	Ec-00_003460.1	putative tRNA methyltransferase	GO:0006400;GO:0008176	NA	NA
comp32443_c0_seq5.p1	Ec-00_003470.1	Potassium channel	GO:0006813	PTHR10027: ; G3DSA:1.10.287.70: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF81324: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016040: NAD(P)-binding domain; IPR003091: Potassium channel; IPR013099: Two pore domain potassium channel domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28705_c0_seq6.p1	Ec-00_003480.1	expressed unknown protein	GO:0003824;GO:0009058;GO:0030170	Coil:	NA
comp12585_c0_seq1.p1	Ec-00_003490.1	D1LIC, cytoplasmic dynein 1 light intermediate chain	GO:0007018;GO:0003774;GO:0005868;GO:0003777	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR022780: Dynein family light intermediate chain; IPR008467: Dynein 1 light intermediate chain	NA
comp28139_c0_seq1.p1	Ec-00_003500.1	expressed unknown protein	GO:0000166;GO:0004812;GO:0005524;GO:0005737;GO:0006412;GO:0006418	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12390_c0_seq2.p1	Ec-00_003530.1	Biotin/lipoate A/B protein ligase	GO:0004077;GO:0006464	SSF55681: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR004143: Biotinyl protein ligase (BPL) and lipoyl protein ligase (LPL), catalytic domain; G3DSA:3.30.930.10: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR004408: Biotin--acetyl-CoA-carboxylase ligase	NA
comp30739_c0_seq2.p1	Ec-00_003540.1	hypothetical protein	GO:0005488	Coil:	NA
comp32292_c0_seq17.p1	Ec-00_003560.1	PCI domain protein	n/a;n/a;n/a	SSF48452: ; IPR000717: Proteasome component (PCI) domain; IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; PTHR10678: ; IPR011990: Tetratricopeptide-like helical domain; IPR013143: PCI/PINT associated module	NA
comp31629_c0_seq4.p1	Ec-00_003720.1	DNA helicase Pif1 like	GO:0006281;GO:0003678;GO:0000723	IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR23274: ; IPR010285: DNA helicase Pif1-like	NA
comp30558_c0_seq3.p6	Ec-00_003730.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32955_c0_seq6.p1	Ec-00_003740.1	Harbinger transposase-derived protein	GO:0016788	NA	NA
comp33269_c0_seq12.p1	Ec-00_003770.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp33020_c0_seq1.p1	Ec-00_003820.1	MULE transposase domain	GO:0006355;GO:0008270	IPR018289: MULE transposase domain; IPR031052: FHY3/FAR1 family	NA
comp31895_c3_seq2.p1	Ec-00_003920.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp29851_c0_seq2.p1	Ec-00_004280.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21525_c0_seq1.p1	Ec-00_004290.1	Lactate/malate dehydrogenase, C-terminal	GO:0016616;GO:0003824;GO:0055114;GO:0005975	SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; IPR001236: Lactate/malate dehydrogenase, N-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR010945: Malate dehydrogenase, type 2; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR022383: Lactate/malate dehydrogenase, C-terminal; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR015955: Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal	NA
comp34737_c0_seq1.p1	Ec-00_004300.3	lipase	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11005:SF9: ; IPR029058: Alpha/Beta hydrolase fold; IPR025483: Lipase, eukaryotic; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11005: ; IPR000073: Alpha/beta hydrolase fold-1; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2624
comp20492_c0_seq1.p1	Ec-00_004310.1	Serine O-acetyltransferase	GO:0006535;GO:0009001;GO:0005737	NA	KOG4750
comp30926_c0_seq2.p1	Ec-00_004320.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp30097_c0_seq1.p1	Ec-00_004350.3	WD40 repeat	GO:0005515	PTHR18359: ; IPR011659: WD40-like Beta Propeller; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp23868_c0_seq1.p1	Ec-00_004430.1	Zinc finger, FYVE/PHD-type	GO:0008270	IPR011011: Zinc finger, FYVE/PHD-type	NA
comp33259_c0_seq9.p1	Ec-00_004460.2	PiggyBac transposable element-derived protein	n/a;n/a;n/a	IPR013762: Integrase-like, catalytic domain	NA
comp28633_c0_seq3.p1	Ec-00_004460.3	PiggyBac transposable element-derived protein	n/a;n/a;n/a	NA	NA
comp32782_c0_seq2.p1	Ec-00_004470.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp23149_c0_seq2.p1	Ec-00_004520.2	RecName: Full=Mucin-1; Short=MUC-1; AltName: Full=Polymorphic epithelial mucin; Short=PEM; AltName: Full=PEMT; AltName: Full=Episialin; AltName: Full=Tumor-associated mucin; AltName: Full=Carcinoma-as	GO:0016740	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp22119_c0_seq1.p1	Ec-00_004540.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp20244_c0_seq2.p1	Ec-00_004550.1	Glucose/ribitol dehydrogenase	GO:0008152;GO:0016491	PTHR24322: ; SSF51735: ; IPR016040: NAD(P)-binding domain; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR	NA
comp30372_c1_seq2.p1	Ec-00_004560.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; IPR002885: Pentatricopeptide repeat; PTHR24015:	NA
comp29496_c0_seq3.p2	Ec-00_004590.1	Riboflavin synthase, putative	NA	Coil:	NA
comp31073_c0_seq5.p1	Ec-00_004570.1	Riboflavin synthase, putative	GO:0009231;GO:0004746	SIGNAL_PEPTIDE: Signal peptide region; IPR023366: ATP synthase subunit alpha-like domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001783: Lumazine-binding protein; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR026017: Lumazine-binding domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR017938: Riboflavin synthase-like beta-barrel; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29496_c0_seq3.p1	Ec-00_004610.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp29496_c0_seq3.p3	Ec-00_004620.1	Arv1 protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR007290: Arv1 protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28798_c0_seq1.p1	Ec-00_004630.1	ornithine transcarbamoylase	GO:0016597;GO:0016743;GO:0006520	IPR006132: Aspartate/ornithine carbamoyltransferase, carbamoyl-P binding; IPR006130: Aspartate/ornithine carbamoyltransferase; PTHR11405: ; IPR006131: Aspartate/ornithine carbamoyltransferase, Asp/Orn-binding domain; IPR002292: Ornithine/putrescine carbamoyltransferase	KOG1504
comp32092_c0_seq5.p1	Ec-00_004670.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp32879_c0_seq2.p1	Ec-00_004740.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32963_c1_seq21.p1	Ec-00_005000.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp33204_c0_seq1.p1	Ec-00_005010.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp32944_c0_seq11.p1	Ec-00_005030.3	expressed unknown protein	n/a;n/a;n/a	G3DSA:2.170.270.10: ; Coil: ; SSF82199:	NA
comp48650_c0_seq1.p1	Ec-00_005050.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp50326_c0_seq1.p1	Ec-00_005060.1	3'-5' exonuclease domain	GO:0006139;GO:0003676;GO:0008408	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR13620: ; IPR012337: Ribonuclease H-like domain; IPR002562: 3'-5' exonuclease domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19421_c0_seq4.p1	Ec-00_005150.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; Coil: ; IPR002110: Ankyrin repeat	NA
comp20494_c0_seq1.p2	Ec-00_005190.1	Hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30001_c0_seq2.p1	Ec-00_005200.1	Nck-associated protein 1	n/a;n/a;n/a	IPR019137: Nck-associated protein 1; PTHR12093:	NA
comp30065_c2_seq2.p1	Ec-00_005210.2	Pentatricopeptide repeat	n/a;n/a;n/a	IPR002885: Pentatricopeptide repeat; PTHR24015:	NA
comp31735_c0_seq2.p1	Ec-00_005220.1	Small GTPase superfamily, Ras type	GO:0016020;GO:0007165;GO:0006184;GO:0005622;GO:0007264;GO:0005525	IPR002041: Ran GTPase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; IPR003579: Small GTPase superfamily, Rab type; IPR020849: Small GTPase superfamily, Ras type; PS51419: small GTPase Rab1 family profile.; PTHR24073:	NA
comp26547_c0_seq2.p1	Ec-00_005230.1	Nitroreductase	GO:0006118;GO:0016491	IPR000415: Nitroreductase-like; PTHR23026: ; IPR029479: Nitroreductase	NA
comp31400_c1_seq5.p1	Ec-00_005240.3	WD40 repeat	GO:0005515	IPR019775: WD40 repeat, conserved site; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR14344: ; Coil: ; PTHR14344:SF3: ; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily	NA
comp33241_c0_seq7.p1	Ec-00_005280.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp29894_c0_seq1.p2	Ec-00_005450.2	Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase, family GT57	GO:0005789;GO:0016758	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR12413:SF1: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004856: Glycosyl transferase, ALG6/ALG8	KOG2575
comp29894_c0_seq2.p1	Ec-00_005450.4	Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase, family GT57	GO:0005789;GO:0016758	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR12413:SF1: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004856: Glycosyl transferase, ALG6/ALG8	KOG2575
comp32523_c0_seq2.p1	Ec-00_005540.1	Dynein regulator LIS1	n/a;n/a;n/a	IPR017252: Dynein regulator LIS1; SSF109925: ; IPR019775: WD40 repeat, conserved site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001680: WD40 repeat; IPR020472: G-protein beta WD-40 repeat; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22847: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33040_c1_seq2.p1	Ec-00_005550.1	High mobility group domain protein	GO:0003677;GO:0005634;GO:0005515;GO:0006355	PTHR13711: ; IPR009071: High mobility group box domain; Coil:	NA
comp32458_c0_seq19.p2	Ec-00_005560.1	ISC system FeS cluster assembly, IscU scaffold	GO:0005506;GO:0051536;GO:0016226	SSF82649: ; IPR002871: NIF system FeS cluster assembly, NifU, N-terminal; PTHR10093: ; IPR011339: ISC system FeS cluster assembly, IscU scaffold; G3DSA:3.90.1010.10:	NA
comp12988_c0_seq1.p1	Ec-00_005570.1	Light harvesting complex protein (probable pseudogene)	GO:0016020;GO:0009765	NA	NA
comp26098_c0_seq2.p1	Ec-00_005580.1	Nug1, nuclear ribosome-associated GTPase	GO:0005525	PTHR11089: ; IPR006073: GTP binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR023179: GTP-binding protein, orthogonal bundle domain; IPR030378: Circularly permuted (CP)-type guanine nucleotide-binding (G) domain; IPR014813: Guanine nucleotide-binding protein-like 3, N-terminal domain	NA
comp24381_c0_seq2.p1	Ec-00_005640.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp26225_c0_seq1.p1	Ec-00_005770.1	Pectin lyase fold/virulence factor	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR003368: Polymorphic outer membrane protein repeat; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12423_c0_seq1.p1	Ec-00_005780.1	ribosome recycling factor	GO:0006412	G3DSA:1.10.132.20: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002661: Ribosome recycling factor; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023584: Ribosome recycling factor domain; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG4759
comp32103_c0_seq29.p1	Ec-00_005790.1	Zinc finger, RING/FYVE/PHD-type	GO:0005515;GO:0006281;GO:0006310;GO:0008270	SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; PF13920: Zinc finger, C3HC4 type (RING finger); PTHR10360:	NA
comp25116_c0_seq1.p1	Ec-00_005800.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	PF13489: Methyltransferase domain; IPR026113: Methyltransferase-like; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase	NA
comp30834_c0_seq2.p1	Ec-00_005850.1	cytochrome P450	GO:0005506;GO:0016705;GO:0020037;GO:0055114	IPR001128: Cytochrome P450; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR017972: Cytochrome P450, conserved site; IPR002401: Cytochrome P450, E-class, group I; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR24286:	KOG0157
comp26375_c0_seq1.p5	Ec-00_005860.1	Harbinger transposase-derived nuclease domain	n/a;n/a;n/a	PTHR22930: ; IPR027806: Harbinger transposase-derived nuclease domain	NA
comp31095_c1_seq7.p1	Ec-00_005890.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp24857_c0_seq2.p1	Ec-00_005900.1	WD40 repeat	GO:0005515	IPR019775: WD40 repeat, conserved site; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001680: WD40 repeat; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22847: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25124_c0_seq2.p1	Ec-00_005920.1	Glucose-methanol-choline oxidoreductase	GO:0016614;GO:0050660;GO:0006066;GO:0055114;GO:0008812	IPR000172: Glucose-methanol-choline oxidoreductase, N-terminal; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR007867: Glucose-methanol-choline oxidoreductase, C-terminal; PTHR11552: ; SSF54373: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.50.50.60: ; SSF51905: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33134_c0_seq8.p1	Ec-00_005930.1	Chalcone Isomerase-like	GO:0016872	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR016087: Chalcone isomerase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11785_c0_seq1.p1	Ec-00_005940.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30780_c0_seq1.p1	Ec-00_005950.2	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002372: Pyrrolo-quinoline quinone repeat; SignalP-TM: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000719: Protein kinase domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily; G3DSA:3.30.200.20: ; SIGNAL_PEPTIDE: Signal peptide region; IPR018391: Pyrrolo-quinoline quinone beta-propeller repeat; PTHR13954: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR13954:SF6: ; SignalP-noTM: ; IPR027295: Quinoprotein alcohol dehydrogenase-like domain; G3DSA:1.10.510.10: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp58028_c0_seq1.p1	Ec-00_005960.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp25798_c0_seq1.p1	Ec-00_006040.1	Vesicle coat complex COPI, beta sub-unit	GO:0005198;GO:0005515;GO:0006886;GO:0016192;GO:0030117	PTHR19876: ; IPR006692: Coatomer, WD associated region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; IPR020472: G-protein beta WD-40 repeat	KOG0276
comp49645_c0_seq1.p1	Ec-00_006180.1	histidine kinase-like protein	GO:0016310;GO:0016772	PTHR24423: ; IPR005467: Signal transduction histidine kinase, core; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR003594: Histidine kinase-like ATPase, C-terminal domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR011006: CheY-like superfamily; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001789: Signal transduction response regulator, receiver domain; G3DSA:3.40.50.2300: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR004358: Signal transduction histidine kinase-related protein, C-terminal	NA
comp30886_c0_seq3.p1	Ec-00_006320.1	DNA polymerase mu	GO:0003677;GO:0003887;GO:0006260	SSF81585: ; IPR029398: DNA polymerase beta, thumb domain; IPR010996: DNA polymerase beta-like, N-terminal domain; SSF81301: ; IPR018944: DNA polymerase lambda, fingers domain; IPR027421: DNA polymerase family X lyase domain; PTHR11276: ; G3DSA:1.10.150.20: ; G3DSA:3.30.460.10: ; IPR028207: DNA polymerase beta, palm domain; IPR002054: DNA-directed DNA polymerase X; IPR022312: DNA polymerase family X	NA
comp34852_c0_seq1.p1	Ec-00_006400.1	Hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp33647_c0_seq1.p1	Ec-00_006420.1	putative kinase wee 1	GO:0006468;GO:0004672;GO:0016772	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR000719: Protein kinase domain; PTHR11042: ; G3DSA:1.10.510.10: ; Coil:	KOG0601
comp28388_c0_seq1.p1	Ec-00_006470.1	Rad21/Rec8-like protein, C-terminal, eukaryotic	GO:0000228;GO:0005515	IPR006909: Rad21/Rec8-like protein, C-terminal, eukaryotic; SSF46785: ; IPR023093: Rad21/Rec8-like protein, C-terminal; PTHR12585: ; IPR006910: Rad21/Rec8-like protein, N-terminal	NA
comp30937_c0_seq3.p1	Ec-00_006520.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19359_c0_seq1.p1	Ec-00_006530.1	PDZ domain	GO:0005515	IPR009003: Trypsin-like cysteine/serine peptidase domain; IPR001940: Peptidase S1C; PF13365: Trypsin-like peptidase domain; PTHR22939: ; IPR001478: PDZ domain; G3DSA:2.40.10.10:	NA
comp20067_c0_seq1.p2	Ec-00_006540.1	Transcription initiation Spt4	GO:0005634;GO:0006355;GO:0008270;GO:0032786	IPR022800: Spt4/RpoE2 zinc finger; IPR016046: Transcription initiation Spt4-like; IPR029040: RNA polymerase subunit RPABC4/transcription elongation factor Spt4	NA
comp25636_c0_seq1.p1	Ec-00_006550.1	conserved unknown protein	GO:0008270	IPR002893: Zinc finger, MYND-type; SSF144232:	NA
comp28200_c0_seq3.p1	Ec-00_006560.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.40.140.10: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF14421: A distinct subfamily of CDD/CDA-like deaminases; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp12506_c0_seq1.p1	Ec-00_006580.1	Glutathione peroxidase	GO:0004602;GO:0055114;GO:0006979	IPR029759: Glutathione peroxidase active site; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR012336: Thioredoxin-like fold; IPR000889: Glutathione peroxidase	KOG1651
comp32747_c0_seq4.p1	Ec-00_006620.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	SSF50729: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR13140: ; IPR001849: Pleckstrin homology domain; IPR000048: IQ motif, EF-hand binding site; IPR020683: Ankyrin repeat-containing domain; IPR011993: Pleckstrin homology-like domain; IPR001609: Myosin head, motor domain; IPR025939: Axin interactor dorsalization-associated protein, C-terminal domain; IPR002110: Ankyrin repeat	NA
comp26805_c0_seq2.p2	Ec-00_006630.1	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR11227:SF18: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; PTHR11227:	NA
comp26937_c0_seq2.p1	Ec-00_006640.1	RAN binding protein 16-like, protein transporter	GO:0005488	IPR001494: Importin-beta, N-terminal domain; IPR011989: Armadillo-like helical; PTHR12596: ; IPR016024: Armadillo-type fold	NA
comp12378_c0_seq1.p5	Ec-00_006650.1	Protein of unknown function DUF872, transmembrane	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR008590: Protein of unknown function DUF872, transmembrane; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21186_c0_seq1.p2	Ec-00_006660.1	Peptide methionine sulphoxide reductase MrsB	GO:0033743;GO:0055114	PTHR10173:SF19: ; IPR028427: Peptide methionine sulfoxide reductase; IPR002579: Peptide methionine sulphoxide reductase MrsB; IPR011057: Mss4-like	NA
comp29332_c0_seq1.p1	Ec-00_006690.1	Mucin	n/a;n/a;n/a	NA	NA
comp31946_c0_seq2.p1	Ec-00_006720.1	Origin recognition complex, subunit 2	GO:0005515;GO:0008270	NA	NA
comp32140_c0_seq10.p1	Ec-00_006770.1	Jumonji domain and TPR repeat protein	GO:0005515	NA	NA
comp29812_c0_seq1.p1	Ec-00_006790.1	Amino acid transporter, transmembrane	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR22950:SF282: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR22950: ; IPR013057: Amino acid transporter, transmembrane domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26361_c0_seq1.p1	Ec-00_006810.1	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a	IPR005135: Endonuclease/exonuclease/phosphatase; PTHR12121:	NA
comp32999_c0_seq7.p1	Ec-00_006840.2	Ribonuclease H-like domain	GO:0003676	NA	NA
comp32749_c0_seq5.p4	Ec-00_006840.3	Ribonuclease H-like domain	GO:0003676	PTHR13620:SF0: ; PTHR13620: ; IPR012337: Ribonuclease H-like domain; IPR002562: 3'-5' exonuclease domain	NA
comp28576_c0_seq1.p1	Ec-00_006870.2	Carbamoyltransferase	GO:0003824;GO:0009058	SIGNAL_PEPTIDE: Signal peptide region; IPR031730: Carbamoyltransferase, C-terminal; SSF53067: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR34847: ; SignalP-noTM: ; IPR003696: Carbamoyltransferase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25557_c0_seq1.p1	Ec-00_006950.1	Peptidase S8/S53 domain	GO:0004252;GO:0008236;GO:0006508	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000209: Peptidase S8/S53 domain; IPR030400: Sedolisin domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14218: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR015366: Peptidase S53, propeptide	NA
comp29028_c0_seq1.p1	Ec-00_006970.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; Coil: ; IPR002110: Ankyrin repeat; PTHR24188:	NA
comp29020_c0_seq1.p1	Ec-00_007000.1	Protein-tyrosine phosphatase-like	GO:0016311;GO:0016791	IPR029021: Protein-tyrosine phosphatase-like; IPR016130: Protein-tyrosine phosphatase, active site; IPR000387: Tyrosine specific protein phosphatases domain; PTHR23339:SF70: ; PTHR23339:	NA
comp26424_c0_seq1.p1	Ec-00_007030.1	Sphingosine-1-phosphate phosphatase	GO:0016020;GO:0003824	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14969: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000326: Phosphatidic acid phosphatase type 2/haloperoxidase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2822
comp29083_c1_seq1.p1	Ec-00_007050.1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A, N-terminal fragment, family GT66	GO:0016020;GO:0006486;GO:0004576	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003674: Oligosaccharyl transferase, STT3 subunit; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR13872: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	KOG2292
comp32268_c0_seq3.p1	Ec-00_007080.2	Harbinger transposase-derived nuclease domain	n/a;n/a;n/a	Coil:	NA
comp32794_c1_seq2.p1	Ec-00_007160.2	Domain of unknown function DUF4414	GO:0004842;GO:0005622;GO:0006464;GO:0006512;GO:0016881	PTHR11254:SF291: ; IPR025527: Domain of unknown function DUF4414; IPR000569: HECT domain; Coil: ; G3DSA:3.30.2160.10: ; PTHR11254:	NA
comp32976_c1_seq2.p1	Ec-00_007270.1	Unsaturated glucuronyl hydrolase, family GH88	GO:0003824	IPR012341: Six-hairpin glycosidase; IPR010905: Glycosyl hydrolase, family 88; IPR008928: Six-hairpin glycosidase-like	NA
comp24945_c0_seq2.p1	Ec-00_007310.1	Sodium/potassium/calcium exchanger	GO:0016020;GO:0005432;GO:0055085;GO:0006816;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004481: Sodium/potassium/calcium exchanger; IPR004837: Sodium/calcium exchanger membrane region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	NA
comp13549_c0_seq1.p1	Ec-00_007320.1	ICln	GO:0006884;GO:0034709;GO:0034715;GO:0006821;GO:0005829;GO:0005886;GO:0000387	IPR003521: ICln; PF03517: Regulator of volume decrease after cellular swelling	NA
comp26118_c0_seq3.p1	Ec-00_007340.1	Novel Sm-like protein with long N- and C-terminal domains.	NA	PTHR13542: ; IPR019181: Anticodon-binding domain	NA
comp30799_c0_seq3.p1	Ec-00_007350.1	UbiA prenyltransferase family	GO:0004659;GO:0016021	IPR030470: UbiA prenyltransferase conserved site; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006370: 4-hydroxybenzoate polyprenyltransferase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11048: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR000537: UbiA prenyltransferase family; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29079_c0_seq1.p1	Ec-00_007380.1	conserved unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29649_c0_seq1.p1	Ec-00_007390.1	Molybdenum cofactor sulfurase, C-terminal	GO:0003824;GO:0006777;GO:0008265;GO:0030151;GO:0030170	IPR005303: MOSC, N-terminal beta barrel; IPR011037: Pyruvate kinase-like, insert domain; IPR015424: Pyridoxal phosphate-dependent transferase; PTHR14237: ; IPR000192: Aminotransferase class V domain; IPR028886: Molybdenum cofactor sulfurase; IPR005302: Molybdenum cofactor sulfurase, C-terminal; SSF141673: ; PTHR14237:SF19: ; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2	NA
comp33593_c0_seq1.p1	Ec-00_007410.1	EsV-1-166	GO:0004553;GO:0005576;GO:0005975;GO:0019028;GO:0030248	SIGNAL_PEPTIDE: Signal peptide region; IPR004302: Chitin-binding, domain 3; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR21113: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000254: Cellulose-binding domain, fungal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30954_c0_seq6.p1	Ec-00_007480.1	Glycosyltransferase, family GT4	GO:0009058	SSF53756: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001296: Glycosyl transferase, family 1; PTHR12526: ; G3DSA:3.40.50.2000: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR028098: Glycosyltransferase subfamily 4, N-terminal domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30954_c0_seq6.p6	Ec-00_007540.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp33159_c0_seq10.p1	Ec-00_007560.2	MULE transposase domain	n/a;n/a;n/a	IPR018289: MULE transposase domain; IPR031052: FHY3/FAR1 family; PTHR31669:SF3:	NA
comp21080_c0_seq1.p1	Ec-00_007580.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28831_c0_seq3.p1	Ec-00_007590.1	5'-3' exoribonuclease	GO:0005622;GO:0003676;GO:0004527	IPR027073: 5'-3' exoribonuclease; IPR017151: 5'-3' exoribonuclease 2/3; Coil: ; IPR004859: Putative 5-3 exonuclease	NA
comp32239_c0_seq20.p2	Ec-00_007680.4	Telomerase ribonucleoprotein complex - RNA-binding domain	GO:0003964	PTHR12066:SF0: ; PTHR12066:	NA
comp27026_c0_seq1.p1	Ec-00_007690.1	serine/threonine protein kinase	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PTHR24362: ; SSF57997: ; IPR011009: Protein kinase-like domain; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	NA
comp25955_c0_seq1.p1	Ec-00_007720.1	Protein of unknown function DUF2854	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR021275: Protein of unknown function DUF2854; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30433_c0_seq4.p5	Ec-00_007730.1	Complex 1 LYR protein	n/a;n/a;n/a	IPR008011: Complex 1 LYR protein	NA
comp30433_c0_seq4.p1	Ec-00_007740.1	PHflX, plastid HflX GTPase	GO:0005525	IPR025121: GTPase HflX N-terminal domain; IPR016496: GTPase HflX; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR030394: HflX-type guanine nucleotide-binding (G) domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006073: GTP binding domain; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28127_c0_seq3.p1	Ec-00_007810.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp23570_c0_seq1.p1	Ec-00_007820.1	GDP-mannose transporter	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004853: Triose-phosphate transporter domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11132: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp22386_c0_seq4.p1	Ec-00_007830.1	Domain of unknown function DUF4168	n/a;n/a;n/a	IPR025433: Domain of unknown function DUF4168	NA
comp26919_c1_seq2.p1	Ec-00_007840.1	EamA domain	GO:0016020;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF103481: ; PTHR12715: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000620: EamA domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31752_c1_seq6.p1	Ec-00_007900.2	Cyclin, N-terminal	n/a;n/a;n/a	PTHR22896:SF0: ; IPR013763: Cyclin-like; IPR006671: Cyclin, N-terminal; IPR012388: CDK5 and ABL1 enzyme substrate 1/2	NA
comp34201_c0_seq1.p1	Ec-00_008050.1	conserved unknown protein	n/a;GO:0005515	PTHR16263: ; IPR011990: Tetratricopeptide-like helical domain; SignalP-TM:	NA
comp11771_c0_seq1.p1	Ec-00_008060.1	Cathepsin-like proteinase	GO:0006508;GO:0008234	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF54001: ; IPR000169: Cysteine peptidase, cysteine active site; IPR013201: Proteinase inhibitor I29, cathepsin propeptide; IPR013128: Peptidase C1A; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR025661: Cysteine peptidase, asparagine active site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR025660: Cysteine peptidase, histidine active site; IPR000668: Peptidase C1A, papain C-terminal; G3DSA:3.90.70.10: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1543
comp32867_c0_seq8.p1	Ec-00_008110.2	expressed unknown protein	n/a;n/a;n/a	PTHR33129:SF2: ; PTHR33129: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp32290_c0_seq4.p1	Ec-00_008200.1	Zinc finger, MYND-type	GO:0008270	IPR002893: Zinc finger, MYND-type; SSF144232:	NA
comp29592_c0_seq3.p1	Ec-00_008240.1	Catalase decomposes hydrogen peroxide to molecular oxygen and water.	GO:0004601;GO:0006979;GO:0020037;GO:0055114	PTHR30555: ; IPR010255: Haem peroxidase; IPR000763: Catalase-peroxidase haem; G3DSA:1.10.520.10: ; G3DSA:1.10.420.10: ; IPR019793: Peroxidases heam-ligand binding site; IPR002016: Haem peroxidase, plant/fungal/bacterial	NA
comp76814_c0_seq1.p1	Ec-00_008290.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp24556_c0_seq2.p1	Ec-00_008340.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp26647_c0_seq2.p1	Ec-00_008350.1	Amino acid/polyamine transporter I	GO:0016020;GO:0003333;GO:0015171	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002293: Amino acid/polyamine transporter I; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp17254_c0_seq2.p1	Ec-00_008400.1	hypothetical protein	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat	NA
comp29279_c0_seq3.p1	Ec-00_008430.1	Ribonuclease Zc3h12a-like	NA	SSF48452: ; IPR021869: Ribonuclease Zc3h12a-like; PTHR12876: ; IPR011990: Tetratricopeptide-like helical domain; IPR018834: DNA/RNA-binding domain, Est1-type	NA
comp27711_c0_seq1.p1	Ec-00_008440.1	Protein kinase, C-terminal	GO:0004674;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; SignalP-TM: ; PTHR24351:SF65: ; IPR017892: Protein kinase, C-terminal; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000961: AGC-kinase, C-terminal; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; PTHR24351:	NA
comp33056_c1_seq6.p1	Ec-00_008460.2	Pleckstrin homology-like domain	n/a;n/a;n/a	IPR011993: PH domain-like; IPR001849: Pleckstrin homology domain	NA
comp31821_c0_seq5.p2	Ec-00_008480.1	Myosin head, motor domain	GO:0005524;GO:0003774;GO:0016459	NA	NA
comp25045_c0_seq3.p1	Ec-00_008530.1	WD40-repeat-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; IPR006595: CTLH, C-terminal LisH motif; PTHR22848:	NA
comp51584_c0_seq1.p1	Ec-00_008560.1	Armadillo-type fold	GO:0005488	IPR026683: Serine/threonine-protein kinase TOR; IPR018392: LysM domain; IPR011989: Armadillo-like helical; PTHR11139: ; IPR016024: Armadillo-type fold	NA
comp31003_c0_seq3.p1	Ec-00_008670.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32060_c0_seq9.p1	Ec-00_008690.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp32060_c0_seq13.p1	Ec-00_008700.1	P-loop containing nucleoside triphosphate hydrolase	GO:0000155;GO:0003924;GO:0005525;GO:0007165;n/a	PTHR23408: ; IPR005129: SIMIBI class G3E GTPase, ArgK/MeaB; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:1.20.5.170: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF101447: ; PF03308: ArgK protein; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR003661: Signal transduction histidine kinase, dimerisation/phosphoacceptor domain; PTHR23408:SF3:	NA
comp23622_c0_seq1.p1	Ec-00_008720.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp31390_c0_seq2.p1	Ec-00_008730.1	Phox homologous domain	GO:0035091	IPR001683: Phox homologous domain	NA
comp15288_c0_seq1.p1	Ec-00_008760.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp34271_c0_seq1.p1	Ec-00_008830.1	Cysteine synthase	GO:0008152;GO:0004124;GO:0055114;GO:0006535;GO:0016491	IPR001216: Cysteine synthase/cystathionine beta-synthase, pyridoxal-phosphate attachment site; IPR005859: Cysteine synthase CysK; IPR001926: Tryptophan synthase beta subunit-like PLP-dependent enzyme; IPR005856: Cysteine synthase; PTHR10314: ; G3DSA:3.40.50.1100:	KOG1252
comp28860_c0_seq4.p1	Ec-00_008910.1	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	n/a;n/a;n/a	PTHR22870: ; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II; IPR000408: Regulator of chromosome condensation, RCC1; mobidb-lite: consensus disorder prediction	NA
comp32167_c0_seq19.p1	Ec-00_008950.1	Exocyst complex component Sec6	GO:0000145;GO:0006887	IPR010326: Exocyst complex component Sec6	NA
comp23487_c0_seq4.p1	Ec-00_008970.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp26668_c0_seq3.p1	Ec-00_009100.1	Thioredoxin-like fold	GO:0005515;n/a	IPR006577: UAS; G3DSA:3.10.20.90: ; PTHR23322: ; IPR029071: Ubiquitin-related domain; IPR001012: UBX domain; PTHR23322:SF1: ; Coil: ; IPR012336: Thioredoxin-like fold	NA
comp12903_c0_seq1.p1	Ec-00_009110.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001594: Zinc finger, DHHC-type, palmitoyltransferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22883: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31871_c1_seq3.p1	Ec-00_009220.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF103657: ; PF16746: BAR domain of APPL family; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31508_c1_seq1.p1	Ec-00_009290.1	Heat shock protein 70	NA	PTHR19375: ; IPR018181: Heat shock protein 70, conserved site; SSF53067: ; IPR029048: Heat shock protein 70kD, C-terminal domain; G3DSA:3.90.640.10: ; G3DSA:3.30.420.40: ; IPR029047: Heat shock protein 70kD, peptide-binding domain; Coil: ; IPR013126: Heat shock protein 70 family	NA
comp32177_c0_seq1.p1	Ec-00_009340.1	Membrane-associated protein	GO:0016021	NA	NA
comp33019_c1_seq24.p1	Ec-00_009350.1	Heat shock protein 40 like protein	NA	SSF48452: ; PTHR24078: ; PF13414: TPR repeat; IPR011990: Tetratricopeptide-like helical domain; IPR001623: DnaJ domain; IPR013026: Tetratricopeptide repeat-containing domain; Coil: ; IPR019734: Tetratricopeptide repeat; IPR018253: DnaJ domain, conserved site	NA
comp18125_c0_seq1.p1	Ec-00_009355.1	hypothetical protein	NA	mobidb-lite: consensus disorder prediction	NA
comp28947_c0_seq1.p1	Ec-00_009370.1	Homeodomain-like	GO:0003677	SSF109715: ; IPR009057: Homeodomain-like; Coil: ; IPR014876: DEK, C-terminal	NA
comp28188_c0_seq2.p1	Ec-00_009410.2	Ferric reductase transmembrane component-like domain	GO:0005506;GO:0006118;GO:0009055;GO:0016021;GO:0016491;GO:0050660	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF52343: ; IPR013130: Ferric reductase transmembrane component-like domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR11972: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.40.50.80: ; IPR013121: Ferric reductase, NAD binding domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33224_c0_seq2.p1	Ec-00_009440.1	Ribonuclease H-like domain	GO:0003676	IPR008906: HAT dimerisation domain, C-terminal; IPR012337: Ribonuclease H-like domain; PTHR23272: ; Coil:	NA
comp30458_c0_seq1.p1	Ec-00_009600.2	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp27194_c0_seq2.p1	Ec-00_009610.2	hypothetical protein	n/a;n/a;n/a	NA	NA
comp26125_c0_seq1.p1	Ec-00_009620.1	eukaryotic initiation factor 4G	GO:0005515;GO:0016070	IPR003891: Initiation factor eIF-4 gamma, MA3; IPR003890: MIF4G-like, type 3; IPR016024: Armadillo-type fold; Coil: ; PTHR23253: ; IPR016021: MIF4-like, type 1/2/3	NA
comp28654_c0_seq2.p1	Ec-00_009680.1	Rhodanese-like domain	n/a;n/a;n/a	IPR001763: Rhodanese-like domain; PTHR13297:	NA
comp20430_c1_seq1.p1	Ec-00_009740.1	Zinc finger, CCHC-type	GO:0003676;GO:0008270	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR001878: Zinc finger, CCHC-type; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32029_c1_seq9.p2	Ec-00_009880.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp11938_c0_seq1.p1	Ec-00_009890.1	Mpv17/PMP22	GO:0016021	IPR007248: Mpv17/PMP22; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29183_c0_seq1.p1	Ec-00_009950.1	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR16453: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp31195_c0_seq3.p1	Ec-00_009970.1	hypothetical protein	GO:0031177	NA	NA
comp32800_c1_seq4.p1	Ec-00_010010.1	Uridyltransferase	NA	SSF81631: ; IPR002058: PAP/25A-associated; PTHR12271: ; G3DSA:3.30.460.10: ; SSF81301:	NA
comp31061_c0_seq2.p1	Ec-00_010200.2	Fatty acid desaturase, type 1	GO:0006629	IPR018506: Cytochrome b5, heme-binding site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR19353:SF30: ; IPR001199: Cytochrome b5-like heme/steroid binding domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005804: Fatty acid desaturase domain, type 1; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR19353:	NA
comp32342_c0_seq16.p1	Ec-00_010240.1	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0036459;GO:0006511	G3DSA:2.20.210.10: ; IPR018200: Ubiquitin specific protease, conserved site; SSF54001: ; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase; IPR028889: Ubiquitin specific protease domain; PTHR24006:	NA
comp32902_c0_seq7.p1	Ec-00_010400.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28794_c0_seq2.p2	Ec-00_010420.1	Protein kinase-like domain	GO:0016772	PTHR22983: ; IPR017441: Protein kinase, ATP binding site; IPR000719: Protein kinase domain; G3DSA:3.30.200.20: ; IPR008266: Tyrosine-protein kinase, active site; G3DSA:1.10.510.10: ; IPR011009: Protein kinase-like domain	NA
comp32295_c1_seq1.p1	Ec-00_010450.3	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp11870_c0_seq1.p1	Ec-00_010520.1	BSD	n/a;n/a;n/a	SSF140383: ; IPR005607: BSD; Coil:	NA
comp31328_c1_seq1.p1	Ec-00_010540.1	conserved unknown protein	n/a;n/a;n/a	IPR001849: Pleckstrin homology domain	NA
comp31328_c1_seq1.p2	Ec-00_010560.1	Adenosine/AMP deaminase domain	GO:0019239	IPR001365: Adenosine/AMP deaminase domain; PTHR11409: ; SSF51556: ; G3DSA:3.20.20.140:	NA
comp13068_c0_seq1.p2	Ec-00_010570.1	Ribosomal protein S6e	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR001377: Ribosomal protein S6e; IPR014401: Ribosomal protein S6, eukaryotic; Coil: ; IPR018282: Ribosomal protein S6e, conserved site	NA
comp31183_c0_seq1.p1	Ec-00_010600.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31183_c0_seq2.p1	Ec-00_010610.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp20944_c0_seq1.p1	Ec-00_010760.1	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0036459;GO:0006511	IPR018200: Ubiquitin specific protease, conserved site; SSF54001: ; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase; IPR028889: Ubiquitin specific protease domain; PTHR24006:	NA
comp31439_c0_seq3.p1	Ec-16_003370.1	mannuronan C-5 epimerase C-terminal fragment	NA	NA	NA
comp23218_c0_seq2.p1	Ec-00_010860.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp20683_c1_seq2.p1	Ec-00_010880.1	RmlC-like jelly roll fold	n/a;n/a;n/a	PTHR11635: ; IPR000595: Cyclic nucleotide-binding domain; IPR018488: Cyclic nucleotide-binding, conserved site; IPR012198: cAMP-dependent protein kinase regulatory subunit; IPR002373: cAMP/cGMP-dependent protein kinase; IPR018490: Cyclic nucleotide-binding-like; IPR003117: Dimerization-anchoring domain of cAMP-dependent protein kinase, regulatory subunit; IPR014710: RmlC-like jelly roll fold	NA
comp27881_c0_seq1.p1	Ec-00_010890.1	conserved unknown protein	n/a;n/a;n/a	G3DSA:3.90.1410.10: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; PTHR13271: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF82199: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32606_c0_seq6.p1	Ec-00_010920.1	Ubiquitin-related domain	n/a;n/a;n/a	G3DSA:3.10.20.90: ; IPR029071: Ubiquitin-related domain; IPR022617: Rad60/SUMO-like domain	NA
comp11379_c0_seq1.p1	Ec-00_010930.1	Quinonprotein alcohol dehydrogenase-like superfamily	n/a;n/a;n/a	PTHR22847: ; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily	NA
comp32224_c0_seq18.p1	Ec-00_010950.1	Bromodomain	GO:0005515	PTHR22880: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; IPR001487: Bromodomain	NA
comp22532_c0_seq1.p1	Ec-00_010990.1	RmlC-like jelly roll fold	n/a;n/a;n/a	IPR000595: Cyclic nucleotide-binding domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018490: Cyclic nucleotide-binding-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR014710: RmlC-like jelly roll fold	NA
comp31006_c0_seq1.p1	Ec-00_011070.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp12043_c0_seq1.p1	Ec-00_011080.1	Dynein heavy chain family	n/a;n/a;n/a	PTHR10676:SF262: ; IPR013594: Dynein heavy chain, domain-1; Coil: ; IPR026983: Dynein heavy chain	NA
comp32711_c1_seq14.p1	Ec-00_011190.1	conserved unknown protein	n/a;n/a;n/a	G3DSA:1.20.5.170: ; Coil:	NA
comp27064_c0_seq4.p2	Ec-00_011210.1	hypothetical protein	n/a;n/a;n/a	NA	NA

comp30214_c0_seq4.p1	Ec-00_011240.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp24227_c0_seq1.p1	Ec-00_011260.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp30835_c1_seq1.p1	Ec-00_011350.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp17995_c0_seq2.p1	Ec-00_011380.1	expressed unknown protein	n/a;GO:0005515	[illegible]	[illegible]
comp32124_c5_seq2.p1	Ec-00_011390.1	expressed unknown protein	n/a;n/a;n/a	Coil: ; SignalP-TM:	[illegible]
comp12045_c0_seq2.p1	Ec-00_011400.1	Hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp31282_c0_seq5.p2	Ec-00_011420.1	ADP-ribosylation factor-like 2-binding protein, domain	n/a;n/a;n/a	[illegible]	[illegible]
comp30954_c0_seq6.p2	Ec-00_011460.1	Folate-sensitive fragile site protein Fra10Ac1	n/a;n/a;n/a	[illegible]	[illegible]
comp25135_c0_seq1.p1	Ec-00_011470.1	Nucleotide cyclase	GO:0009190;GO:0035556;GO:0016849;GO:0007242	[illegible]	[illegible]
comp55961_c0_seq1.p1	Ec-00_011480.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp32176_c1_seq4.p1	Ec-01_000060.1	diaminopimelate decarboxylase	n/a;GO:0003824	[illegible]	[illegible]
comp30560_c0_seq5.p1	Ec-01_000070.1	P-type ATPase, A domain	GO:0000166;GO:0046872	[illegible]	[illegible]
comp47245_c0_seq1.p1	Ec-01_000080.1	Armadillo-like helical	n/a;GO:0005488	[illegible]	[illegible]
comp28784_c1_seq7.p1	Ec-01_000090.1	Fatty acid desaturase	GO:0006629;GO:0016491;GO:0055114	[illegible]	[illegible]
comp12691_c0_seq1.p1	Ec-01_000100.1	SAP domain	n/a;GO:0006629	[illegible]	[illegible]
comp28569_c0_seq2.p1	Ec-01_000110.1	Serine-threonine/tyrosine-protein kinase catalytic domain	GO:0004672;GO:0006468	[illegible]	[illegible]
comp28569_c0_seq3.p1	Ec-01_000120.1	Peptidase C19, ubiquitin-specific peptidase, DUSP domain	GO:0004843	[illegible]	[illegible]
comp28569_c0_seq3.p2	Ec-01_000130.1	4'-phosphopantetheinyl transferase superfamily	GO:0000287;GO:0009059;GO:0008897	[illegible]	[illegible]
comp29068_c0_seq1.p1	Ec-01_000140.1	Ribosomal RNA large subunit methyltransferase RlmN/Cfr	GO:0008173;GO:0003824;GO:0006364;GO:0005737;GO:0051536	[illegible]	[illegible]
comp33265_c0_seq3.p1	Ec-01_000160.1	Protein of unknown function DUF938	n/a;n/a;n/a	[illegible]	[illegible]
comp109747_c0_seq1.p1	Ec-01_000170.3	C-type lectin-like	GO:0005488	[illegible]	[illegible]
comp20141_c0_seq1.p1	Ec-01_000180.1	Thioredoxin-like fold	n/a;n/a;n/a	[illegible]	[illegible]
comp32113_c0_seq4.p3	Ec-01_000190.1	conserved unknown protein	n/a;n/a;n/a	NA	[illegible]
comp32113_c0_seq4.p2	Ec-01_000200.1	conserved unknown protein	n/a;GO:0005515	[illegible]	[illegible]
comp32113_c0_seq4.p1	Ec-01_000210.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp25171_c0_seq1.p1	Ec-01_000220.2	Short-chain dehydrogenase/reductase SDR	GO:0008152;GO:0016491	[illegible]	[illegible]
comp25171_c0_seq1.p2	Ec-01_000230.1	FAD binding / catalytic/ tRNA dihydrouridine synthase	GO:0017150;GO:0050660;GO:0055114;GO:0008033	[illegible]	[illegible]
comp26257_c0_seq3.p1	Ec-01_000240.1	Alpha/Beta hydrolase fold	GO:0006508;GO:0005515;GO:0008236	[illegible]	[illegible]
comp28070_c0_seq4.p1	Ec-01_000250.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp29779_c0_seq1.p1	Ec-01_000260.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp29779_c0_seq1.p2	Ec-01_000270.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp13083_c0_seq1.p1	Ec-01_000280.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp29433_c1_seq6.p1	Ec-01_000290.1	Mitochondrial matrix Mmp37	n/a;n/a;n/a	[illegible]	[illegible]
comp18159_c0_seq1.p1	Ec-01_000300.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31696_c0_seq2.p1	Ec-01_000310.1	F-box, zinc finger protein	GO:0046872;GO:0005515	[illegible]	[illegible]
comp26735_c0_seq1.p1	Ec-01_000320.1	ABC transporter type 1, transmembrane domain	GO:0006810;GO:0055085;GO:0005524;GO:0042626;GO:0016021;GO:0016887	[illegible]	[illegible]
comp25118_c0_seq1.p1	Ec-01_000330.1	Winged helix-turn-helix DNA-binding domain	GO:0004867	[illegible]	[illegible]
comp21425_c0_seq2.p1	Ec-01_000340.1	Ankyrin repeat-containing domain	n/a;GO:0004733;GO:0010181;GO:0055114	[illegible]	[illegible]
comp29078_c0_seq4.p1	Ec-01_000360.1	Uroporphyrinogen decarboxylase, chloroplast precursor	GO:0004853;GO:0006779	[illegible]	[illegible]
comp10512_c0_seq1.p1	Ec-01_000370.1	EF-hand domain pair	GO:0005509	[illegible]	[illegible]
comp25148_c0_seq1.p1	Ec-01_000400.1	Chlorophyll a/b binding protein domain	n/a;n/a;n/a	[illegible]	[illegible]
comp24287_c0_seq3.p1	Ec-01_000420.1	NADH dehydrogenase (ubiquinone)	GO:0016491;GO:0050660;GO:0055114	[illegible]	[illegible]
comp12981_c0_seq1.p1	Ec-01_000430.1	Glutamyl-tRNA Reductase, chloroplast precursor	GO:0050661;GO:0008883;GO:0033014;GO:0055114	[illegible]	[illegible]
comp12283_c0_seq1.p1	Ec-01_000440.1	conserved unknown protein	GO:0005515	NA	[illegible]
comp33019_c1_seq3.p1	Ec-01_000450.1	expressed unknown protein	GO:0006520;GO:0030170;n/a	[illegible]	[illegible]
comp32591_c1_seq5.p1	Ec-01_000460.1	Ankyrin repeat-containing domain	n/a;GO:0005515	[illegible]	[illegible]
comp34447_c0_seq1.p1	Ec-01_000490.1	Programmed cell death protein 2, C-terminal	GO:0005737	[illegible]	[illegible]
comp29041_c0_seq2.p1	Ec-01_000500.1	Exonuclease	GO:0004527	[illegible]	[illegible]
comp29041_c0_seq2.p3	Ec-01_000510.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp32318_c1_seq8.p4	Ec-01_000520.1	Uncharacterised protein family UPF0001	n/a;n/a;n/a	[illegible]	[illegible]
comp26102_c0_seq3.p2	Ec-01_000530.1	NC2alpha class protein with histone-like transcription factor (NF-YC subunit) domain	GO:0046982	NA	[illegible]
comp32318_c1_seq7.p1	Ec-01_000540.1	Kinesin motor domain	GO:0003777;GO:0005524;GO:0005871;GO:0007018;GO:0008017	[illegible]	[illegible]
comp26102_c0_seq3.p1	Ec-01_000560.1	expressed unknown protein	GO:0005515;GO:0016020;GO:0016192	[illegible]	[illegible]
comp28929_c0_seq1.p1	Ec-01_000570.1	NMD3	n/a;n/a;n/a	[illegible]	[illegible]
comp59100_c0_seq1.p2	Ec-01_000580.1	Guanine nucleotide binding protein beta subunit	NA	[illegible]	[illegible]
comp25364_c0_seq5.p4	Ec-01_000590.1	WD40/YVTN repeat-like-containing domain	GO:0005515	[illegible]	[illegible]
comp32367_c0_seq9.p1	Ec-01_000600.1	Similar to Rrp6, which is a component of the exosome 3'->5' exoribonuclease complex, a complex that degrades mRNAs.	GO:0005622;GO:0003676;GO:0008408;GO:0006139	[illegible]	[illegible]
comp21553_c0_seq2.p1	Ec-01_000620.1	conserved unknown protein	GO:0016813;GO:0046872	[illegible]	[illegible]
comp29018_c0_seq2.p1	Ec-01_000630.1	NatC N(alpha)-terminal acetyltransferase, Mak10 subunit	n/a;n/a;n/a	[illegible]	[illegible]
comp32409_c0_seq4.p1	Ec-01_000640.1	Chloride channel protein EriC	GO:0016020;GO:0055085;GO:0005216;GO:0006821;GO:0005247	[illegible]	[illegible]
comp28839_c1_seq2.p1	Ec-01_000660.1	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	n/a;n/a;n/a	[illegible]	[illegible]
comp25276_c0_seq1.p1	Ec-01_000680.1	Cyclic nucleotide-binding domain	n/a;n/a;n/a	[illegible]	[illegible]
comp20147_c0_seq2.p1	Ec-01_000690.1	Pseudouridine synthase I, TruA, C-terminal	GO:0003723;GO:0009451;GO:0009982;GO:0001522	[illegible]	[illegible]
comp31644_c0_seq2.p1	Ec-01_000710.3	High mobility group and PHD zinc finger domain protein	GO:0008270	[illegible]	[illegible]
comp53188_c0_seq1.p1	Ec-01_000720.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp28513_c0_seq1.p1	Ec-01_000740.1	Putative cyclin A	n/a;n/a;n/a	[illegible]	[illegible]
comp28900_c0_seq2.p1	Ec-01_000750.1	Phosphatidylinositol 3- and 4-kinase family protein	GO:0006464;GO:0005515	[illegible]	[illegible]
comp26997_c1_seq1.p1	Ec-01_000760.1	tRNA-splicing ligase, RtcB	GO:0006396;GO:0008452	[illegible]	[illegible]
comp31452_c0_seq1.p1	Ec-01_000780.1	vacuolar protein sorting vps16	GO:0005737;GO:0006886	[illegible]	[illegible]
comp32322_c1_seq3.p1	Ec-01_000790.1	Protein kinase	NA	NA	[illegible]
comp32006_c1_seq14.p2	Ec-01_000800.1	NADH-ubiquinone oxidoreductase, subunit 10	n/a;n/a;n/a	[illegible]	[illegible]
comp31836_c0_seq4.p3	Ec-01_000810.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp31836_c0_seq4.p2	Ec-01_000820.1	Beta-lactamase-like	GO:0016787	[illegible]	[illegible]
comp31465_c0_seq4.p2	Ec-01_000830.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31465_c0_seq4.p1	Ec-01_000840.1	Mg2+ transporter protein, CorA-like/Zinc transport protein ZntB	GO:0016020;GO:0015693;GO:0055085;GO:0046873;GO:0015095;GO:0030001	[illegible]	[illegible]
comp31465_c0_seq4.p3	Ec-01_000850.1	Solute carrier family 35 member SLC35F1/F2/F6	GO:0006810;GO:0016021	[illegible]	[illegible]
comp32167_c0_seq32.p1	Ec-01_000860.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp30842_c0_seq2.p2	Ec-01_000870.1	B1358B12.18	n/a;n/a;n/a	[illegible]	[illegible]
comp30842_c0_seq2.p1	Ec-01_000890.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp28004_c0_seq1.p1	Ec-01_000930.1	von Willebrand factor, type A	GO:0005515;GO:0006886;GO:0006888;GO:0030127	[illegible]	[illegible]
comp26666_c0_seq2.p1	Ec-01_000960.1	Mitochondrial carrier protein	GO:0055085	[illegible]	[illegible]
comp26666_c0_seq4.p3	Ec-01_000970.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp34508_c0_seq1.p1	Ec-01_000980.1	plastid phosphoglycerate mutase protein precursor	GO:0003824;GO:0008152	[illegible]	[illegible]
comp138891_c0_seq1.p1	Ec-01_000990.2	RNA ligase/cyclic nucleotide phosphodiesterase	GO:0003824;GO:0005622;GO:0016070	[illegible]	[illegible]
comp11544_c0_seq1.p1	Ec-01_001000.1	Tetratricopeptide-like helical domain	GO:0005515	[illegible]	[illegible]
comp27150_c0_seq1.p1	Ec-01_001010.1	Zinc finger, CCHC-type	GO:0003676;GO:0008270	[illegible]	[illegible]
comp12398_c0_seq1.p1	Ec-01_001020.1	Mediator complex, subunit Med4	GO:0006357;GO:0016592;GO:0001104	[illegible]	[illegible]
comp32667_c0_seq4.p1	Ec-01_001040.1	Cation efflux protein	GO:0055085;GO:0016021;GO:0006812;GO:0008324	[illegible]	[illegible]
comp28492_c1_seq1.p1	Ec-01_001060.2	TFIIH p62 subunit, N-terminal	n/a;n/a;n/a	[illegible]	[illegible]
comp29888_c0_seq2.p1	Ec-01_001070.1	SET domain and Rubisco LSMT substrate-binding domain protein	GO:0005515	NA	[illegible]
comp28671_c0_seq2.p1	Ec-01_001080.1	SelB, translation elongation factor specific to Sec-tRNA	GO:0003924;GO:0005525	[illegible]	[illegible]
comp30596_c0_seq2.p1	Ec-01_001090.1	ADP/ATP carrier protein	GO:0005471;GO:0005524;GO:0006810;GO:0016021	[illegible]	[illegible]
comp26706_c0_seq1.p1	Ec-01_001100.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp33451_c0_seq1.p1	Ec-01_001120.1	Cytochrome c oxidase subunit Vb.	GO:0004129;GO:0005740;GO:0006118	[illegible]	[illegible]
comp22748_c0_seq1.p1	Ec-01_001140.2	WW domain	GO:0005515	[illegible]	[illegible]
comp19451_c0_seq1.p1	Ec-01_001150.1	Domain of unknown function DUF1279	n/a;n/a;n/a	[illegible]	[illegible]
comp35373_c0_seq1.p1	Ec-01_001160.1	Defective-in-cullin neddylation protein	n/a;n/a;n/a	[illegible]	[illegible]
comp26851_c0_seq2.p1	Ec-01_001170.1	Acetyltransferase (GNAT) domain protein	GO:0008080	NA	[illegible]
comp21611_c0_seq1.p1	Ec-01_001180.1	SGF29 tudor-like domain	n/a;n/a;n/a	[illegible]	[illegible]
comp28506_c0_seq2.p1	Ec-01_001210.1	Pathogenesis-related transcriptional factor and ERF	GO:0003700;GO:0006355	[illegible]	[illegible]
comp12480_c0_seq2.p1	Ec-01_001220.1	ion channel nompc, putative	n/a;GO:0005515	[illegible]	[illegible]
comp27130_c0_seq1.p1	Ec-01_001230.1	Histidine phosphatase superfamily, clade-1	GO:0003824;GO:0005524;GO:0006003	[illegible]	[illegible]
comp29184_c0_seq3.p1	Ec-01_001250.3	WW domain	GO:0005515	[illegible]	[illegible]
comp31383_c0_seq3.p1	Ec-01_001260.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp25375_c0_seq1.p1	Ec-01_001270.1	Citrate transporter-like domain	GO:0016020;GO:0055085;GO:0016021;GO:0006814;GO:0005215	[illegible]	[illegible]
comp26587_c0_seq1.p1	Ec-01_001340.2	Citrate transporter-like domain	GO:0016021;GO:0055085	[illegible]	[illegible]
comp21452_c0_seq1.p1	Ec-01_001350.1	phosphoglycerate kinase	GO:0006096;GO:0004618	[illegible]	[illegible]
comp30643_c0_seq3.p2	Ec-01_001370.1	UBX domain	GO:0005515	[illegible]	[illegible]
comp30643_c0_seq3.p1	Ec-01_001410.1	Citrate transporter-like domain	GO:0016020;GO:0055085;GO:0016021;GO:0006814;GO:0005215	[illegible]	[illegible]
comp16765_c0_seq2.p1	Ec-01_001430.1	EF-hand domain pair	GO:0005509	[illegible]	[illegible]
comp33662_c0_seq1.p1	Ec-01_001440.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp34128_c0_seq1.p1	Ec-01_001450.1	ferredoxin-NADP oxidoreductase	GO:0055114;GO:0016491	[illegible]	[illegible]
comp30978_c0_seq1.p1	Ec-01_001460.1	villin	GO:0003779	[illegible]	[illegible]
comp30112_c0_seq3.p1	Ec-01_001470.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp30112_c0_seq13.p1	Ec-01_001480.1	Protein phosphatase 2C (PP2C)-like domain	GO:0004672;GO:0006468;GO:0003824	[illegible]	[illegible]
comp29067_c0_seq1.p3	Ec-01_001510.1	Resolvase, holliday junction-type, YqgF-like	GO:0031564;GO:0006281;GO:0006974;GO:0005737;GO:0006310;GO:0016788	[illegible]	[illegible]
comp29067_c0_seq1.p1	Ec-01_001540.1	Armadillo-like helical	GO:0005488	[illegible]	[illegible]
comp31098_c0_seq4.p1	Ec-01_001550.1	SNF2-related, winged helix-turn-helix DNA-binding and zinc finger domain protein	GO:0003677;GO:0005524	NA	[illegible]
comp29756_c0_seq1.p1	Ec-01_001550.2	Winged helix-turn-helix DNA-binding domain	GO:0003677;GO:0005524	[illegible]	[illegible]
comp12515_c0_seq1.p1	Ec-01_001560.1	long chain acyl-coA synthetase	GO:0008152;GO:0003824	[illegible]	[illegible]
comp27410_c0_seq1.p1	Ec-01_001600.1	Guanosine polyphosphate pyrophosphohydrolases/synthetases	GO:0015969	[illegible]	[illegible]
comp20588_c0_seq1.p1	Ec-01_001610.1	Serine O-acetyltransferase, incomplete	GO:0009001;GO:0006535;GO:0005737	[illegible]	[illegible]
comp30116_c1_seq2.p1	Ec-01_001620.1	Tetratricopeptide-like helical domain	GO:0005515	[illegible]	[illegible]
comp30647_c0_seq2.p1	Ec-01_001630.1	Helicase-associated domain	GO:0004386	[illegible]	[illegible]
comp29450_c0_seq6.p1	Ec-01_001650.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31327_c0_seq4.p1	Ec-01_001660.1	HECT	GO:0005515;GO:0004842	[illegible]	[illegible]
comp29908_c0_seq2.p1	Ec-01_001700.1	Pyruvate/Phosphoenolpyruvate kinase-like domain	GO:0015940;GO:0003864;GO:0003824	[illegible]	[illegible]
comp21245_c0_seq1.p1	Ec-01_001710.1	TUP1-like enhancer of split	GO:0005634;GO:0006355;GO:0006351;GO:0016568	[illegible]	[illegible]
comp29370_c0_seq1.p2	Ec-01_001710.2	TUP1-like enhancer of split	GO:0005634;GO:0006355	[illegible]	[illegible]
comp29370_c0_seq1.p1	Ec-01_001720.1	Putative S-adenosyl-L-methionine-dependent methyltransferase MidA	n/a;n/a;n/a	[illegible]	[illegible]
comp20236_c0_seq1.p2	Ec-01_001740.1	Phytanoyl-CoA dioxygenase	n/a;n/a;n/a	[illegible]	[illegible]
comp20236_c0_seq2.p1	Ec-01_001750.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524	[illegible]	[illegible]
comp26885_c0_seq1.p1	Ec-01_001780.1	Armadillo-type fold	GO:0005488	[illegible]	[illegible]
comp26604_c0_seq2.p1	Ec-01_001840.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp24357_c0_seq4.p1	Ec-01_001860.1	conserved unknown protein	NA	[illegible]	[illegible]
comp25001_c0_seq2.p1	Ec-01_001870.1	argininosuccinate synthetase	GO:0005524;GO:0004055;GO:0006526	[illegible]	[illegible]
comp12321_c0_seq1.p1	Ec-01_001880.1	Uncharacterised protein family Cys-rich	n/a;n/a;n/a	[illegible]	[illegible]
comp32983_c1_seq46.p6	Ec-01_001900.1	Arf GTPase activating protein	GO:0032312;GO:0008060;GO:0008270;GO:0005096	NA	[illegible]
comp32983_c1_seq46.p1	Ec-01_001910.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp29452_c1_seq1.p1	Ec-01_001920.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp27441_c2_seq1.p1	Ec-01_001930.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp27441_c2_seq1.p2	Ec-01_001940.1	FUN14	n/a;n/a;n/a	[illegible]	[illegible]
comp28913_c0_seq3.p1	Ec-01_001950.1	CobW/HypB/UreG domain	n/a;n/a;n/a	[illegible]	[illegible]
comp20478_c0_seq2.p1	Ec-01_001960.1	conserved unknown protein	n/a;n/a;n/a	NA	[illegible]
comp32368_c1_seq4.p1	Ec-01_001970.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	[illegible]	[illegible]
comp31427_c0_seq4.p2	Ec-01_001990.1	Protein of unknown function DUF1350	NA	[illegible]	[illegible]
comp56038_c0_seq1.p1	Ec-01_002000.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	[illegible]	[illegible]
comp28238_c0_seq3.p1	Ec-01_002020.1	Six-hairpin glycosidase	GO:0003824	[illegible]	[illegible]
comp31426_c1_seq9.p1	Ec-01_002030.1	F-box domain	GO:0005515	[illegible]	[illegible]
comp32368_c1_seq4.p2	Ec-01_002040.1	Rrp46 is a component of the exosome 3'->5' exoribonuclease complex, a complex that degrades mRNAs.	GO:0000175;GO:0003723;GO:0006396	[illegible]	[illegible]
comp28716_c0_seq1.p1	Ec-01_002050.1	alternative oxidase, mitochondrial protein	GO:0009916;GO:0055114	[illegible]	[illegible]
comp31427_c0_seq4.p1	Ec-01_002060.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp24205_c0_seq1.p1	Ec-01_002070.1	UBX domain	GO:0005515	[illegible]	[illegible]
comp24205_c0_seq1.p2	Ec-01_002080.1	RNA-binding domain, S1, IF1 type	GO:0006413;GO:0003723;GO:0003743	[illegible]	[illegible]
comp24124_c0_seq1.p1	Ec-01_002090.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp27539_c0_seq3.p1	Ec-01_002100.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp21053_c0_seq1.p1	Ec-01_002110.1	SAP domain	GO:0003676	[illegible]	[illegible]
comp30928_c0_seq4.p1	Ec-01_002130.1	SOUL haem-binding protein	n/a;n/a;n/a	[illegible]	[illegible]
comp27850_c0_seq1.p1	Ec-01_002150.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	[illegible]	[illegible]
comp32105_c1_seq6.p1	Ec-01_002180.1	Alpha/Beta hydrolase fold	GO:0004091;n/a	[illegible]	[illegible]
comp29735_c0_seq4.p1	Ec-01_002190.1	JAB1/MPN/MOV34 metalloenzyme domain	GO:0005515	[illegible]	[illegible]
comp24906_c0_seq1.p1	Ec-01_002200.1	Apoptosis inducing factor	GO:0050660;GO:0055114;GO:0016491	[illegible]	[illegible]
comp35585_c0_seq1.p1	Ec-01_002220.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp12834_c0_seq1.p1	Ec-01_002250.1	carboxyvinyl-carboxyphosphonate phosphorylmutase	GO:0008152;GO:0003824	[illegible]	[illegible]
comp12834_c0_seq1.p2	Ec-01_002260.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp20088_c0_seq1.p1	Ec-01_002270.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp29367_c0_seq1.p1	Ec-01_002280.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp26158_c0_seq2.p1	Ec-01_002290.1	Transcription elongation factor 1	n/a;n/a;n/a	[illegible]	[illegible]
comp33621_c0_seq1.p1	Ec-01_002300.1	Prohibitin complex subunit 1	NA	[illegible]	[illegible]
comp29636_c0_seq5.p1	Ec-01_002310.1	Armadillo-type fold	GO:0005488	[illegible]	[illegible]
comp32581_c0_seq1.p1	Ec-01_002320.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp28813_c0_seq7.p1	Ec-01_002330.1	Methyltransferase type 11	GO:0008152;GO:0008168	[illegible]	[illegible]
comp28813_c0_seq7.p3	Ec-01_002340.1	AhpD-like	n/a;GO:0055114;GO:0051920	[illegible]	[illegible]
comp29381_c0_seq4.p1	Ec-01_002350.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	[illegible]	[illegible]
comp29381_c0_seq6.p2	Ec-01_002360.1	conserved unknown protein	n/a;n/a;n/a	NA	[illegible]
comp25534_c0_seq1.p1	Ec-01_002370.1	Hydrolase, carbon-nitrogen family protein	GO:0006807;GO:0016810	[illegible]	[illegible]
comp32851_c0_seq1.p1	Ec-01_002380.1	Short-chain dehydrogenase/reductase SDR	GO:0008152;GO:0016491	[illegible]	[illegible]
comp32243_c2_seq13.p1	Ec-01_002400.1	LsmAD domain	n/a;n/a;n/a	[illegible]	[illegible]
comp29426_c0_seq2.p1	Ec-01_002410.1	HAD-like domain	GO:0008270;GO:0016491;GO:0055114	[illegible]	[illegible]
comp25141_c0_seq1.p1	Ec-01_002420.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	[illegible]	[illegible]
comp20039_c0_seq1.p1	Ec-01_002460.1	heat shock protein Hsp90	GO:0005524;GO:0006457;GO:0006950;GO:0051082	[illegible]	[illegible]
comp24595_c0_seq2.p1	Ec-01_002470.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp25428_c0_seq1.p1	Ec-01_002500.1	LRR-GTPase of the ROCO family	GO:0007264;GO:0005622;GO:0005525	[illegible]	[illegible]
comp20693_c0_seq1.p1	Ec-01_002520.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp29284_c0_seq5.p1	Ec-01_002530.1	Proliferating cell nuclear antigen, PCNA, C-terminal	GO:0003677;GO:0006275	[illegible]	[illegible]
comp29713_c0_seq5.p2	Ec-01_002540.1	ubiquinol cytochrome c reductase cytochrome c1 prec (ISS)	GO:0009055;GO:0020037;GO:0005506	[illegible]	[illegible]
comp29284_c0_seq4.p1	Ec-01_002550.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp29713_c0_seq5.p1	Ec-01_002570.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp27552_c0_seq2.p1	Ec-01_002580.1	EGF-like calcium-binding domain	GO:0005509	[illegible]	[illegible]
comp26934_c1_seq1.p1	Ec-01_002600.1	EamA domain	GO:0016020;GO:0016021	[illegible]	[illegible]
comp33012_c2_seq1.p1	Ec-01_002610.1	Zinc finger, RING/FYVE/PHD-type	GO:0005515;GO:0008270	[illegible]	[illegible]
comp27568_c0_seq2.p1	Ec-01_002650.1	Heat Shock transcription factor	GO:0005634;GO:0006355;GO:0043565;GO:0003700	NA	[illegible]
comp20533_c0_seq1.p1	Ec-01_002660.1	zinc finger, FYVE domain containing 19, isoform CRA_g	n/a;n/a;n/a	[illegible]	[illegible]
comp20533_c0_seq2.p2	Ec-01_002670.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp29434_c4_seq1.p1	Ec-01_002680.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31051_c2_seq12.p1	Ec-01_002690.1	Pleckstrin homology-like domain	n/a;n/a;n/a	[illegible]	[illegible]
comp25395_c1_seq1.p1	Ec-01_002700.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp21518_c0_seq1.p1	Ec-01_002710.1	Alpha/Beta hydrolase fold	GO:0016787	[illegible]	[illegible]
comp31818_c0_seq2.p1	Ec-01_002720.1	ferredoxin nitrite reductase	GO:0016491;GO:0055114	[illegible]	[illegible]
comp29365_c0_seq1.p6	Ec-01_002730.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp29720_c0_seq1.p1	Ec-01_002740.1	hypothetical protein	NA	[illegible]	[illegible]
comp31818_c0_seq4.p1	Ec-01_002750.1	C2H2 zinc finger protein	GO:0003676;GO:0005622;GO:0008270	[illegible]	[illegible]
comp26830_c0_seq2.p1	Ec-01_002770.3	AP endonuclease 1	GO:0004518;GO:0006281	[illegible]	[illegible]
comp32370_c0_seq15.p2	Ec-01_002780.1	Aldolase-type TIM barrel	GO:0005975;GO:0003824	[illegible]	[illegible]
comp26609_c0_seq1.p1	Ec-01_002790.1	Poly(ADP-ribose) polymerase, catalytic domain	GO:0003950	[illegible]	[illegible]
comp31981_c0_seq3.p1	Ec-01_002810.1	xylulose kinase	GO:0016773;GO:0005975	[illegible]	[illegible]
comp21537_c0_seq1.p1	Ec-01_002820.1	AAA+ ATPase domain	GO:0005524	[illegible]	[illegible]
comp31112_c0_seq1.p1	Ec-01_002840.1	Magnesium chelatase subunit H, putative chloroplast precursor	GO:0016851;GO:0015995	[illegible]	[illegible]
comp33959_c0_seq1.p1	Ec-01_002890.1	conserved unknown protein	n/a;n/a;n/a	NA	[illegible]
comp33959_c0_seq1.p2	Ec-01_002900.1	proteasome subunit alpha type 7	GO:0004175;GO:0019773;GO:0006511;GO:0004298	[illegible]	[illegible]
comp19906_c0_seq1.p1	Ec-01_002920.1	Thioredoxin-like fold	GO:0006457;n/a;GO:0051082;GO:0031072	[illegible]	[illegible]
comp18619_c0_seq1.p1	Ec-01_002940.1	RGS domain	GO:0038032	[illegible]	[illegible]
comp32374_c1_seq2.p1	Ec-01_002950.1	YHS domain-containing protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31226_c1_seq9.p1	Ec-01_002960.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31555_c0_seq13.p2	Ec-01_002970.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31555_c0_seq13.p1	Ec-01_002980.1	Ribokinase-like	GO:0004001;GO:0006166	[illegible]	[illegible]
comp28971_c1_seq1.p1	Ec-01_002990.1	mitochondrial ADP/ATP translocator	GO:0006810;GO:0055085;GO:0005743;GO:0005215	[illegible]	[illegible]
comp34122_c0_seq1.p1	Ec-01_003040.1	Glycogen synthase kinase-3 beta (GSK-3 beta)	GO:0004672;GO:0005524;GO:0006468	[illegible]	[illegible]
comp28486_c0_seq3.p1	Ec-01_003050.1	conserved unknown protein	GO:0003677;n/a	[illegible]	[illegible]
comp21083_c0_seq1.p1	Ec-01_003060.1	EF-hand domain pair	GO:0005509;n/a	[illegible]	[illegible]
comp26965_c0_seq1.p1	Ec-01_003080.1	Major facilitator superfamily domain	n/a;n/a;n/a	[illegible]	[illegible]
comp65956_c0_seq1.p2	Ec-01_003110.2	Auxin efflux carrier	GO:0016021;GO:0055085	[illegible]	[illegible]
comp31440_c0_seq9.p1	Ec-01_003120.1	Auxin efflux carrier	GO:0055085;GO:0016021	[illegible]	[illegible]
comp20572_c1_seq1.p1	Ec-01_003130.1	GDP-4-keto-6-deoxy-D-mannose epimerase-reductase	GO:0003824;GO:0005488;GO:0008152	[illegible]	[illegible]
comp33424_c0_seq1.p1	Ec-01_003150.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	[illegible]	[illegible]
comp29957_c0_seq11.p1	Ec-01_003160.1	Rubisco LSMT, substrate-binding domain	n/a;n/a;n/a	[illegible]	[illegible]
comp27918_c0_seq2.p1	Ec-01_003170.1	Hypothetical leucine rich repeat protein	GO:0005515;GO:0005509	[illegible]	[illegible]
comp30732_c0_seq5.p1	Ec-01_003180.2	Transmembrane protein TauE like	GO:0016021	[illegible]	[illegible]
comp11241_c0_seq2.p1	Ec-01_003190.1	Cyclophilin-like domain	GO:0006457;GO:0003755	[illegible]	[illegible]
comp31745_c0_seq5.p2	Ec-01_003210.1	Aldehyde dehydrogenase	GO:0016620;GO:0008152;GO:0055114;GO:0016491	NA	[illegible]
comp31745_c0_seq5.p1	Ec-01_003220.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp13133_c0_seq1.p1	Ec-01_003240.1	Amino acid transporter, transmembrane	n/a;n/a;n/a	[illegible]	[illegible]
comp29927_c1_seq3.p1	Ec-01_003250.1	sec23/sec24 transport protein-related	NA	[illegible]	[illegible]
comp28777_c0_seq4.p1	Ec-01_003260.1	Glucose-methanol-choline oxidoreductase, C-terminal	GO:0016614;GO:0055114	[illegible]	[illegible]
comp34580_c0_seq1.p1	Ec-01_003290.1	Protein of unknown function DUF2009	n/a;n/a;n/a	[illegible]	[illegible]
comp32843_c0_seq2.p2	Ec-01_003300.1	small nuclear ribonucleoprotein D2-like protein	GO:0030529;GO:0016071	[illegible]	[illegible]
comp20165_c0_seq2.p1	Ec-01_003330.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp12916_c0_seq1.p1	Ec-01_003340.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp21049_c0_seq1.p1	Ec-01_003350.1	MutS protein homolog 6	GO:0006298	[illegible]	[illegible]
comp25618_c0_seq5.p1	Ec-01_003370.1	GWT1	GO:0006506;GO:0016746;GO:0016021;GO:0005789	[illegible]	[illegible]
comp22598_c0_seq2.p1	Ec-01_003380.1	RNA recognition motif domain	GO:0000166;GO:0003676	[illegible]	[illegible]
comp24312_c0_seq1.p1	Ec-01_003410.1	Nucleolar protein 14	GO:0032040	[illegible]	[illegible]
comp28689_c0_seq2.p1	Ec-01_003420.1	Armadillo-like helical	GO:0005488;GO:0006402;GO:0030014	[illegible]	[illegible]
comp12967_c0_seq1.p1	Ec-01_003470.1	Brix domain	n/a;n/a;n/a	[illegible]	[illegible]
comp32408_c2_seq13.p1	Ec-01_003490.1	Ribosomal protein S6 kinase	GO:0005524;GO:0004674;GO:0004672;GO:0006468	[illegible]	[illegible]
comp20884_c0_seq1.p1	Ec-01_003500.1	Anthranilate Phosphoribosyltransferase	GO:0000162;GO:0004048;GO:0008152;GO:0016757	NA	[illegible]
comp26455_c0_seq1.p1	Ec-01_003520.1	conserved unknown protein	GO:0005509	[illegible]	[illegible]
comp21600_c0_seq1.p1	Ec-01_003540.1	elongation factor EF-3	GO:0005524;GO:0016887	[illegible]	[illegible]
comp27009_c0_seq4.p1	Ec-01_003550.1	Diphthamide biosynthesis protein 1, putative	NA	[illegible]	[illegible]
comp27009_c0_seq3.p2	Ec-01_003560.1	Domain of unknown function DUF1777	n/a;n/a;n/a	[illegible]	[illegible]
comp30442_c0_seq4.p1	Ec-01_003570.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	[illegible]	[illegible]
comp24638_c0_seq2.p2	Ec-01_003590.1	Peptidyl-prolyl cis-trans isomerase, FKBP-type	GO:0006457	[illegible]	[illegible]
comp24638_c0_seq2.p1	Ec-01_003600.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp17814_c1_seq1.p1	Ec-01_003610.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp20741_c0_seq1.p1	Ec-01_003620.1	Armadillo-type fold	GO:0005488	[illegible]	[illegible]
comp32167_c4_seq1.p1	Ec-01_003630.1	RNA recognition motif domain	GO:0000166;GO:0003676	[illegible]	[illegible]
comp21439_c0_seq1.p1	Ec-01_003640.1	Arginyl-tRNA Synthetase	GO:0004814;GO:0005524;GO:0006420	[illegible]	[illegible]
comp31439_c0_seq6.p1	Ec-01_003650.1	GRIP	GO:0005515;GO:0000042	[illegible]	[illegible]
comp26573_c0_seq1.p1	Ec-01_003660.1	Peroxiredoxin-like protein	NA	[illegible]	[illegible]
comp25032_c0_seq1.p1	Ec-01_003680.1	malate dehydrogenase	GO:0004470;GO:0004471;GO:0006108;GO:0055114	[illegible]	[illegible]
comp28198_c0_seq4.p1	Ec-01_003690.2	AAA+ ATPase domain	GO:0000166;GO:0005524;GO:0017111	[illegible]	[illegible]
comp32253_c0_seq7.p1	Ec-01_003730.1	Type III pantothenate kinase	GO:0004594	[illegible]	[illegible]
comp30081_c0_seq1.p1	Ec-01_003740.1	hypothetical protein	GO:0005515;GO:0008270	[illegible]	[illegible]
comp27096_c0_seq2.p1	Ec-01_003750.1	BRCT domain	GO:0005622	[illegible]	[illegible]
comp31552_c0_seq7.p1	Ec-01_003760.1	Protein of unknown function DUF3172	n/a;n/a;n/a	[illegible]	[illegible]
comp33076_c0_seq24.p1	Ec-01_003770.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp33834_c0_seq1.p1	Ec-01_003780.1	Sterol C-5 desaturase	GO:0005506;GO:0006633;GO:0016491;GO:0055114	[illegible]	[illegible]
comp57686_c0_seq1.p1	Ec-01_003800.1	Ribosomal protein S21e	GO:0005840;GO:0006412;GO:0005622;GO:0003735	[illegible]	[illegible]
comp29077_c0_seq1.p1	Ec-01_003810.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp29640_c0_seq3.p1	Ec-01_003830.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp27914_c0_seq3.p1	Ec-01_003840.1	plastid division protein FtsZ	GO:0051258;GO:0006184;GO:0043234;GO:0005525;GO:0003924	[illegible]	[illegible]
comp15128_c0_seq1.p1	Ec-01_003850.1	disproportionate superoxide radical into hydrogen peroxide	GO:0006801;GO:0046872;GO:0055114	[illegible]	[illegible]
comp82902_c0_seq1.p1	Ec-01_003860.2	Ankyrin, TRAF-type zinc finger protein	GO:0005515	[illegible]	[illegible]
comp26088_c0_seq1.p1	Ec-01_003870.1	Anoctamin	n/a;n/a;n/a	[illegible]	[illegible]
comp11841_c0_seq1.p1	Ec-01_003880.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]

comp27636_c0_seq1.p1	Ec-01_003890.1	PObg1, plastid Obg/CgtA-like GTPase 1	GO:0000287;GO:0005525;GO:0003924	IPR006169: GTP1/OBG domain; SIGNAL_PEPTIDE: Signal peptide region; IPR031167: OBG-type guanine nucleotide-binding (G) domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR11702: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR014100: GTP-binding protein Obg/CgtA; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015349: GTP-binding protein OBG, C-terminal; IPR006073: GTP binding domain; IPR006074: GTP1/OBG, conserved site; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp23085_c0_seq1.p1	Ec-01_003910.1	Cyclophilin-like domain	GO:0006457;GO:0003755	IPR024936: Cyclophilin-type peptidyl-prolyl cis-trans isomerase; IPR002130: Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain; IPR020892: Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site; IPR029000: Cyclophilin-like domain; Coil:	NA
comp33024_c1_seq25.p1	Ec-01_003920.1	Uncharacterised domain SAYSvFN	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR13527: ; IPR019387: Uncharacterised domain SAYSvFN; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32957_c0_seq18.p1	Ec-01_003930.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30585_c0_seq1.p1	Ec-01_003960.1	Glycerol-3-phosphate O-acyltransferase	GO:0008152;GO:0016746	NA	NA
comp32665_c0_seq6.p1	Ec-01_003970.1	hypothetical protein	n/a;GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; IPR000048: IQ motif, EF-hand binding site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27008_c0_seq1.p1	Ec-01_003990.1	putative respiratory burst oxidase homolog protein	GO:0055114;GO:0016491	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:2.40.30.10: ; SSF52343: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR11972: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013121: Ferric reductase, NAD binding; G3DSA:3.40.50.80: ; IPR013112: FAD-binding 8; IPR017938: Riboflavin synthase-like beta-barrel; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0039
comp25633_c0_seq1.p1	Ec-01_004000.1	Basic-leucine zipper domain	GO:0006355;GO:0043565;GO:0003700	IPR004827: Basic-leucine zipper domain; SSF57959: ; G3DSA:1.20.5.170: ; Coil:	NA
comp29994_c0_seq3.p1	Ec-01_004020.1	Protein kinase-like domain	GO:0004672;GO:0006468;GO:0016772	PTHR24349: ; IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33238_c0_seq6.p1	Ec-01_004030.1	C2 domain	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR12546: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000008: C2 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28181_c0_seq2.p1	Ec-01_004040.3	WD repeat-containing protein	n/a;n/a;n/a	PTHR22844: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; IPR020472: G-protein beta WD-40 repeat	NA
comp33669_c0_seq1.p1	Ec-01_004050.1	WD40/YVTN repeat-like-containing domain	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29939_c0_seq2.p1	Ec-01_004060.1	Ferlin domain	n/a;GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR12546: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR012968: Ferlin domain; Coil: ; IPR000008: C2 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29988_c1_seq1.p1	Ec-01_004100.1	Armadillo-like helical	GO:0005634;GO:0005488	PTHR16199: ; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold; IPR024741: Condensin-2 complex subunit G2	NA
comp11825_c0_seq1.p1	Ec-01_004120.1	inorganic pyrophosphatase	GO:0016020;GO:0004427;GO:0015992;GO:0009678	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004131: Pyrophosphate-energised proton pump; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR31998:	NA
comp34069_c0_seq1.p1	Ec-01_004140.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29111_c0_seq2.p1	Ec-01_004150.1	SH3 domain	GO:0005515;GO:0005737	IPR027267: Arfaptin homology (AH) domain/BAR domain; G3DSA:2.30.30.40: ; IPR001452: SH3 domain; SSF103657: ; PR00499: Neutrophil cytosol factor 2 signature; IPR004148: BAR domain; Coil: ; PTHR10661:	NA
comp32279_c0_seq1.p1	Ec-01_004160.1	Protein for assembly of pre-ribosomal particles containing 18S rRNA	GO:0000166	PTHR24012: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; SSF54928: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000504: RNA recognition motif domain; PF14259: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain); IPR012677: Nucleotide-binding alpha-beta plait domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20075_c0_seq1.p2	Ec-01_004190.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp32954_c3_seq1.p1	Ec-01_004200.1	BIG2, ArfGEF protein of the BIG/GBF family	NA	IPR000904: Sec7 domain; IPR011989: Armadillo-like helical; G3DSA:1.10.220.20: ; PTHR10663: ; IPR023394: Sec7 domain, alpha orthogonal bundle; PF12783: Guanine nucleotide exchange factor in Golgi transport N-terminal; IPR016024: Armadillo-type fold; IPR015403: Domain of unknown function DUF1981, Sec7 associated	NA
comp31233_c0_seq4.p2	Ec-01_004230.1	Jumonji and C5HC2 zinc finger domain protein	n/a;n/a;n/a	NA	NA
comp32702_c0_seq7.p1	Ec-01_004240.1	Phox homologous domain	GO:0035091	IPR001683: Phox homologous domain	NA
comp24499_c0_seq1.p1	Ec-01_004250.1	3-deoxy-7-phosphoheptulonate synthase	GO:0003849;GO:0009073	IPR002480: DAHP synthetase, class II; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SSF51569: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp28858_c0_seq6.p1	Ec-01_004260.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp12429_c0_seq2.p1	Ec-01_004270.1	MtN3-like protein	GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004316: SWEET sugar transporter; PTHR10791: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19672_c1_seq1.p1	Ec-01_004280.1	similar to metallopeptidase family M24 containing protein, expressed	NA	NA	NA
comp26344_c0_seq1.p1	Ec-01_004300.2	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp31233_c0_seq4.p1	Ec-01_004320.1	Ca2+-ATPase	GO:0005524;GO:0006754;GO:0006812;GO:0015662;GO:0016020	IPR023298: P-type ATPase, transmembrane domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR008250: P-type ATPase, A domain; SSF81653: ; IPR006408: P-type ATPase, subfamily IIB; IPR023214: HAD-like domain; IPR004014: Cation-transporting P-type ATPase, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PR00121: Sodium/potassium-transporting ATPase signature; IPR001757: P-type ATPase; SSF81665: ; IPR006068: Cation-transporting P-type ATPase, C-terminal; IPR018303: P-type ATPase, phosphorylation site; IPR023299: P-type ATPase, cytoplasmic domain N; PTHR24093: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28198_c0_seq5.p2	Ec-01_004330.1	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	GO:0008152;GO:0016491	PTHR24322: ; SSF51735: ; IPR020904: Short-chain dehydrogenase/reductase, conserved site; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013968: Polyketide synthase, ketoreductase domain	NA
comp21595_c0_seq1.p1	Ec-01_004340.2	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR019410: Lysine methyltransferase; PTHR14614:	NA
comp27731_c0_seq4.p1	Ec-01_004350.1	Uncharacterised domain NUC130/133, N-terminal	n/a;n/a;n/a	IPR007949: SDA1 domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR012977: Uncharacterised domain NUC130/133, N-terminal; Coil: ; IPR016024: Armadillo-type fold; IPR027312: Sda1; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR12730:	NA
comp31909_c0_seq24.p1	Ec-01_004380.1	ABC membrane transporter	GO:0005524;GO:0016887	IPR003439: ABC transporter-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017871: ABC transporter, conserved site; PTHR19241: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013525: ABC-2 type transporter	NA
comp31909_c0_seq42.p2	Ec-01_004390.1	Sugar/inositol transporter	GO:0016020;GO:0055085;GO:0016021;GO:0022891;GO:0022857	IPR005829: Sugar transporter, conserved site; IPR005828: General substrate transporter; IPR003663: Sugar/inositol transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR24063: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32066_c0_seq2.p1	Ec-01_004420.2	AT hook-like	GO:0006355	SSF63748: ; IPR020478: AT hook-like; IPR017956: AT hook, DNA-binding motif; IPR000116: High mobility group protein HMGA; IPR000637: HMG-I/HMG-Y, DNA-binding, conserved site; G3DSA:2.30.30.160: ; Coil: ; IPR000313: PWWP domain	NA
comp31862_c0_seq1.p4	Ec-01_004430.1	Cytochrome b5-like heme/steroid binding domain	GO:0020037	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR018506: Cytochrome b5, heme-binding site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001199: Cytochrome b5-like heme/steroid binding domain; PTHR19359: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30915_c0_seq16.p1	Ec-01_004460.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR000073: Alpha/beta hydrolase fold-1; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR10992: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24613_c0_seq2.p1	Ec-01_004480.1	FAD dependent oxidoreductase	GO:0055114;GO:0016491	IPR006076: FAD dependent oxidoreductase; G3DSA:3.50.50.60: ; SSF51905:	NA
comp11777_c0_seq1.p1	Ec-01_004490.1	expressed unknown protein	n/a;GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015943: WD40/YVTN repeat-like-containing domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33846_c0_seq1.p1	Ec-01_004500.1	lactoylglutathione lyase family protein / glyoxalase I family protein	n/a;n/a;n/a	IPR025870: Glyoxalase-like domain; PTHR21366: ; IPR029068: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	NA
comp26245_c0_seq1.p1	Ec-01_004510.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28444_c0_seq1.p2	Ec-01_004530.1	Metallo-dependent phosphatase-like	GO:0016787	IPR029052: Metallo-dependent phosphatase-like; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; IPR006186: Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase; PTHR11668:	NA
comp28444_c0_seq1.p1	Ec-01_004540.1	Uncharacterised domain, di-copper centre	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR008922: Uncharacterised domain, di-copper centre; IPR002227: Tyrosinase copper-binding domain; PTHR11474: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32558_c0_seq5.p1	Ec-01_004550.1	FAD-linked oxidoreductase-like	NA	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR029041: FAD-linked oxidoreductase-like	NA
comp34016_c0_seq1.p1	Ec-01_004560.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30671_c0_seq2.p1	Ec-01_004580.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp60119_c0_seq1.p2	Ec-01_004600.1	transcription factor C-MYB	NA	PTHR10641: ; IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; PTHR10641:SF221: ; Coil: ; IPR017930: Myb domain; IPR017877: Myb-like domain	NA
comp20743_c0_seq3.p1	Ec-01_004630.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; IPR000073: Alpha/beta hydrolase fold-1; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR10992: ; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp13119_c0_seq1.p1	Ec-01_004640.1	ATP-dependent Clp protease, proteolytic subunit ClpP	GO:0004252;GO:0006508;GO:0008462	IPR029045: ClpP/crotonase-like domain; SIGNAL_PEPTIDE: Signal peptide region; IPR018215: ClpP, active site; IPR001907: ATP-dependent Clp protease proteolytic subunit; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023562: Clp protease proteolytic subunit /Translocation-enhancing protein TepA	NA
comp32953_c10_seq1.p2	Ec-01_004660.2	beta tubulin	GO:0005874;GO:0007017	IPR002453: Beta tubulin; IPR000217: Tubulin; IPR003008: Tubulin/FtsZ, GTPase domain; IPR023123: Tubulin, C-terminal; PTHR11588:SF97: ; IPR008280: Tubulin/FtsZ, C-terminal; Coil: ; IPR018316: Tubulin/FtsZ, 2-layer sandwich domain	KOG1375
comp29419_c0_seq3.p1	Ec-01_004670.1	Guanylate-binding protein, N-terminal	GO:0003924;GO:0005525	SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR015894: Guanylate-binding protein, N-terminal; PTHR10751: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31193_c0_seq7.p4	Ec-01_004680.1	Ankyrin repeat-containing domain	GO:0005515	NA	NA
comp12231_c0_seq2.p1	Ec-01_004690.1	Amino acid/polyamine transporter I	GO:0016020;GO:0003333;GO:0015171	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002293: Amino acid/polyamine transporter I; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	NA
comp31193_c0_seq5.p2	Ec-01_004720.1	Caffeate O-Methyltransferase	GO:0008168	IPR008576: Alpha-N-methyltransferase NTM1; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase	KOG3178
comp30300_c0_seq2.p1	Ec-01_004730.1	Heat shock protein 40 like protein	GO:0031072	SSF48452: ; IPR001440: Tetratricopeptide TPR1; PF14559: Tetratricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; IPR001623: DnaJ domain; IPR018253: DnaJ domain, conserved site; PTHR24078: ; PF13414: TPR repeat; Coil: ; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat	NA
comp32523_c0_seq13.p3	Ec-01_004740.2	Hypothetical protein	n/a;n/a;n/a	SSF57716: ; IPR001510: Zinc finger, PARP-type	NA
comp31536_c0_seq3.p1	Ec-01_004760.1	putative serine/threonine phosphatase 2C ptc2	GO:0005515	IPR008984: SMAD/FHA domain; IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C; IPR000253: Forkhead-associated (FHA) domain	NA
comp15766_c0_seq1.p1	Ec-01_004780.1	RNA recognition motif domain	GO:0003676	PTHR24012: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25907_c0_seq2.p1	Ec-01_004800.1	WD40-repeat-containing domain	GO:0005515	PTHR22844:SF191: ; PTHR22844: ; IPR018247: EF-Hand 1, calcium-binding site; IPR019775: WD40 repeat, conserved site; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR001680: WD40 repeat; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; Coil: ; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily	NA
comp25612_c0_seq2.p1	Ec-01_004800.3	WD40-repeat-containing domain	GO:0005515	PTHR22844:SF191: ; PTHR22844: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; Coil:	NA
comp29315_c0_seq1.p2	Ec-01_004810.1	Calponin homology domain	GO:0005515	PTHR18959: ; IPR001715: Calponin homology domain; Coil: ; IPR003096: Smooth muscle protein/calponin	NA
comp29315_c0_seq1.p1	Ec-01_004820.1	Protein kinase C-like, phorbol ester/diacylglycerol-binding domain	GO:0035556	SSF57889: ; IPR002219: Protein kinase C-like, phorbol ester/diacylglycerol-binding domain; SSF109993: ; G3DSA:3.30.60.20:	NA
comp30326_c1_seq2.p1	Ec-01_004830.1	FANCI helical domain 1	n/a;n/a;n/a	IPR029308: FANCI solenoid 1 domain; IPR026171: Fanconi anemia group I protein; IPR029310: FANCI helical domain 1; IPR029314: FANCI solenoid 4 domain; PTHR21818: ; Coil: ; IPR029315: FANCI solenoid 2 domain	NA
comp29644_c0_seq2.p1	Ec-01_004840.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp34523_c0_seq1.p1	Ec-01_004870.1	Zinc finger, HIT-type	n/a;n/a;n/a	PTHR13241: ; IPR007529: Zinc finger, HIT-type; SSF144232:	NA
comp24788_c0_seq1.p2	Ec-01_004880.1	Thioredoxin-like fold	n/a;GO:0045454	SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR18929: ; Coil: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24788_c0_seq1.p1	Ec-01_004890.1	Ribonuclease CAF1	GO:0005634;GO:0003676	IPR006941: Ribonuclease CAF1; IPR012337: Ribonuclease H-like domain; PTHR15092:	NA
comp20558_c0_seq2.p1	Ec-01_004900.1	Histone H4 acetyltransferase, NuA4 complex, Eaf6	n/a;n/a;n/a	Coil: ; PTHR13476: ; IPR015418: Histone H4 acetyltransferase, NuA4 complex, Eaf6	NA
comp29462_c0_seq2.p2	Ec-01_004910.1	Vacuolar fusion protein MON1	n/a;n/a;n/a	IPR004353: Vacuolar fusion protein MON1	NA
comp29462_c0_seq2.p1	Ec-01_004920.1	ABC transporter-like	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR004147: UbiB domain; PTHR10566: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011009: Protein kinase-like domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30741_c0_seq6.p1	Ec-01_004930.1	SET domain protein	GO:0005515	NA	NA
comp30741_c0_seq5.p1	Ec-01_004940.1	Mitogen-activated protein kinase kinase (MAP2K)	GO:0016772	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PTHR24361:SF408: ; PTHR24361: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	KOG0581
comp27471_c0_seq3.p1	Ec-01_004980.3	Folylpolyglutamate synthase, mitochondrial	GO:0004326;GO:0005524;GO:0009396	IPR023600: Folylpolyglutamate synthase, eukaryota; IPR018109: Folylpolyglutamate synthetase, conserved site; IPR013221: Mur ligase, central; IPR004101: Mur ligase, C-terminal; IPR001645: Folylpolyglutamate synthetase	NA
comp12075_c0_seq2.p1	Ec-01_004990.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp26890_c0_seq3.p1	Ec-01_005000.1	Homoserine dehydrogenase	GO:0016597;GO:0008152;GO:0006520;GO:0055114	PTHR21499: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR005106: Aspartate/homoserine dehydrogenase, NAD-binding; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR019811: Homoserine dehydrogenase, conserved site; SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; IPR001342: Homoserine dehydrogenase, catalytic; IPR002912: ACT domain; SSF55021: ; SSF55347: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; G3DSA:3.30.360.10: ; SignalP-noTM: ; IPR016040: NAD(P)-binding domain	KOG0455
comp34601_c0_seq1.p1	Ec-01_005010.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28039_c0_seq2.p1	Ec-01_005020.1	DnaJ domain	GO:0031072	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR001623: DnaJ domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp25627_c0_seq2.p1	Ec-01_005030.1	short-chain alcohol dehydrogenase-like protein	GO:0008152;GO:0016491	SSF51735: ; PTHR24322: ; IPR016040: NAD(P)-binding domain; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR	NA
comp27617_c0_seq3.p1	Ec-01_005040.1	DNA-directed RNA polymerase III subunit Rpc5	GO:0003899;GO:0005634;GO:0006351	IPR006886: DNA-directed RNA polymerase III subunit Rpc5; PTHR12069:	NA
comp27512_c0_seq2.p1	Ec-01_005050.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp11675_c0_seq1.p2	Ec-01_005060.1	Uncharacterised protein family UPF0136, Transmembrane	GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005349: Uncharacterised protein family UPF0136, Transmembrane; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20645_c0_seq1.p1	Ec-01_005070.1	Renin receptor-like	GO:0004872;GO:0016021	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012493: Renin receptor-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28774_c0_seq4.p1	Ec-01_005090.1	Dimeric alpha-beta barrel	n/a;n/a;n/a	IPR011008: Dimeric alpha-beta barrel; G3DSA:3.30.70.1060: ; IPR005545: YCII-related	NA
comp31642_c0_seq8.p1	Ec-01_005100.1	Ribonuclease Zc3h12a-like	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR021869: Ribonuclease Zc3h12a-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002885: Pentatricopeptide repeat; PTHR13547: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24122_c0_seq1.p1	Ec-01_005110.1	imidazoleglycerol-phosphate dehydratase	GO:0008152;GO:0016787	G3DSA:3.30.230.40: ; IPR006438: HAD hydrolase, TIGR01548 family; SIGNAL_PEPTIDE: Signal peptide region; PTHR23133: ; IPR006439: HAD hydrolase, subfamily IA; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023214: HAD-like domain; IPR000807: Imidazoleglycerol-phosphate dehydratase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR020565: Imidazoleglycerol-phosphate dehydratase, conserved site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR020568: Ribosomal protein S5 domain 2-type fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG3143
comp31326_c0_seq1.p1	Ec-01_005130.1	VRR-NUC domain	GO:0016788	PTHR15749: ; Coil: ; IPR014883: VRR-NUC domain	NA
comp26285_c0_seq3.p1	Ec-01_005140.1	Transcription factor TFIIB	GO:0006352;GO:0006355;GO:0008270	IPR000812: Transcription factor TFIIB; IPR013137: Zinc finger, TFIIB-type; IPR013763: Cyclin-like; SSF57783: ; G3DSA:2.20.25.10:	NA
comp31193_c0_seq5.p1	Ec-01_005150.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24015: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002885: Pentatricopeptide repeat; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp23525_c0_seq2.p1	Ec-01_005190.3	Tetratricopeptide-like helical domain	GO:0005515	NA	NA
comp29962_c0_seq6.p1	Ec-01_005200.1	Pim1 homolog, ATP-dependent protease	GO:0004176;GO:0004252;GO:0006508	IPR027503: Lon protease homolog, chloroplastic/mitochondrial; IPR015947: PUA-like domain; IPR003959: ATPase, AAA-type, core; IPR004815: Lon protease, bacterial/eukaryotic-type; IPR008268: Peptidase S16, active site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003111: Peptidase S16, lon N-terminal; IPR008269: Peptidase S16, Lon C-terminal; IPR003593: AAA+ ATPase domain; PR00830: Endopeptidase La (Lon) serine protease (S16) signature; G3DSA:1.10.8.60: ; IPR020568: Ribosomal protein S5 domain 2-type fold; IPR027065: Lon protease; Coil: ; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup	NA
comp30400_c0_seq4.p1	Ec-01_005220.1	Ribokinase, bacterial	GO:0004747;GO:0006014	IPR011611: Carbohydrate kinase PfkB; IPR011877: Ribokinase, bacterial; SIGNAL_PEPTIDE: Signal peptide region; IPR002139: Ribokinase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR10584: ; IPR029056: Ribokinase-like	NA
comp30400_c0_seq4.p2	Ec-01_005240.1	Clathrin light chain	GO:0006886;GO:0030132;GO:0030130;GO:0005198;GO:0016192	IPR000996: Clathrin light chain; Coil:	NA
comp26523_c0_seq1.p1	Ec-01_005250.1	selenide, water dikinase also called selenophosphate synthase	GO:0055114;GO:0016491	IPR016188: PurM, N-terminal-like; IPR000728: AIR synthase related protein, N-terminal domain; PR00368: FAD-dependent pyridine nucleotide reductase signature; IPR001327: Pyridine nucleotide-disulphide oxidoreductase, NAD-binding domain; IPR010918: AIR synthase-related protein, C-terminal domain; G3DSA:3.50.50.60: ; IPR004536: Selenophosphate synthetase; PTHR22915: ; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	KOG3939
comp29962_c0_seq6.p6	Ec-01_005300.1	NUDIX hydrolase domain-like	GO:0016787	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR015797: NUDIX hydrolase domain-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22769: ; IPR020476: NUDIX hydrolase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000086: NUDIX hydrolase domain	NA
comp28795_c0_seq3.p1	Ec-01_005310.1	Gamma-tubulin complex component protein	GO:0005815;GO:0000922;GO:0000226	IPR007259: Gamma-tubulin complex component protein; Coil:	NA
comp20127_c0_seq1.p1	Ec-01_005320.1	Predicted E3 ubiquitin ligase	GO:0008270	IPR031127: E3 ubiquitin ligase RBR family; IPR017907: Zinc finger, RING-type, conserved site; IPR001841: Zinc finger, RING-type; IPR002867: Zinc finger, C6HC-type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1815
comp29112_c0_seq1.p1	Ec-01_005340.1	Clathrin assembly complex, medium subunit	GO:0006810;GO:0006886;GO:0016192;GO:0030131	IPR028565: Mu homology domain; PTHR10529: ; IPR001392: Clathrin adaptor, mu subunit; G3DSA:3.30.450.60: ; G3DSA:2.60.40.1170: ; IPR022775: AP complex, mu/sigma subunit; IPR011012: Longin-like domain	KOG2740
comp26024_c0_seq2.p1	Ec-01_005350.1	conserved unknown protein	n/a;n/a;n/a	SignalP-noTM:	NA
comp25867_c1_seq1.p1	Ec-01_005360.1	Ferrochelatase-2, putative chloroplast precursor	GO:0004325;GO:0006783	SSF53800: ; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.40.50.1400: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001015: Ferrochelatase; IPR019772: Ferrochelatase, active site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29112_c0_seq1.p2	Ec-01_005380.1	Aminoalcohol phosphotransferase	GO:0016020;GO:0008654;GO:0016780	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000462: CDP-alcohol phosphatidyltransferase; IPR014472: Choline/ethanolamine phosphotransferase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2877
comp30680_c0_seq1.p1	Ec-01_005420.1	Major facilitator superfamily	GO:0016021;GO:0055085	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR23504:SF18: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR23504: ; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31984_c1_seq8.p1	Ec-01_005430.1	Tetracycline resistance protein, TetA/multidrug resistance protein MdtG	GO:0055085;GO:0016021;GO:0005886;GO:0005215	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24003: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001958: Tetracycline resistance protein, TetA/multidrug resistance protein MdtG; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34044_c0_seq1.p1	Ec-01_005440.1	Arf GTPase activating protein	GO:0032312;GO:0008060;GO:0008270;GO:0005096	IPR001164: Arf GTPase activating protein; SSF57863: ; PTHR23180:	NA
comp16204_c0_seq1.p1	Ec-01_005470.1	putative: flagellar/basal body protein, PACRG (parkin co-regulated gene) -like protein	n/a;n/a;n/a	PTHR21207: ; IPR019399: Parkin co-regulated protein	KOG3961
comp21148_c0_seq3.p1	Ec-01_005480.1	Small-subunit processome, Utp11	GO:0032040;GO:0006364	IPR007144: Small-subunit processome, Utp11; Coil:	NA
comp28678_c0_seq2.p1	Ec-01_005490.1	Ubiquitin fusion degradation protein UFD1	GO:0006511	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR004854: Ubiquitin fusion degradation protein UFD1; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28678_c0_seq3.p1	Ec-01_005500.1	Alpha-ketoglutarate-dependent dioxygenase AlkB-like	GO:0016491;n/a	SSF51197: ; IPR005123: Oxoglutarate/iron-dependent dioxygenase; PTHR13069: ; IPR027450: Alpha-ketoglutarate-dependent dioxygenase AlkB-like	NA
comp26958_c0_seq1.p1	Ec-01_005510.1	enoyl-CoA hydratase domain-containing protein	GO:0008152;GO:0003824	IPR018376: Enoyl-CoA hydratase/isomerase, conserved site; IPR029045: ClpP/crotonase-like domain; IPR001753: Crotonase superfamily; PTHR11941:	KOG1680
comp29383_c0_seq2.p1	Ec-01_005520.1	conserved unknown protein	n/a;n/a;n/a	IPR021827: Nucleoporin Nup186/Nup192/Nup205; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12407_c0_seq1.p1	Ec-01_005540.1	expressed unknown protein	n/a;GO:0005515	IPR000225: Armadillo	NA
comp26183_c0_seq1.p1	Ec-01_005550.1	5-oxoprolinase (ATP-hydrolysing)	NA	PTHR11365: ; IPR003692: Hydantoinase B/oxoprolinase; IPR002821: Hydantoinase/oxoprolinase; IPR008040: Hydantoinaseoxoprolinase, N-terminal	NA
comp26920_c0_seq2.p1	Ec-01_005560.1	Dimethylaniline monooxygenase, N-oxide-forming	GO:0050661;GO:0050660;GO:0004499;GO:0055114	IPR000960: Flavin monooxygenase FMO; IPR012143: Dimethylaniline monooxygenase, N-oxide-forming; G3DSA:3.50.50.60: ; PTHR23023: ; IPR020946: Flavin monooxygenase-like; SSF51905:	NA
comp31831_c0_seq1.p1	Ec-01_005570.1	tRNA-guanine(15) transglycosylase-like	GO:0008616;GO:0006400;GO:0008479	IPR004803: Queuine tRNA-ribosyltransferase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; IPR002616: tRNA-guanine(15) transglycosylase-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20260_c0_seq1.p1	Ec-01_005580.1	eukaryotic initiation factor 3H1 subunit	GO:0003743;GO:0005852;GO:0005737	IPR000555: JAB1/MPN/MOV34 metalloenzyme domain; PTHR10410: ; Coil: ; IPR027524: Eukaryotic translation initiation factor 3 subunit H	NA
comp31306_c0_seq1.p1	Ec-01_005590.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp31978_c0_seq4.p1	Ec-01_005600.1	Short-chain dehydrogenase/reductase SDR	GO:0008152;GO:0016491	SSF51735: ; IPR020904: Short-chain dehydrogenase/reductase, conserved site; IPR016040: NAD(P)-binding domain; PTHR24320: ; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR; IPR013968: Polyketide synthase, ketoreductase domain	NA
comp28864_c0_seq1.p1	Ec-01_005610.1	BTB/Kelch-associated	GO:0005515	PTHR24412: ; IPR013069: BTB/POZ; IPR011333: BTB/POZ fold; IPR011705: BTB/Kelch-associated; IPR000210: BTB/POZ-like; G3DSA:3.30.710.10:	NA
comp19381_c0_seq2.p1	Ec-01_005620.1	PSP, proline-rich	GO:0006397;GO:0005634	IPR006568: PSP, proline-rich; IPR007180: Domain of unknown function DUF382; Coil: ; PTHR12785:	NA
comp24809_c0_seq1.p1	Ec-01_005630.2	possible ferredoxin (2Fe-2S)	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; IPR001041: 2Fe-2S ferredoxin-type iron-sulfur binding domain; IPR001478: PDZ domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR23426: ; IPR012675: Beta-grasp domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21478_c0_seq1.p1	Ec-01_005640.1	conserved unknown protein	GO:0008152;GO:0016491;GO:0055114	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp24360_c0_seq2.p1	Ec-01_005650.1	Basic-leucine zipper and PAS domains	GO:0007165;GO:0004871	NA	NA
comp32504_c1_seq26.p1	Ec-01_005660.1	Similar to photosystem II oxygen evolving complex protein PsbP in Synechococcus	GO:0005509;GO:0009523;GO:0009654;GO:0015979;GO:0019898	IPR002683: Photosystem II PsbP, oxygen evolving complex; PTHR31407: ; IPR016123: Mog1/PsbP, alpha/beta/alpha sandwich	NA
comp29995_c0_seq6.p1	Ec-01_005700.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR14614:SF29: ; IPR019410: Lysine methyltransferase; PTHR14614:	NA
comp29995_c0_seq4.p1	Ec-01_005710.1	Proteasome component ECM29/Translational activator GCN1	GO:0005488	IPR011989: Armadillo-like helical; IPR026827: Proteasome component ECM29/Translational activator GCN1; IPR024372: Proteasome stabiliser ECM29; IPR016024: Armadillo-type fold; Coil:	NA
comp31396_c0_seq10.p1	Ec-01_005720.1	Sorting nexin 1	GO:0005515;GO:0007154;GO:0035091	IPR015404: Vps5 C-terminal; IPR027267: Arfaptin homology (AH) domain/BAR domain; SSF103657: ; PTHR10555: ; IPR001683: Phox homologous domain	KOG2273
comp32012_c0_seq3.p1	Ec-01_005730.1	hypothetical protein	GO:0003677;GO:0005665;GO:0006366	NA	NA
comp12766_c1_seq1.p1	Ec-01_005740.1	Proteasome component (PCI) domain	GO:0005515	PTHR14145: ; IPR011991: Winged helix-turn-helix DNA-binding domain; IPR000717: Proteasome component (PCI) domain; PTHR14145:SF2: ; IPR011990: Tetratricopeptide-like helical domain; IPR019585: 26S proteasome, regulatory subunit Rpn7; Coil:	NA
comp30947_c0_seq5.p1	Ec-01_005750.1	Bifunctional dethiobiotin synthetase/7,8-diamino-pelargonic acid aminotransferase	GO:0003824;GO:0030170	IPR015424: Pyridoxal phosphate-dependent transferase; IPR005814: Aminotransferase class-III; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PF13500: AAA domain; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2; IPR004472: Dethiobiotin synthase BioD	NA
comp31212_c0_seq2.p1	Ec-01_005760.1	Bax inhibitor 1-related	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006214: Bax inhibitor 1-related; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31212_c0_seq1.p1	Ec-01_005770.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp13004_c0_seq1.p1	Ec-01_005790.1	Lysyl-tRNA ligase	GO:0006430;GO:0005524;GO:0000166;GO:0006412;GO:0004824;GO:0005737	IPR012340: Nucleic acid-binding, OB-fold; IPR014038: Translation elongation factor EF1B, beta/delta subunit, guanine nucleotide exchange; IPR004365: OB-fold nucleic acid binding domain, AA-tRNA synthetase-type; IPR006195: Aminoacyl-tRNA synthetase, class II; SSF55681: ; IPR004364: Aminoacyl-tRNA synthetase, class II (D/K/N); IPR014717: Translation elongation factor EF1B/ribosomal protein S6; IPR018149: Lysyl-tRNA synthetase, class II, C-terminal; IPR018150: Aminoacyl-tRNA synthetase, class II (D/K/N)-like; G3DSA:3.30.930.10: ; IPR002313: Lysine-tRNA ligase, class II; Coil:	KOG1885
comp30303_c0_seq1.p1	Ec-01_005800.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31254_c2_seq1.p1	Ec-01_005810.1	expressed unknown protein	GO:0004526;GO:0008033	NA	NA
comp27685_c0_seq1.p1	Ec-01_005830.3	Rho GTPase-activating protein domain	GO:0007165	SSF103657:	NA
comp19954_c0_seq1.p1	Ec-01_005840.1	ATPase, dynein-related, AAA domain	GO:0005524;GO:0016887	IPR011704: ATPase, dynein-related, AAA domain; IPR030553: Torsin-like protein; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001270: ClpA/B family; IPR010448: Torsin; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32609_c1_seq2.p1	Ec-01_005860.1	thaumatin-domain containing protein	NA	IPR013994: Carbohydrate-binding WSC, subgroup; PTHR19297: ; IPR002889: Carbohydrate-binding WSC; IPR001938: Thaumatin	NA
comp32177_c3_seq1.p1	Ec-01_005880.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp12286_c0_seq1.p1	Ec-01_005890.1	Hypothetical protein	n/a;n/a;n/a	SignalP-TM:	NA
comp20031_c0_seq1.p3	Ec-01_005900.1	ERCC4 domain containing protein	GO:0003677;GO:0006259;GO:0004518	PTHR13451: ; IPR006166: ERCC4 domain; IPR011335: Restriction endonuclease type II-like; IPR020819: DNA repair nuclease, XPF-type/Helicase	KOG2379
comp27699_c0_seq4.p1	Ec-01_005920.1	Phosphatidylserine synthase	GO:0006659	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004277: Phosphatidyl serine synthase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2735
comp39861_c0_seq1.p1	Ec-01_005930.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp29745_c0_seq8.p1	Ec-01_005940.1	AT hook-like	GO:0005634;GO:0003677;GO:0000785;GO:0006355	IPR017956: AT hook, DNA-binding motif; IPR020478: AT hook-like; Coil:	NA
comp19659_c0_seq1.p1	Ec-01_005950.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp26918_c0_seq3.p1	Ec-01_005960.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0005634;GO:0000981;GO:0006355;GO:0008270	IPR001138: Zn(2)-C6 fungal-type DNA-binding domain	NA
comp31441_c0_seq2.p1	Ec-01_005970.1	Acetyltransferase (GNAT) domain protein	n/a;n/a;n/a	NA	NA
comp26172_c0_seq1.p1	Ec-01_005990.1	Acetyltransferase (GNAT) domain protein	n/a;n/a;n/a	NA	NA
comp19453_c0_seq2.p1	Ec-01_006010.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp27360_c0_seq4.p1	Ec-01_006040.1	HAD-like domain	n/a;n/a;n/a	IPR008380: HAD-superfamily hydrolase, subfamily IG, 5'-nucleotidase; IPR023214: HAD-like domain	NA
comp27288_c0_seq3.p1	Ec-01_006050.1	Cation/H+ exchanger	GO:0055085;GO:0016021;GO:0015299;GO:0006812	IPR030152: Na(+)/H(+) antiporter NhaS3/S5; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR32468: ; IPR006153: Cation/H+ exchanger; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30154_c0_seq4.p1	Ec-01_006070.1	Myo-inositol dehydrogenase myo-inositol dehydrogenase	GO:0008152;GO:0016491;GO:0055114	SSF51735: ; IPR004104: Oxidoreductase, C-terminal; SIGNAL_PEPTIDE: Signal peptide region; IPR030827: Inositol 2-dehydrogenase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF55347: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000683: Oxidoreductase, N-terminal; SignalP-noTM: ; G3DSA:3.30.360.10: ; IPR016040: NAD(P)-binding domain; PTHR22604: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2741
comp29703_c0_seq1.p1	Ec-01_006080.1	DNA polymerase, Y-family, little finger domain	GO:0003887;GO:0006281;GO:0003684	SSF56672: ; IPR017961: DNA polymerase, Y-family, little finger domain; G3DSA:1.10.150.20: ; G3DSA:3.30.70.270: ; IPR001126: DNA-repair protein, UmuC-like; IPR017963: DNA-repair protein, UmuC-like, N-terminal; PTHR11076:	NA
comp12886_c0_seq1.p1	Ec-01_006090.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp54809_c0_seq1.p1	Ec-01_006100.1	hypothetical protein	n/a;n/a;n/a	IPR001202: WW domain; G3DSA:2.20.70.10:	NA
comp33882_c0_seq1.p1	Ec-01_006110.1	Peptidase M24, structural domain	GO:0006508;GO:0008235;GO:0009987	IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; IPR000994: Peptidase M24, structural domain; PTHR10804:	NA
comp21272_c0_seq1.p1	Ec-01_006140.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp20031_c0_seq1.p1	Ec-01_006170.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168;n/a	IPR001763: Rhodanese-like domain; PF13489: Methyltransferase domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21376_c0_seq1.p1	Ec-01_006180.2	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	PTHR22957:SF212: ; G3DSA:1.10.8.270: ; IPR020683: Ankyrin repeat-containing domain; PTHR22957: ; IPR000195: Rab-GTPase-TBC domain	NA
comp12090_c0_seq2.p1	Ec-01_006200.1	Zn dependent hydrolase or glyoxylase	GO:0016787	SIGNAL_PEPTIDE: Signal peptide region; IPR001279: Beta-lactamase-like; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR23131: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0813
comp23210_c0_seq1.p1	Ec-01_006280.1	Beta-lactamase-like	n/a;n/a;n/a	IPR001279: Metallo-beta-lactamase	NA
comp31848_c0_seq9.p1	Ec-01_006290.1	Domain of unknown function DUF4209	n/a;n/a;n/a	IPR025209: Domain of unknown function DUF4209; PTHR31701:SF2: ; Coil: ; PTHR31701:	NA
comp29694_c0_seq1.p1	Ec-01_006300.1	Importin-beta, N-terminal domain	GO:0006886;GO:0008536;GO:0005488	IPR000357: HEAT; IPR001494: Importin-beta, N-terminal domain; IPR011989: Armadillo-like helical; IPR021133: HEAT, type 2; PTHR10527: ; IPR016024: Armadillo-type fold	NA
comp19828_c0_seq2.p3	Ec-01_006310.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19828_c0_seq2.p1	Ec-01_006320.1	transketolase	n/a;n/a;n/a	IPR005474: Transketolase, N-terminal; IPR005476: Transketolase, C-terminal; SIGNAL_PEPTIDE: Signal peptide region; IPR009014: Transketolase, C-terminal/Pyruvate-ferredoxin oxidoreductase, domain II; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR029061: Thiamin diphosphate-binding fold; IPR005475: Transketolase-like, pyrimidine-binding domain; IPR020826: Transketolase binding site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005478: Transketolase, bacterial-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11624: ; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp19828_c0_seq2.p2	Ec-01_006330.1	mono-or diacylglycerol acyltransferase type 2	GO:0016747	IPR007130: Diacylglycerol acyltransferase	KOG0831
comp25225_c0_seq1.p1	Ec-01_006350.1	DNA glycosylase/AP lyase, catalytic domain	GO:0003906;GO:0016799;GO:0006284;GO:0003684;GO:0008270	G3DSA:1.10.8.50: ; IPR010979: Ribosomal protein S13-like, H2TH; IPR012319: DNA glycosylase/AP lyase, catalytic domain; IPR015886: DNA glycosylase/AP lyase, H2TH DNA-binding; G3DSA:3.20.190.10: ; PTHR22993:	NA
comp30270_c0_seq3.p1	Ec-01_006370.1	Bromodomain	GO:0005515	PTHR22880: ; IPR018359: Bromodomain, conserved site; IPR001487: Bromodomain	NA
comp32768_c0_seq16.p1	Ec-01_006380.1	adenylate kinase	GO:0005975;GO:0016868	IPR016066: Alpha-D-phosphohexomutase, conserved site; IPR005843: Alpha-D-phosphohexomutase, C-terminal; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR22573: ; IPR016055: Alpha-D-phosphohexomutase, alpha/beta/alpha I/II/III; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR006259: Adenylate kinase subfamily; IPR000850: Adenylate kinase/UMP-CMP kinase; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007862: Adenylate kinase, active site lid domain; PTHR22573:SF2: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR005844: Alpha-D-phosphohexomutase, alpha/beta/alpha domain I; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PF00406: Adenylate kinase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005846: Alpha-D-phosphohexomutase, alpha/beta/alpha domain III; SignalP-noTM: ; IPR005845: Alpha-D-phosphohexomutase, alpha/beta/alpha domain II	KOG3078
comp32768_c0_seq2.p1	Ec-01_006380.3	adenylate kinase	GO:0005975;GO:0016868	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR006259: Adenylate kinase subfamily; PF00406: Adenylate kinase; IPR000850: Adenylate kinase/UMP-CMP kinase; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR007862: Adenylate kinase, active site lid domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG3078
comp27169_c0_seq1.p1	Ec-01_006390.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp34286_c0_seq1.p1	Ec-01_006400.1	FK506-binding protein 1	GO:0006457	SSF54534: ; G3DSA:3.10.50.40: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023566: Peptidyl-prolyl cis-trans isomerase, FKBP-type; IPR006311: Twin-arginine translocation pathway, signal sequence; IPR001179: Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0549
comp33605_c0_seq1.p1	Ec-01_006410.1	Clathrin assembly complex, small subunit	GO:0006810;GO:0008565;GO:0015031	IPR016635: Adaptor protein complex, sigma subunit; G3DSA:3.30.450.60: ; IPR000804: Clathrin adaptor complex, small chain; IPR027155: AP-3 complex subunit sigma; IPR011012: Longin-like domain; IPR022775: AP complex, mu/sigma subunit	KOG0936
comp27709_c0_seq2.p1	Ec-01_006420.1	Zinc finger, DNL-type	GO:0005515;GO:0008270	IPR013883: Transcription factor Iwr1; IPR020683: Ankyrin repeat-containing domain; IPR002110: Ankyrin repeat	NA
comp24190_c0_seq2.p2	Ec-01_006425.1	hypothetical protein	NA	IPR024158: Mitochondrial import protein TIM15; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007853: Zinc finger, DNL-type; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24190_c0_seq2.p1	Ec-01_006430.1	Protein of unknown function DUF2358	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018790: Protein of unknown function DUF2358; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SSF54427: ; G3DSA:3.10.450.50: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp28173_c0_seq2.p1	Ec-01_006440.1	Putative calcium-activated chloride channel	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007632: Anoctamin; PTHR12308:SF12: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24469_c0_seq2.p1	Ec-01_006460.1	Poly(A) polymerase, RNA-binding domain	GO:0003723;GO:0004652;GO:0005634;GO:0043631	SSF81631: ; IPR007012: Poly(A) polymerase, central domain; IPR002934: Polymerase, nucleotidyl transferase domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF81301: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR014492: Poly(A) polymerase; IPR011068: Nucleotidyltransferase, class I, C-terminal-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.10.1410.10: ; IPR007010: Poly(A) polymerase, RNA-binding domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28239_c1_seq3.p1	Ec-01_006470.1	conserved unknown protein	NA	IPR004147: UbiB domain; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.30.200.20: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011009: Protein kinase-like domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10566: ; IPR000719: Protein kinase domain; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28694_c0_seq1.p1	Ec-01_006480.1	Phosphoribosyltransferase-like	GO:0004422;GO:0005737;GO:0006166;GO:0016740	IPR005904: Hypoxanthine phosphoribosyl transferase; IPR000836: Phosphoribosyltransferase domain; PTHR22573: ; IPR029057: Phosphoribosyltransferase-like	NA
comp27584_c0_seq1.p1	Ec-01_006500.1	Plastid lipid-associated protein/fibrillin conserved domain	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; PTHR31906: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; IPR006843: Plastid lipid-associated protein/fibrillin conserved domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24508_c0_seq2.p1	Ec-01_006510.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type	NA
comp21436_c0_seq2.p2	Ec-01_006520.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp29023_c0_seq2.p1	Ec-01_006540.1	Sel1-like	n/a;n/a;n/a	PTHR11102: ; IPR011990: Tetratricopeptide-like helical domain; SSF81901: ; Coil: ; IPR006597: Sel1-like	NA
comp29950_c1_seq4.p1	Ec-01_006580.1	RecF/RecN/SMC, N-terminal	GO:0005524;GO:0005694;GO:0006259;GO:0016887	IPR010935: SMCs flexible hinge; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR003395: RecF/RecN/SMC, N-terminal; PTHR18937:	NA
comp28545_c0_seq1.p1	Ec-01_006590.1	Heat shock protein 70kD, peptide-binding domain	n/a;n/a;n/a	PTHR19375: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029048: Heat shock protein 70kD, C-terminal domain; G3DSA:3.30.420.40: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR018181: Heat shock protein 70, conserved site; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF53067: ; SignalP-noTM: ; G3DSA:3.90.640.10: ; Coil: ; IPR029047: Heat shock protein 70kD, peptide-binding domain; IPR013126: Heat shock protein 70 family; G3DSA:3.30.30.30:	KOG0100
comp25996_c0_seq2.p1	Ec-01_006600.1	protein tyrosine phosphatase, receptor type	GO:0005515	PTHR10891: ; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; IPR003961: Fibronectin type III; IPR014819: Primase, C-terminal 2; SSF47473: ; IPR013783: Immunoglobulin-like fold; Coil:	NA
comp33877_c0_seq1.p1	Ec-01_006620.2	Protein of unknown function DUF1826	n/a;n/a;n/a	IPR014955: Protein of unknown function DUF1826	NA
comp24130_c0_seq1.p2	Ec-01_006630.1	G-patch domain	GO:0003676	PTHR23149: ; IPR000467: G-patch domain	NA
comp25073_c0_seq2.p1	Ec-01_006640.1	RNA polymerase Rpb7, N-terminal	GO:0003899;GO:0006351	PTHR12709: ; IPR005576: RNA polymerase Rpb7, N-terminal; Coil:	NA
comp34584_c0_seq1.p1	Ec-01_006670.1	FAD synthetase	GO:0008152;GO:0016740;GO:0003824	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF52402: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002500: Phosphoadenosine phosphosulphate reductase; PTHR23293: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30191_c0_seq3.p2	Ec-01_006680.1	Glycosyl transferase, family 31	GO:0016020;GO:0006486;GO:0008378	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002659: Glycosyl transferase, family 31; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30553_c0_seq9.p1	Ec-01_006700.1	Mitochondrial carrier domain	GO:0005215;GO:0005488;GO:0005743;GO:0006810;GO:0016020;GO:0055085	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR24089: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30553_c0_seq1.p1	Ec-01_006710.1	Uracil-DNA glycosylase-like	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005122: Uracil-DNA glycosylase-like; IPR015637: DNA glycosylase, G/T mismatch; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33803_c0_seq1.p1	Ec-01_006720.2	Ribosomal protein S17	GO:0003735;GO:0005622;GO:0005840;GO:0006412	IPR012340: Nucleic acid-binding, OB-fold; IPR032440: 40S ribosomal protein S11, N-terminal; PTHR10744:SF9: ; IPR019979: Ribosomal protein S17, conserved site; IPR000266: Ribosomal protein S17/S11	NA
comp20534_c0_seq1.p1	Ec-01_006730.1	Sterile alpha motif, type 2	GO:0005515	IPR013761: Sterile alpha motif/pointed domain; IPR001660: Sterile alpha motif domain; IPR011510: Sterile alpha motif, type 2	NA
comp21027_c0_seq1.p1	Ec-01_006740.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	IPR003613: U box domain; IPR010734: Copine; PTHR10857: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR002035: von Willebrand factor, type A; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26881_c0_seq1.p1	Ec-01_006760.1	alpha-Glucosidase II, beta subunit	GO:0005515	SIGNAL_PEPTIDE: Signal peptide region; IPR009011: Mannose-6-phosphate receptor binding domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR12630: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PF13015: Glucosidase II beta subunit-like protein; IPR026874: Glucosidase 2 subunit beta; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; IPR028146: Glucosidase II beta subunit, N-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2397
comp12466_c0_seq1.p1	Ec-01_006770.1	Similar to ATP binding / alanine-tRNA ligase	GO:0000166;GO:0004813;GO:0005524;GO:0005737;GO:0006412;GO:0006419	IPR012947: Threonyl/alanyl tRNA synthetase, SAD; IPR018164: Alanyl-tRNA synthetase, class IIc, N-terminal; IPR018163: Threonyl/alanyl tRNA synthetase, class II-like, putative editing domain; PTHR11777: ; IPR009000: Translation protein, beta-barrel domain	KOG0188
comp27916_c0_seq1.p1	Ec-01_006780.1	K Homology domain	GO:0003676	IPR004087: K Homology domain; IPR004088: K Homology domain, type 1; IPR013761: Sterile alpha motif/pointed domain; IPR001660: Sterile alpha motif domain; IPR021129: Sterile alpha motif, type 1	NA
comp34049_c0_seq1.p1	Ec-01_006800.1	WD40 repeat	GO:0005515	IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; PTHR14205:	NA
comp26859_c0_seq2.p1	Ec-01_006810.1	Transmembrane receptor, eukaryota	GO:0016021	IPR009637: Transmembrane receptor, eukaryota; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp49487_c0_seq1.p1	Ec-01_006820.2	Hypothetical leucine rich repeat and MORN domain-containing protein	GO:0005515	SSF52047: ; IPR006553: Leucine-rich repeat, cysteine-containing subtype; IPR032675: Leucine-rich repeat domain, L domain-like; SSF82185: ; PTHR24006: ; IPR000048: IQ motif, EF-hand binding site; IPR000421: Coagulation factor 5/8 C-terminal domain; G3DSA:2.20.110.10: ; Coil: ; IPR000008: C2 domain; IPR003409: MORN motif; IPR008979: Galactose-binding domain-like	NA
comp63968_c0_seq1.p1	Ec-01_006820.3	Hypothetical leucine rich repeat and MORN domain-containing protein	GO:0005515	SSF52047: ; IPR006553: Leucine-rich repeat, cysteine-containing subtype; IPR032675: Leucine-rich repeat domain, L domain-like; PTHR24006: ; IPR000048: IQ motif, EF-hand binding site; IPR000421: Coagulation factor 5/8 C-terminal domain; Coil: ; IPR000008: C2 domain; IPR008979: Galactose-binding domain-like	NA
comp31719_c1_seq2.p1	Ec-01_006830.2	Hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11754_c0_seq1.p1	Ec-01_006840.1	DBC1/CARP1 catalytically inactive NUDIX hydrolase domain	n/a;n/a;n/a	IPR025224: Cell cycle and apoptosis regulator protein; Coil: ; PTHR14304:SF11: ; IPR025954: DBC1/CARP1 catalytically inactive NUDIX hydrolase domain	NA
comp26178_c0_seq1.p1	Ec-01_006870.1	Cleavage and polyadenylation specificity factor subunit 2	GO:0005847;GO:0006378;GO:0006379	IPR025069: Cleavage and polyadenylation specificity factor 2, C-terminal; IPR022712: Beta-Casp domain; PTHR11203: ; IPR027075: Cleavage and polyadenylation specificity factor subunit 2; IPR001279: Metallo-beta-lactamase; Coil:	NA
comp31461_c0_seq1.p1	Ec-01_006880.1	Putative sodium bile acid cotransporter	GO:0006814;GO:0008508;GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR016833: Putative sodium bile acid cotransporter; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	NA
comp89827_c0_seq1.p1	Ec-01_006910.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp24167_c0_seq2.p1	Ec-01_006920.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp26719_c0_seq1.p1	Ec-01_006930.1	Protein phosphatase 2C (PP2C)-like domain	GO:0006470;GO:0003824;GO:0004722	IPR000222: PPM-type phosphatase, divalent cation binding; IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C	NA
comp30920_c0_seq2.p5	Ec-01_006940.1	Sybindin-like protein	GO:0006810;GO:0006888;GO:0005801	IPR007233: Sybindin-like protein; IPR011012: Longin-like domain; G3DSA:3.30.450.70:	NA
comp30920_c0_seq2.p1	Ec-01_006950.1	Chromodomain helicase-DNA-binding protein, putative	GO:0005515	IPR019786: Zinc finger, PHD-type, conserved site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001965: Zinc finger, PHD-type; IPR001471: AP2/ERF domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR016177: DNA-binding domain; IPR011011: Zinc finger, FYVE/PHD-type; IPR019787: Zinc finger, PHD-finger	NA
comp28091_c0_seq3.p1	Ec-01_006960.1	Cathepsin H	GO:0006508;GO:0004197	SIGNAL_PEPTIDE: Signal peptide region; SSF54001: ; IPR000169: Cysteine peptidase, cysteine active site; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR013201: Proteinase inhibitor I29, cathepsin propeptide; IPR013128: Peptidase C1A; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR025661: Cysteine peptidase, asparagine active site; IPR000668: Peptidase C1A, papain C-terminal; SignalP-noTM: ; G3DSA:3.90.70.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1543
comp28091_c0_seq3.p2	Ec-01_006980.1	CS domain	n/a;n/a;n/a	IPR007052: CS domain; PTHR13164: ; IPR007699: SGS; IPR008978: HSP20-like chaperone	NA
comp20070_c0_seq1.p1	Ec-01_006990.1	Ribosomal protein S4/S9, N-terminal	GO:0003723;GO:0005622;GO:0019843	IPR001912: Ribosomal protein S4/S9, N-terminal; SSF55174: ; IPR022801: Ribosomal protein S4/S9; IPR002942: RNA-binding S4 domain	NA
comp32617_c5_seq1.p1	Ec-01_007000.1	Nicotinamide nucleotide transhydrogenase	GO:0008746;GO:0015992;GO:0055114	IPR007698: Alanine dehydrogenase/pyridine nucleotide transhydrogenase, NAD(H)-binding domain; SSF51735: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR012136: NADP transhydrogenase, beta subunit; IPR024605: NAD(P) transhydrogenase, alpha subunit, C-terminal; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR026255: NAD(P) transhydrogenase, alpha subunit; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.40.50.1770: ; IPR029035: DHS-like NAD/FAD-binding domain; IPR007886: Alanine dehydrogenase/pyridine nucleotide transhydrogenase, N-terminal; SSF52283: ; PTHR10160: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28579_c0_seq1.p1	Ec-01_007010.1	Armadillo-type fold	GO:0005488	IPR022162: Protein of unknown function DUF3689; IPR016024: Armadillo-type fold; Coil: ; PTHR31743:	NA
comp28548_c1_seq3.p2	Ec-01_007020.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28548_c1_seq3.p1	Ec-01_007030.1	Tetratricopeptide-like helical domain	GO:0005515	IPR002885: Pentatricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; PTHR24015:	NA
comp13069_c0_seq1.p1	Ec-01_007060.1	EamA domain	GO:0016020;GO:0016021	PTHR12715: ; SSF103481: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000620: EamA domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30165_c0_seq2.p1	Ec-01_007070.1	expressed unknown protein	NA	Coil:	NA
comp30165_c0_seq2.p2	Ec-01_007080.1	Protein of unknown function DUF2838	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR31201: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR021261: Protein of unknown function DUF2838; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28581_c0_seq7.p1	Ec-01_007090.1	hypothetical protein	GO:0005524	NA	NA
comp33777_c0_seq1.p1	Ec-01_007100.1	3-ketoacyl-(acyl-carrier-protein) reductase, 3-oxoacyl-[acyl-carrier-protein] reductase.	GO:0008152;GO:0016491	PTHR24312: ; SSF51735: ; IPR020904: Short-chain dehydrogenase/reductase, conserved site; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011284: 3-oxoacyl-(acyl-carrier-protein) reductase; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013968: Polyketide synthase, ketoreductase domain	KOG1200
comp31339_c0_seq2.p1	Ec-01_007110.1	Domain of unknown function DUF4206	GO:0005515;GO:0008270;n/a	IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR025258: Domain of unknown function DUF4206; Coil: ; PTHR12326:	NA
comp31339_c0_seq15.p1	Ec-01_007120.1	Prolyl 4-hydroxylase, alpha subunit	GO:0005506;GO:0016705;GO:0031418;GO:0055114	IPR006620: Prolyl 4-hydroxylase, alpha subunit; PTHR10869:SF80: ; PTHR10869:	NA
comp31339_c0_seq5.p2	Ec-01_007130.1	possible haloacid dehalogenase-like hydrolase family protein	GO:0003824;GO:0008152	PTHR19288: ; IPR006356: HAD-superfamily hydrolase, subfamily IIA, hypothetical 3; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR006439: HAD hydrolase, subfamily IA; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR023214: HAD-like domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR19288:SF3: ; IPR006357: HAD-superfamily hydrolase, subfamily IIA; PF13242: HAD-hydrolase-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2882
comp32768_c0_seq14.p3	Ec-01_007150.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32567_c0_seq3.p1	Ec-01_007160.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0005524;GO:0004672;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PTHR24361: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	KOG0589
comp20640_c0_seq1.p1	Ec-01_007180.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32728_c0_seq31.p1	Ec-01_007190.2	DNA double-strand break repair rad50 ATPase	GO:0005524;GO:0005694;GO:0006259;GO:0016887	IPR029052: Metallo-dependent phosphatase-like; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR32114:SF2: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027050: Nuclease SbcCD subunit C; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32958_c0_seq4.p1	Ec-01_007230.1	AAA+ ATPase domain	GO:0004176;GO:0004252;GO:0006508	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003593: AAA+ ATPase domain; IPR003959: ATPase, AAA-type, core; PR00830: Endopeptidase La (Lon) serine protease (S16) signature; IPR003960: ATPase, AAA-type, conserved site; PTHR23070: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp35191_c0_seq1.p1	Ec-01_007240.1	Ribosomal protein S24e	GO:0005840;GO:0000166;GO:0006412;GO:0005622;GO:0003735	IPR001976: Ribosomal protein S24e; IPR012678: Ribosomal protein L23/L15e core domain; IPR012677: Nucleotide-binding alpha-beta plait domain; Coil:	NA
comp11726_c0_seq1.p1	Ec-01_007250.1	Mini-chromosome maintenance, DNA-dependent ATPase	GO:0003677;GO:0005524;GO:0006260;GO:0042555;GO:0006270;GO:0003678	IPR001208: Mini-chromosome maintenance, DNA-dependent ATPase; IPR012340: Nucleic acid-binding, OB-fold; IPR018525: Mini-chromosome maintenance, conserved site; IPR004039: Rubredoxin-type fold; IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:3.30.1640.10: ; PTHR11630: ; IPR027925: MCM N-terminal domain; IPR008047: Mini-chromosome maintenance complex protein 4	NA
comp30552_c0_seq5.p1	Ec-01_007270.1	Fanconi Anaemia group E protein, C-terminal	n/a;n/a;n/a	IPR021025: Fanconi Anaemia group E protein, C-terminal; PTHR32094:	NA
comp26815_c0_seq1.p1	Ec-01_007280.1	expressed unknown protein	GO:0004553;GO:0005975;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp41981_c0_seq1.p1	Ec-01_007300.1	Hypothetical protein	n/a;n/a;n/a	IPR000048: IQ motif, EF-hand binding site	NA
comp32379_c1_seq2.p1	Ec-01_007320.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp32379_c3_seq1.p2	Ec-01_007340.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; IPR002110: Ankyrin repeat; PTHR24188:	NA
comp32522_c0_seq1.p1	Ec-01_007350.1	UDP-glucuronate decarboxylase	GO:0048040	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001509: NAD-dependent epimerase/dehydratase, N-terminal domain; SSF51735: ; IPR016040: NAD(P)-binding domain; G3DSA:3.90.25.10: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10366:	NA
comp32522_c0_seq1.p2	Ec-01_007370.1	Endonuclease/exonuclease/phosphatase	GO:0004518;GO:0006281	IPR020848: AP endonuclease 1, conserved site; IPR020847: AP endonuclease 1, binding site; IPR005135: Endonuclease/exonuclease/phosphatase; IPR004808: AP endonuclease 1	NA
comp32522_c0_seq1.p3	Ec-01_007380.1	Hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp9550_c0_seq1.p2	Ec-01_007390.1	flagellar associated protein	GO:0005515	IPR008962: PapD-like; IPR001715: Calponin homology domain; PF14874: Flagellar-associated PapD-like; PTHR23053:	NA
comp32360_c0_seq8.p1	Ec-01_007420.1	Anoctamin	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007632: Anoctamin; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19364_c0_seq1.p1	Ec-01_007440.1	EF-hand domain pair	n/a;GO:0005509	PF13833: EF-hand domain pair; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; SSF47473: ; PTHR23056:	NA
comp34336_c0_seq1.p1	Ec-01_007450.1	Tetratricopeptide-like helical domain	GO:0005515	IPR011990: Tetratricopeptide-like helical domain; SSF81901: ; PTHR13891: ; IPR006597: Sel1-like	NA
comp28644_c0_seq2.p1	Ec-01_007470.1	aspartate-semialdehyde dehydrogenase	GO:0016620;GO:0051287;GO:0009097;GO:0009088;GO:0055114;GO:0050661;GO:0009089;GO:0004073;GO:0009086	PTHR10174: ; IPR012280: Semialdehyde dehydrogenase, dimerisation domain; SSF51735: ; IPR000534: Semialdehyde dehydrogenase, NAD-binding; G3DSA:3.30.360.10: ; IPR016040: NAD(P)-binding domain; IPR005986: Aspartate-semialdehyde dehydrogenase, beta-type; SSF55347: ; IPR012080: Aspartate-semialdehyde dehydrogenase	KOG4777
comp26213_c0_seq1.p1	Ec-01_007480.1	Aspartate Aminotransferase	GO:0003824;GO:0030170	IPR004839: Aminotransferase, class I/classII; IPR015424: Pyridoxal phosphate-dependent transferase; IPR004838: Aminotransferases, class-I, pyridoxal-phosphate-binding site; PTHR11751: ; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	KOG0257
comp33006_c1_seq12.p1	Ec-01_007490.1	HECT	GO:0004842	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR11254: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000569: HECT; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:3.30.2160.10:	NA
comp26724_c0_seq1.p1	Ec-01_007500.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp83831_c0_seq1.p1	Ec-01_007520.3	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp26308_c0_seq1.p1	Ec-01_007540.1	Histone acetyltransferase type B, catalytic subunit	GO:0004402;GO:0005634;GO:0006348;GO:0016573	IPR017380: Histone acetyltransferase type B, catalytic subunit; IPR016181: Acyl-CoA N-acyltransferase; IPR019467: Histone acetyl transferase HAT1 N-terminal	NA
comp26308_c0_seq1.p2	Ec-01_007550.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp31542_c0_seq9.p1	Ec-01_007560.1	Tubulin-tyrosine ligase/Tubulin polyglutamylase	GO:0006464	SSF56059: ; IPR004344: Tubulin-tyrosine ligase/Tubulin polyglutamylase; PTHR12241:	NA
comp31542_c0_seq6.p1	Ec-01_007570.1	PDZ domain	GO:0005515	IPR009003: Trypsin-like cysteine/serine peptidase domain; IPR001940: Peptidase S1C; PF13365: Trypsin-like peptidase domain; PTHR22939: ; IPR001478: PDZ domain; G3DSA:2.40.10.10:	NA
comp32666_c0_seq15.p1	Ec-01_007590.1	CRAL-TRIO domain	n/a;n/a;n/a	PTHR10174: ; IPR001251: CRAL-TRIO lipid binding domain	NA
comp27882_c0_seq4.p1	Ec-01_007600.1	Dynein light chain	GO:0005875;GO:0007017	SSF54648: ; IPR001372: Dynein light chain, type 1/2	KOG3430
comp19685_c0_seq2.p1	Ec-01_007610.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp107079_c0_seq1.p1	Ec-01_007640.1	conserved unknown protein	n/a;n/a;n/a	PTHR33667: ; PTHR33667:SF2:	NA
comp30269_c0_seq1.p1	Ec-01_007660.1	ENTH/VHS	n/a;n/a;n/a	IPR013809: ENTH domain; Coil: ; IPR008942: ENTH/VHS	NA
comp33006_c1_seq22.p1	Ec-01_007690.1	EF-hand domain pair	GO:0005509	IPR018247: EF-Hand 1, calcium-binding site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; SSF47473: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp18556_c0_seq1.p1	Ec-01_007700.1	Chorismate Mutase	GO:0004106;GO:0009073	IPR008238: Chorismate mutase, AroQ class, eukaryotic type; IPR020822: Chorismate mutase, type II; SignalP-TM:	KOG0795
comp29424_c0_seq1.p1	Ec-01_007720.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20064_c0_seq1.p1	Ec-01_007750.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; PF13414: TPR repeat; IPR013105: Tetratricopeptide TPR2; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; PTHR22904:	NA
comp34494_c0_seq1.p1	Ec-01_007760.1	Superoxide dismutase	GO:0006801;GO:0004784;GO:0046872;GO:0055114	NA	KOG0876
comp20917_c0_seq2.p1	Ec-01_007770.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA

comp26831_c0_seq1.p2	Ec-01_007800.1	methionine sulfoxide reductase	GO:0055114;GO:0008113	[illegible]	KOG1635
comp26831_c0_seq1.p1	Ec-01_007810.1	Magnesium-protoporphyrin IX methyltransferase, putative chloroplast precursor	GO:0046406;GO:0015979;GO:0015995	[illegible]	NA
comp33133_c7_seq1.p1	Ec-01_007820.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp32298_c0_seq1.p1	Ec-01_007830.1	putative tRNA isopentenyltransferase	GO:0004811;GO:0005524;GO:0008033	[illegible]	KOG1384
comp24668_c0_seq1.p1	Ec-01_007840.1	Peptidase C2, calpain, catalytic domain	GO:0004198;GO:0005622;GO:0006508	[illegible]	NA
comp34120_c0_seq1.p1	Ec-01_007850.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32233_c0_seq1.p1	Ec-01_007860.1	Gametogenetin-binding protein 2	n/a;n/a;n/a	[illegible]	NA
comp32233_c1_seq1.p3	Ec-01_007870.1	Protein of unknown function DUF866, eukaryotic	n/a;n/a;n/a	IPR008584: Protein of unknown function DUF866, eukaryotic; SSF141678:	NA
comp19114_c0_seq1.p1	Ec-01_007880.1	Alkaline-phosphatase-like, core domain	GO:0008152;GO:0003824	[illegible]	NA
comp33136_c0_seq6.p1	Ec-01_007890.1	Exonuclease	GO:0004527	IPR006055: Exonuclease; IPR012337: Ribonuclease H-like domain; PTHR12801: ; IPR013520: Exonuclease, RNase T/DNA polymerase III; Coil:	NA
comp31249_c0_seq12.p1	Ec-01_007930.1	Metallo-dependent phosphatase-like	n/a;GO:0016787	IPR029052: Metallo-dependent phosphatase-like; IPR004843: Calcineurin-like phosphoesterase domain, apaH type	NA
comp25256_c1_seq1.p1	Ec-01_007940.1	Dolichol-phosphate mannosyltransferase, family GT2	NA	IPR029044: Nucleotide-diphospho-sugar transferases; PTHR10859: ; IPR001173: Glycosyltransferase 2-like	KOG2978
comp12467_c0_seq1.p1	Ec-01_007950.1	Root UVB sensitive family	n/a;n/a;n/a	[illegible]	NA
comp33559_c0_seq1.p1	Ec-01_007990.1	Translation elongation factor EFTs/EF1B	GO:0005622;GO:0003746;GO:0006414	[illegible]	NA
comp32373_c0_seq2.p1	Ec-01_008000.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp30248_c0_seq2.p1	Ec-01_008010.1	similar to CTF18, chromosome transmission fidelity factor 18 homolog isoform 3	GO:0004176;GO:0004252;GO:0005524;GO:0006508	IPR003959: ATPase, AAA-type, core; IPR003593: AAA+ ATPase domain; G3DSA:1.10.8.60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR23389:	NA
comp31413_c0_seq7.p1	Ec-01_008020.1	Tetratricopeptide-like helical domain	GO:0005515	[illegible]	NA
comp31413_c0_seq6.p1	Ec-01_008030.1	Putative Glutathione S-transferase	n/a;GO:0005515	[illegible]	KOG2903
comp24688_c0_seq3.p1	Ec-01_008040.1	fructose-1,6-bisphosphate aldolase	GO:0004332;GO:0006096	[illegible]	NA
comp26997_c0_seq1.p1	Ec-01_008050.2	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29521_c0_seq1.p1	Ec-01_008070.1	Glycoside-hydrolase family GH114, TIM-barrel domain	n/a;n/a;n/a	[illegible]	NA
comp30155_c0_seq4.p1	Ec-01_008100.1	cryptochrome 2	GO:0003913;GO:0006281	[illegible]	KOG0133
comp26195_c0_seq1.p1	Ec-01_008110.2	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp32198_c0_seq12.p1	Ec-01_008120.1	Zinc finger, UBP-type	GO:0008270	PTHR24007: ; IPR011422: BRCA1-associated 2; IPR001607: Zinc finger, UBP-type; IPR001841: Zinc finger, RING-type; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; Coil:	NA
comp31093_c0_seq1.p1	Ec-01_008140.1	NLI interacting factor	GO:0005515	[illegible]	NA
comp14277_c0_seq1.p2	Ec-01_008160.3	Fibronectin type III	GO:0005515	IPR013783: Immunoglobulin-like fold; IPR003961: Fibronectin type III; Coil:	NA
comp52182_c0_seq1.p1	Ec-01_008170.1	hypothetical protein	n/a;n/a;n/a	Coil: ; IPR000048: IQ motif, EF-hand binding site	NA
comp29063_c0_seq13.p1	Ec-01_008180.1	ATPase, V0 complex, subunit 116kDa, eukaryotic	GO:0000220	[illegible]	NA
comp20593_c0_seq1.p1	Ec-01_008190.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp20518_c0_seq1.p1	Ec-01_008200.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp32363_c0_seq4.p2	Ec-01_008210.1	Peroxisomal targeting signal 1 receptor family	n/a;n/a;n/a	[illegible]	NA
comp35686_c0_seq1.p1	Ec-01_008220.1	Nicotinamide N-methyltransferase-like	n/a;n/a;n/a	[illegible]	NA
comp32363_c0_seq4.p1	Ec-01_008230.1	FACT complex subunit SPT16	NA	[illegible]	NA
comp24339_c0_seq1.p1	Ec-01_008240.1	Tubulin/FtsZ, GTPase domain	GO:0003924;GO:0005525;GO:0043234;GO:0051258	[illegible]	NA
comp30735_c0_seq3.p2	Ec-01_008250.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp30735_c0_seq3.p1	Ec-01_008260.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	[illegible]	NA
comp30735_c0_seq10.p1	Ec-01_008270.1	Dynein light chain flagellar outer dynein arm light chain LC1	GO:0005515;n/a	[illegible]	NA
comp24371_c0_seq1.p1	Ec-01_008280.1	pyruvate dehydrogenase kinase	GO:0005524;GO:0016310;GO:0016772	[illegible]	NA
comp35023_c0_seq1.p1	Ec-01_008300.1	Hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp72094_c0_seq1.p1	Ec-01_008310.1	Dbl homology (DH) domain	GO:0005089;GO:0035023	[illegible]	NA
comp30041_c0_seq1.p1	Ec-01_008330.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp31503_c1_seq1.p1	Ec-01_008340.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp19918_c0_seq1.p1	Ec-01_008370.1	UDP-galactose transporter	GO:0005338;GO:0015780;GO:0016021	[illegible]	NA
comp25273_c0_seq1.p1	Ec-01_008380.1	Winged helix-turn-helix DNA-binding domain	GO:0003677;GO:0006355;GO:0006352;GO:0016987;GO:0003700	[illegible]	NA
comp28381_c0_seq1.p1	Ec-01_008390.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp27385_c0_seq1.p1	Ec-01_008400.1	RNA polymerase sigma-70 region 2	GO:0003677;GO:0006355;GO:0006352;GO:0016987;GO:0003700	[illegible]	NA
comp33826_c0_seq1.p1	Ec-01_008410.1	Acetyltransferase (GNAT) domain protein	GO:0008080	[illegible]	NA
comp34504_c0_seq1.p1	Ec-01_008420.1	Zinc finger, AN1-type	GO:0008270	[illegible]	NA
comp33112_c0_seq1.p1	Ec-01_008430.1	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0036459;GO:0006511;GO:0005515	[illegible]	NA
comp33112_c1_seq2.p1	Ec-01_008440.1	protein-L-isoaspartate (D-aspartate) O-methyltransferase	GO:0004719;GO:0006464	[illegible]	NA
comp22526_c0_seq1.p1	Ec-01_008450.1	6-phosphogluconate dehydrogenase, NADP-binding	GO:0004616;GO:0055114;GO:0006098;GO:0016491	[illegible]	NA
comp32079_c1_seq16.p1	Ec-01_008470.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp25161_c0_seq1.p1	Ec-01_008480.1	STAS domain	GO:0016020;n/a;GO:0055085;GO:0008272;GO:0008271	[illegible]	NA
comp20862_c0_seq1.p1	Ec-01_008510.1	conserved unknown protein	n/a;GO:0005515	[illegible]	NA
comp26309_c0_seq2.p1	Ec-01_008520.1	tRNA (guanine-N(7)-)-methyltransferase	GO:0006400;GO:0008176	[illegible]	NA
comp28972_c0_seq1.p1	Ec-01_008550.1	EF-hand domain pair	GO:0005509	[illegible]	NA
comp15138_c0_seq2.p1	Ec-01_008560.1	putative dipeptidyl peptidase IV	GO:0016020;GO:0004252;GO:0003676;GO:0006508	[illegible]	NA
comp33764_c0_seq1.p1	Ec-01_008570.1	Nascent polypeptide-associated complex NAC domain	n/a;n/a;n/a	[illegible]	NA
comp29744_c0_seq6.p1	Ec-01_008580.1	Multi antimicrobial extrusion protein	GO:0016020;GO:0055085;GO:0015238;GO:0015297;GO:0006855	[illegible]	NA
comp13370_c0_seq1.p1	Ec-01_008590.1	Protein kinase domain	GO:0005524;GO:0006468;GO:0004672	[illegible]	NA
comp30457_c1_seq3.p2	Ec-01_008610.1	Probable serine/threonine-protein kinase, C-terminal half	NA	[illegible]	NA
comp12460_c0_seq1.p1	Ec-01_008620.2	Lipoyl-[acyl-carrier-protein]-protein-N-lipoyltransferase (Lipoate-protein ligase B)	GO:0006464	[illegible]	NA
comp24162_c0_seq1.p1	Ec-01_008630.1	NADH dehydrogenase (ubiquinone)	GO:0003824;GO:0005488;GO:0008152	[illegible]	KOG2865
comp30385_c0_seq6.p2	Ec-01_008640.1	pseudouridine synthase	GO:0003723	[illegible]	NA
comp30385_c0_seq6.p1	Ec-01_008650.1	Protofilament ribbon protein of flagellar microtubules	n/a;n/a;n/a	[illegible]	KOG0043
comp27738_c0_seq5.p1	Ec-01_008660.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp21838_c0_seq1.p1	Ec-01_008670.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp20651_c0_seq1.p1	Ec-01_008680.2	hypothetical protein	n/a;n/a;n/a	SSF101447:	NA
comp12849_c0_seq1.p1	Ec-01_008690.1	Cullin repeat-like-containing domain	n/a;n/a;n/a	[illegible]	NA
comp12778_c0_seq1.p1	Ec-01_008730.1	conserved unknown protein	GO:0000166;GO:0004812;GO:0005524;GO:0005737;GO:0006412;GO:0006418	[illegible]	NA
comp31229_c1_seq3.p1	Ec-01_008740.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp33149_c0_seq7.p1	Ec-01_008750.1	Helicase, C-terminal	GO:0003676;GO:0004386;GO:0005524	[illegible]	NA
comp31158_c0_seq3.p1	Ec-01_008760.1	conserved unknown protein	n/a;n/a;n/a	PTHR38899:	NA
comp27102_c0_seq1.p1	Ec-01_008790.1	Pseudouridine synthase, catalytic domain	GO:0003723;GO:0001522;GO:0009451;GO:0009982	[illegible]	NA
comp27102_c0_seq1.p2	Ec-01_008800.1	Protein of unknown function DUF583	NA	[illegible]	NA
comp25122_c0_seq1.p1	Ec-01_008810.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	[illegible]	NA
comp11014_c0_seq1.p1	Ec-01_008830.1	Ankyrin repeat	GO:0005515	[illegible]	NA
comp11894_c0_seq1.p1	Ec-01_008840.1	Sec61	GO:0009306;GO:0015031;GO:0015450;GO:0016020	[illegible]	NA
comp24648_c0_seq1.p1	Ec-01_008850.1	aureochrome 5	GO:0004871;GO:0007165	[illegible]	NA
comp32067_c0_seq31.p1	Ec-01_008860.1	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative	NA	[illegible]	NA
comp23621_c0_seq2.p1	Ec-01_008890.1	gamma hydroxybutyrate dehydrogenase	GO:0016616;GO:0055114;GO:0050662;GO:0016491	[illegible]	NA
comp30629_c0_seq1.p1	Ec-01_008900.1	HECT	GO:0004842;GO:0008270	[illegible]	NA
comp33921_c0_seq1.p1	Ec-01_008910.1	CS domain	n/a;n/a;n/a	[illegible]	NA
comp33921_c0_seq1.p3	Ec-01_008920.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp31521_c0_seq5.p1	Ec-01_008930.1	early-responsive to dehydration protein-related	GO:0016020	[illegible]	NA
comp34070_c0_seq1.p1	Ec-01_008960.1	Light harvesting complex protein	GO:0009765;GO:0016020	[illegible]	NA
comp33956_c0_seq1.p1	Ec-01_008970.1	Putative subunit of the Anaphase Promoting Complex	GO:0005515	[illegible]	KOG1155
comp32885_c1_seq1.p1	Ec-01_008980.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp28802_c0_seq3.p1	Ec-01_009010.1	Argonaute 1	GO:0003676	[illegible]	KOG1041
comp34093_c0_seq1.p1	Ec-01_009030.1	Heat shock protein 40	GO:0006457;GO:0031072;GO:0051082	[illegible]	NA
comp29009_c0_seq1.p1	Ec-01_009040.2	[Skp1-protein]-hydroxyproline N-acetylglucosaminyltransferase, family GT60	NA	[illegible]	NA
comp21090_c0_seq1.p1	Ec-01_009050.1	actin	GO:0005515	[illegible]	KOG0676
comp24295_c0_seq2.p1	Ec-01_009060.2	XPG-I domain	GO:0004518	[illegible]	NA
comp31047_c0_seq3.p1	Ec-01_009070.1	Yip1 domain	GO:0016020	[illegible]	NA
comp26984_c0_seq2.p1	Ec-01_009100.1	eukaryotic initiation factor 4A	n/a;n/a;n/a	[illegible]	NA
comp34349_c0_seq1.p1	Ec-01_009140.1	5-formyltetrahydrofolate cyclo-ligase	GO:0005524;GO:0009396;GO:0030272	[illegible]	NA
comp23424_c0_seq2.p1	Ec-01_009160.1	Tyrosine--tRNA ligase	GO:0005524;GO:0006437;GO:0005737;GO:0006418;GO:0000166;GO:0006412;GO:0004831;GO:0004812	[illegible]	KOG2144
comp50176_c0_seq1.p1	Ec-01_009170.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp23424_c0_seq2.p2	Ec-01_009180.1	conserved carbohydrate binding protein	GO:0003824;GO:0005975;GO:0030246	[illegible]	NA
comp30146_c0_seq1.p1	Ec-01_009200.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp26720_c0_seq2.p1	Ec-01_009220.1	DNA repair protein Rad50, eukaryotes	GO:0005634;GO:0006281;GO:0030870;GO:0000723;GO:0016887	NA	NA
comp26148_c0_seq1.p1	Ec-01_009250.1	expressed unknown protein	n/a;n/a;n/a	SignalP-TM:	NA
comp30068_c0_seq7.p1	Ec-01_009320.1	Ribosomal protein S5 domain 2-type fold	n/a;n/a;n/a	[illegible]	NA
comp31062_c0_seq5.p1	Ec-01_009350.1	Condensin complex subunit 3	GO:0000796;GO:0007076	[illegible]	NA
comp19832_c0_seq3.p1	Ec-01_009360.1	RNA recognition motif domain	GO:0003676;GO:0000166	[illegible]	NA
comp26365_c0_seq2.p1	Ec-01_009390.1	cyclin B2	n/a;n/a;n/a	[illegible]	KOG0653
comp12096_c0_seq1.p1	Ec-01_009400.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0016887	[illegible]	NA
comp20766_c0_seq2.p1	Ec-01_009410.1	carbohydrate kinase, FGGY	GO:0016773;GO:0005975	[illegible]	NA
comp28246_c0_seq1.p1	Ec-01_009420.2	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28918_c0_seq1.p1	Ec-01_009440.1	ADP/ATP carrier protein	GO:0006810;GO:0005524;GO:0005471;GO:0016021	[illegible]	NA
comp28918_c0_seq1.p2	Ec-01_009450.1	Mpv17/PMP22	GO:0016021	[illegible]	NA
comp28323_c0_seq3.p1	Ec-01_009460.1	Rieske [2Fe-2S] iron-sulphur domain	GO:0051537;GO:0055114;GO:0016491	[illegible]	NA
comp32615_c1_seq10.p1	Ec-01_009500.1	eukaryotic translation initiation factor 2B epsilon subunit	GO:0005488	[illegible]	NA
comp16958_c0_seq2.p1	Ec-01_009510.1	Hypothetical leucine rich repeat protein	NA	[illegible]	NA
comp22682_c0_seq3.p1	Ec-01_009520.1	hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp20763_c0_seq1.p1	Ec-01_009550.2	HECT	GO:0004842	[illegible]	NA
comp12328_c0_seq1.p1	Ec-01_009560.1	proteasome beta subunit	GO:0051603;GO:0004298;GO:0005839;GO:0006511	[illegible]	NA
comp20934_c0_seq1.p1	Ec-01_009570.1	Homeodomain-like	GO:0003677	[illegible]	NA
comp26601_c1_seq1.p1	Ec-01_009590.1	HSP20-like chaperone	n/a;n/a;n/a	[illegible]	NA
comp21229_c0_seq1.p2	Ec-01_009600.1	Domain of unknown function DUF11	GO:0005727	[illegible]	NA
comp28493_c0_seq2.p2	Ec-01_009620.1	SMAD/FHA domain	GO:0005515	[illegible]	NA
comp33822_c0_seq1.p2	Ec-01_009630.1	DPB4 class protein with histone-like transcription factor (NF-YB subunit) domain	GO:0046982;GO:0043565;GO:0005622	NA	NA
comp45575_c0_seq1.p1	Ec-01_009650.2	Armadillo-like helical	GO:0005488	[illegible]	NA
comp19869_c0_seq2.p1	Ec-01_009660.1	fatty acid-ACP thioesterase	GO:0016788;GO:0009058	[illegible]	no relat
comp24670_c0_seq1.p1	Ec-01_009670.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	[illegible]	NA
comp32772_c0_seq22.p1	Ec-01_009690.1	Histidine phosphatase superfamily, clade-1	GO:0006096;GO:0016868	[illegible]	NA
comp32283_c4_seq2.p1	Ec-01_009700.1	putative phosphate/phosphoenolpyruvate translocator precursor protein	n/a;n/a;n/a	[illegible]	NA
comp32283_c4_seq2.p3	Ec-01_009710.1	Methylmalonic aciduria and homocystinuria type D protein	GO:0009235	[illegible]	NA
comp30044_c0_seq3.p1	Ec-01_009720.1	carboxylase	GO:0003824;GO:0005524	[illegible]	KOG0238
comp25104_c0_seq1.p1	Ec-01_009730.2	Bromodomain	GO:0005515	[illegible]	NA
comp12731_c0_seq1.p3	Ec-01_009740.1	Light harvesting complex protein	GO:0009765;GO:0016020	[illegible]	NA
comp12335_c0_seq1.p1	Ec-01_009750.1	Citrate synthase-like	GO:0046912;GO:0044262	[illegible]	NA
comp21062_c0_seq2.p1	Ec-01_009770.1	Aldolase-type TIM barrel	GO:0003824	[illegible]	NA
comp15801_c0_seq2.p1	Ec-01_009790.1	WW domain	GO:0005515	[illegible]	NA
comp32711_c0_seq2.p1	Ec-01_009810.1	expressed unknown protein	n/a;n/a;n/a	G3DSA:3.30.70.80:	NA
comp32711_c0_seq1.p1	Ec-01_009820.1	Protein of unknown function DUF1183, TMEM66	n/a;n/a;n/a	[illegible]	NA
comp30317_c0_seq2.p1	Ec-01_009830.1	hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp28218_c0_seq1.p1	Ec-01_009840.3	Hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp31685_c0_seq6.p1	Ec-01_009860.1	hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp30162_c0_seq1.p1	Ec-01_009880.1	Domain of unknown function DUF676, lipase-like	n/a;n/a;n/a	[illegible]	NA
comp24561_c0_seq1.p1	Ec-01_009900.1	Zinc finger, RING/FYVE/PHD-type	n/a;GO:0005515	[illegible]	NA
comp31237_c0_seq3.p1	Ec-01_009980.4	MutS protein homolog 4	GO:0005524;GO:0006298;GO:0030983	[illegible]	KOG0220
comp32399_c4_seq1.p1	Ec-01_010010.1	Protein prenyltransferase, alpha subunit	GO:0018342;GO:0008318	[illegible]	NA
comp29376_c0_seq1.p1	Ec-01_010050.1	Activator of Hsp90 ATPase, N-terminal	GO:0001671;GO:0051087;GO:0005515	[illegible]	NA
comp29376_c0_seq1.p2	Ec-01_010060.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp20218_c0_seq1.p1	Ec-01_010070.1	conserved unknown protein	n/a;n/a;n/a	PTHR31833:	NA
comp12044_c0_seq1.p1	Ec-01_010080.1	Protein of unknown function UPF0301	n/a;n/a;n/a	[illegible]	NA
comp28493_c0_seq3.p1	Ec-01_010090.1	Coatomer protein complex,delta sub-unit	GO:0005488;GO:0016192;GO:0006886;GO:0030117	[illegible]	KOG1059
comp25281_c0_seq1.p1	Ec-01_010140.1	Ribonuclease H2, subunit B	GO:0005634	[illegible]	NA
comp31863_c0_seq4.p1	Ec-01_010150.1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11-like	GO:0005743;GO:0008565;GO:0015031	[illegible]	NA
comp29976_c0_seq1.p1	Ec-01_010170.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31807_c0_seq1.p1	Ec-01_010230.1	GLE1-like	GO:0005643;GO:0016973	[illegible]	NA
comp29406_c0_seq4.p1	Ec-01_010240.1	Hypothetical leucine rich repeat protein	NA	[illegible]	NA
comp33100_c0_seq1.p1	Ec-01_010250.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp30414_c0_seq1.p1	Ec-01_010260.1	DEAD box helicase	GO:0003676;GO:0003677;GO:0003887;GO:0005524;GO:0006260	[illegible]	KOG0950
comp33223_c1_seq1.p1	Ec-01_010270.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp24711_c0_seq1.p1	Ec-01_010330.1	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) containing protein	GO:0003676	[illegible]	NA
comp11897_c0_seq1.p1	Ec-01_010350.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp32659_c0_seq48.p1	Ec-01_010370.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp32846_c0_seq28.p1	Ec-01_010380.1	Chromate transporter	GO:0015109;GO:0015703	[illegible]	NA
comp31214_c1_seq1.p1	Ec-01_010410.1	NLI interacting factor	GO:0005515	[illegible]	NA
comp33844_c0_seq1.p2	Ec-01_010430.1	Hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp31281_c0_seq1.p1	Ec-01_010440.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp20346_c0_seq1.p1	Ec-01_010450.1	Histidine phosphatase superfamily	n/a;n/a;n/a	[illegible]	NA
comp31095_c0_seq3.p1	Ec-01_010460.1	UbiB domain	n/a;n/a;n/a	[illegible]	NA
comp34467_c0_seq1.p1	Ec-01_010470.1	Basic-leucine zipper domain	GO:0003700;GO:0006355;GO:0043565	[illegible]	NA
comp27693_c0_seq2.p1	Ec-01_010480.1	Alpha/beta hydrolase fold-5	GO:0005622;GO:0008270	[illegible]	NA
comp20180_c0_seq1.p1	Ec-01_010490.1	W2 domain	GO:0005515	[illegible]	NA
comp29229_c1_seq2.p1	Ec-01_010510.1	Tetratricopeptide, SHNi-TPR domain	n/a;n/a;n/a	[illegible]	NA
comp29229_c0_seq4.p1	Ec-01_010520.1	tRNA-dihydrouridine synthase	GO:0050660;GO:0055114;GO:0008033;GO:0017150	[illegible]	NA
comp20302_c0_seq1.p1	Ec-01_010535.1	hypothetical protein	GO:0004742;GO:0006090;GO:0008152;GO:0016746;GO:0045254	[illegible]	NA
comp44509_c0_seq1.p1	Ec-01_010540.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	[illegible]	NA
comp27417_c0_seq1.p2	Ec-01_010550.1	SGNH hydrolase-type esterase domain	n/a;n/a;n/a	[illegible]	NA
comp27417_c0_seq1.p1	Ec-01_010560.1	conserved unknown protein	GO:0005524;GO:0016887	[illegible]	NA
comp31151_c0_seq4.p2	Ec-01_010570.1	HECT	GO:0004842	[illegible]	NA
comp31151_c0_seq4.p8	Ec-01_010590.1	Protein of unknown function DUF842, eukaryotic	n/a;n/a;n/a	[illegible]	NA
comp31151_c0_seq4.p1	Ec-01_010600.1	Amino acid permease/ SLC12A domain	GO:0006810;GO:0016020;GO:0055085	[illegible]	NA
comp33728_c0_seq1.p1	Ec-01_010610.2	ATP-dependent Clp protease proteolytic subunit	GO:0004252;GO:0006508	[illegible]	KOG0840
comp26211_c0_seq1.p1	Ec-01_010620.1	Putative Leucine Rich Repeat Protein Kinase	NA	[illegible]	NA
comp26769_c0_seq1.p1	Ec-01_010630.1	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0036459;GO:0006511	[illegible]	NA
comp31611_c4_seq1.p1	Ec-01_010650.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp20256_c0_seq1.p1	Ec-01_010670.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp33194_c1_seq4.p1	Ec-01_010690.1	hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp30613_c0_seq3.p2	Ec-01_010700.1	hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp28771_c0_seq1.p1	Ec-01_010710.1	UDP-galactose transporter	GO:0015780;GO:0005338;GO:0016021	[illegible]	NA
comp28953_c0_seq2.p1	Ec-01_010720.1	Globin, annelid-type	GO:0015671;GO:0020037;GO:0005506;GO:0019825	[illegible]	NA
comp34978_c0_seq1.p2	Ec-01_010750.1	Ribosomal protein/NADH dehydrogenase domain	n/a;n/a;n/a	[illegible]	NA
comp30841_c1_seq2.p1	Ec-01_010760.2	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp31466_c0_seq2.p2	Ec-01_010770.1	Thioredoxin-like fold	n/a;n/a;n/a	[illegible]	NA
comp31466_c0_seq2.p1	Ec-01_010780.1	Cupin-like domain protein	n/a;n/a;n/a	NA	NA
comp19780_c0_seq1.p1	Ec-01_010790.1	similar to TAK1 (TGF-beta-activated kinase)	GO:0016772	[illegible]	NA
comp31626_c0_seq7.p1	Ec-01_010800.2	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0006457;GO:0031072;GO:0051082	[illegible]	NA
comp13984_c0_seq1.p1	Ec-01_010810.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp34084_c0_seq1.p1	Ec-01_010820.1	SPRY domain	GO:0005515	[illegible]	NA
comp33986_c0_seq1.p1	Ec-01_010830.1	CBS domain	n/a;n/a;n/a	[illegible]	NA
comp26027_c0_seq1.p2	Ec-01_010850.1	conserved unknown protein	NA	[illegible]	NA
comp28872_c1_seq1.p2	Ec-01_010860.1	selenoprotein T	n/a;n/a;n/a	[illegible]	NA
comp27213_c0_seq1.p1	Ec-01_010870.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0005634;GO:0000981;GO:0006355;GO:0008270	[illegible]	NA
comp29187_c0_seq1.p1	Ec-01_010880.1	Flavoprotein Monooxygenase	GO:0005515;GO:0008152;GO:0016491	[illegible]	KOG2614
comp24211_c0_seq1.p1	Ec-01_010890.1	Protein of unknown function DUF1092	NA	[illegible]	NA
comp20466_c0_seq1.p1	Ec-01_010910.1	conserved unknown protein	n/a;n/a;n/a	SSF52777:	NA
comp33837_c0_seq1.p1	Ec-01_010920.1	imm downregulated 15	NA	[illegible]	NA
comp19813_c0_seq1.p1	Ec-01_010930.1	SPRY domain	GO:0005515	[illegible]	NA
comp11683_c0_seq2.p1	Ec-01_010940.1	weakly similar Glutamic acid-rich protein precursor	NA	[illegible]	NA
comp30228_c0_seq3.p1	Ec-01_010950.1	Protein of unknown function DUF4239	n/a;n/a;n/a	[illegible]	NA
comp21115_c0_seq1.p1	Ec-01_010970.1	propionyl-CoA carboxylase, alpha subunit	GO:0003824;GO:0005524	[illegible]	KOG0238
comp26572_c0_seq1.p1	Ec-01_010990.1	Amino acid transporter, transmembrane	n/a;n/a;n/a	[illegible]	NA
comp27032_c0_seq1.p1	Ec-01_011000.1	Protein kinase domain containing protein	GO:0004672;GO:0005524;GO:0006468	[illegible]	KOG1165
comp27032_c0_seq1.p2	Ec-01_011010.1	Tetratricopeptide-like helical domain	GO:0005515	[illegible]	NA
comp26687_c0_seq2.p1	Ec-01_011040.1	Glutamate:glyoxylate aminotransferase	GO:0003824;GO:0047810	[illegible]	NA
comp24504_c0_seq2.p1	Ec-01_011050.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	[illegible]	NA
comp29488_c0_seq1.p2	Ec-01_011060.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp29488_c0_seq1.p1	Ec-01_011070.1	Oxidoreductase, molybdopterin-binding domain	GO:0009055;GO:0055114;GO:0042128	[illegible]	NA
comp17785_c0_seq2.p1	Ec-01_011080.1	SNF1-related protein kinase	GO:0004672;GO:0005524;GO:0006468	[illegible]	KOG0583
comp18977_c0_seq1.p1	Ec-01_011110.2	WD40 repeat	GO:0005515	[illegible]	NA
comp29642_c0_seq3.p1	Ec-01_011120.1	C2 domain	GO:0005515	[illegible]	NA
comp30406_c0_seq1.p1	Ec-01_011130.1	Domain of unknown function DUF2470	n/a;n/a;n/a	[illegible]	NA
comp28827_c0_seq1.p1	Ec-01_011140.1	Endoplasmic reticulum vesicle transporter, C-terminal	n/a;n/a;n/a	[illegible]	NA
comp28827_c0_seq1.p2	Ec-01_011150.1	DDRGK domain containing protein	n/a;n/a;n/a	[illegible]	NA
comp11725_c0_seq1.p1	Ec-01_011160.1	membrane acyl-CoA binding protein	n/a;GO:0005515	[illegible]	KOG0817
comp29993_c0_seq2.p1	Ec-01_011180.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp28244_c0_seq1.p1	Ec-01_011210.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp2859_c0_seq1.p1	Ec-01_011220.1	Kelch-type beta propeller	GO:0005515	[illegible]	NA
comp13286_c0_seq1.p1	Ec-01_011230.1	Ankyrin repeat-containing domain	n/a;GO:0005515	[illegible]	NA
comp11248_c0_seq2.p1	Ec-01_011250.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp34164_c0_seq1.p1	Ec-01_011270.1	Coatomer protein complex,delta sub-unit	GO:0006810	[illegible]	KOG2635
comp32489_c0_seq15.p1	Ec-01_011400.2	hypothetical protein	n/a;n/a;n/a	NA	NA
comp34406_c0_seq1.p1	Ec-01_011410.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp31474_c0_seq1.p1	Ec-01_011420.1	NAD(P)-binding domain	GO:0008152;GO:0016491	[illegible]	NA
comp33024_c1_seq35.p1	Ec-01_011430.1	Sulfotransferase	GO:0008146;GO:0016021	[illegible]	NA
comp19914_c0_seq1.p1	Ec-01_011450.1	P-loop containing nucleoside triphosphate hydrolase	n/a;GO:0008146;GO:0016021	[illegible]	NA
comp29529_c0_seq1.p1	Ec-01_011470.1	Protein of unknown function DUF3754	n/a;n/a;n/a	[illegible]	NA
comp10106_c0_seq1.p1	Ec-01_011480.1	SMCs flexible hinge	GO:0005515;GO:0005524;GO:0005694;GO:0051276	[illegible]	NA
comp34098_c0_seq1.p2	Ec-01_011490.1	Glycine cleavage system H-protein	n/a;n/a;n/a	[illegible]	NA
comp34098_c0_seq1.p1	Ec-01_011500.1	NAD(P)-binding domain	n/a;n/a;n/a	[illegible]	NA
comp25462_c0_seq4.p1	Ec-01_011530.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp12702_c0_seq1.p1	Ec-01_011570.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp27600_c0_seq2.p2	Ec-01_011580.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0031072	[illegible]	NA
comp20520_c0_seq1.p1	Ec-01_011590.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp28789_c0_seq1.p1	Ec-01_011610.1	PDZ domain	GO:0005515	[illegible]	NA
comp26418_c0_seq1.p1	Ec-01_011640.1	vacuolar-type H -translocating inorganic pyrophosphatase	GO:0016020;GO:0004427;GO:0015992;GO:0009678	[illegible]	NA
comp30273_c0_seq4.p1	Ec-01_011680.1	DNA ligase, ATP-dependent, C-terminal	GO:0006281;GO:0003910;GO:0051103;GO:0003909;GO:0006310	[illegible]	NA
comp68954_c0_seq1.p1	Ec-01_011700.1	G protein-coupled receptor GCR1 putative	n/a;n/a;n/a	[illegible]	NA
comp26905_c0_seq2.p1	Ec-01_011710.1	putative LuxR domain protein	GO:0003700;GO:0005622;GO:0006355;GO:0043565	NA	NA
comp34116_c0_seq1.p1	Ec-01_011720.1	Tetratricopeptide-like helical domain	GO:0005515	[illegible]	NA
comp31161_c0_seq2.p1	Ec-01_011730.1	UBA-like	GO:0005515	[illegible]	NA
comp28865_c1_seq4.p1	Ec-01_011750.1	tRNA/rRNA methyltransferase, SpoU type	GO:0003723;GO:0006396;GO:0008173	[illegible]	NA
comp35305_c0_seq1.p1	Ec-01_011760.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp31380_c2_seq1.p1	Ec-01_011770.1	CCR4-Not complex component, Not N-terminal domain	GO:0005634;GO:0006355	[illegible]	NA
comp11976_c0_seq1.p1	Ec-01_011790.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	[illegible]	NA
comp32368_c1_seq9.p1	Ec-01_011820.1	MTIF2, mitochondrial translation initiation factor 2	n/a;n/a;n/a	[illegible]	NA
comp13000_c0_seq1.p1	Ec-01_011830.1	DUF1279 domain protein	n/a;n/a;n/a	[illegible]	NA
comp19976_c0_seq1.p1	Ec-01_011850.1	Ribosomal protein L17	GO:0005840;GO:0005622;GO:0006412;GO:0003735	[illegible]	NA
comp21306_c0_seq2.p1	Ec-01_011860.1	Ribosomal protein L22e	GO:0005840;GO:0005622;GO:0006412;GO:0003735	[illegible]	NA
comp33619_c0_seq1.p1	Ec-01_011870.1	Ribosomal protein L10/acidic P0	GO:0005622;GO:0042254	[illegible]	NA
comp31989_c0_seq3.p1	Ec-01_011880.1	separin	GO:0005634;GO:0006508;GO:0008233	Coil:	NA
comp32325_c1_seq1.p2	Ec-01_011910.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270	[illegible]	NA
comp24179_c0_seq1.p1	Ec-01_011930.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp24179_c0_seq1.p2	Ec-01_011940.1	Mediator complex, subunit Med6	GO:0016592;GO:0001104;GO:0006357	[illegible]	NA
comp20690_c0_seq1.p1	Ec-01_011950.1	Ribosomal protein L13, eukaryotic/archaeal	GO:0015934;GO:0006412;GO:0003735	[illegible]	NA
comp20669_c0_seq1.p1	Ec-01_011970.1	50S ribosomal protein L30e-like	GO:0006412;n/a	[illegible]	NA
comp12885_c0_seq1.p1	Ec-01_011980.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp31859_c1_seq2.p1	Ec-01_012000.2	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp30796_c1_seq1.p1	Ec-01_012020.1	NB-ARC and TPR repeat-containing protein	NA	[illegible]	NA
comp29999_c0_seq5.p1	Ec-01_012030.1	gamma tubulin ring complex protein	GO:0005856;GO:0005815;GO:0000922;GO:0000226;GO:0007020	[illegible]	KOG2000
comp28909_c0_seq1.p1	Ec-01_012040.1	Protein phosphatase 2C	n/a;GO:0004722;GO:0006470	[illegible]	NA
comp13001_c0_seq1.p1	Ec-01_012050.1	expressed unknown protein	GO:0008649;GO:0046677	[illegible]	NA
comp33708_c0_seq1.p1	Ec-01_012060.1	possible ABC-like protein kinase	NA	NA	NA
comp25098_c0_seq3.p1	Ec-01_012080.1	Cysteine synthase	GO:0003824;GO:0008152;GO:0030170	[illegible]	KOG1252
comp20773_c0_seq1.p1	Ec-01_012090.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp15942_c0_seq2.p1	Ec-01_012140.1	Protein of unknown function DUF4336	n/a;n/a;n/a	[illegible]	NA
comp34828_c0_seq1.p1	Ec-01_012150.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp20205_c0_seq1.p1	Ec-01_012160.1	hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp30805_c0_seq3.p1	Ec-01_012170.1	Zinc finger, MYND-type	GO:0008270	[illegible]	NA
comp17207_c1_seq1.p1	Ec-01_012180.1	uncharacterized protein	GO:0008236;GO:0016021;n/a	[illegible]	NA
comp32027_c1_seq5.p2	Ec-01_012190.1	tRNA (cytosine-5-)-methyltransferase	GO:0003677;GO:0008168;GO:0006306	[illegible]	NA

comp32027_c1_seq5.p1	Ec-01_012200.1	General substrate transporter	GO:0055085;GO:0016021;GO:0022857	IPR005829: Sugar transporter, conserved site; IPR005828: General substrate transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; PTHR24064: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33990_c0_seq1.p1	Ec-01_012260.2	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29601_c0_seq2.p1	Ec-01_012290.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33215_c1_seq2.p1	Ec-01_012300.1	WSC-domain containing protein	NA	PTHR19328: ; IPR013994: Carbohydrate-binding WSC, subgroup; IPR012938: Glucose/Sorbosone dehydrogenase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR002889: Carbohydrate-binding WSC; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011042: Six-bladed beta-propeller, TolB-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR011041: Soluble quinoprotein glucose/sorbosone dehydrogenase; PTHR19328:SF13: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27115_c0_seq9.p1	Ec-02_000050.1	conserved unknown protein	GO:0005509	IPR018247: EF-Hand 1, calcium-binding site; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; Coil:	NA
comp28753_c0_seq1.p1	Ec-02_000060.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp45219_c0_seq1.p1	Ec-02_000070.1	Domain of unknown function DUF4483	n/a;n/a;n/a	IPR029147: Domain of unknown function DUF4483	NA
comp24510_c0_seq2.p1	Ec-02_000090.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp34869_c0_seq1.p1	Ec-02_000100.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp22313_c0_seq3.p1	Ec-02_000120.1	alpha-SNAP	GO:0006886;GO:0005515	SSF48452: ; IPR000744: NSF attachment protein; IPR011990: Tetratricopeptide-like helical domain; PF14938: Soluble NSF attachment protein, SNAP	KOG1586
comp25106_c0_seq1.p1	Ec-02_000130.1	conserved unknown protein	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp28786_c0_seq1.p1	Ec-02_000170.1	Nucleoporin interacting component Nup93/Nic96	GO:0006810;GO:0005643	IPR007231: Nucleoporin interacting component Nup93/Nic96	NA
comp20503_c0_seq2.p1	Ec-02_000190.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32230_c1_seq9.p1	Ec-02_000210.1	Snf7 family	GO:0007034	IPR005024: Snf7 family; Coil: ; PTHR10476:	NA
comp29923_c0_seq8.p1	Ec-02_000250.1	conserved unknown protein	GO:0008270	IPR007527: Zinc finger, SWIM-type	NA
comp20296_c0_seq2.p2	Ec-02_000260.1	hypothetical protein	GO:0006508;GO:0008236;GO:0016020;GO:0016021	IPR002885: Pentatricopeptide repeat	NA
comp19391_c0_seq2.p1	Ec-02_000270.1	Calcineurin-like phosphoesterase domain, apaH type	GO:0016787	IPR029052: Metallo-dependent phosphatase-like; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; IPR006186: Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase; PTHR11668:	NA
comp20296_c0_seq3.p1	Ec-02_000320.1	Conserved hypothetical protein CHP01589, plant	n/a;n/a;n/a	PTHR31871:SF1 : ; PTHR31871 : ; IPR006476: Conserved hypothetical protein CHP01589, plant; IPR000104: Antifreeze protein, type I	NA
comp27564_c1_seq2.p1	Ec-02_000340.1	EMP/nonaspanin domain family protein	GO:0016021	PTHR10766:SF1 : ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004240: Nonaspanin (TM9SF)	NA
comp27564_c0_seq1.p1	Ec-02_000350.1	UAA transporter	GO:0055085	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR10778:SF13: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013657: UAA transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10778: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30805_c0_seq1.p1	Ec-02_000370.1	Mediator complex, subunit Med22	GO:0016592;GO:0001104;GO:0006357	IPR009332: Mediator of RNA polymerase II transcription subunit 22; Coil:	NA
comp32685_c0_seq18.p1	Ec-02_000410.1	expressed unknown protein	GO:0005783	NA	NA
comp19624_c0_seq3.p1	Ec-02_000430.1	Glutaredoxin	GO:0009055;GO:0015035;GO:0045454	IPR002109: Glutaredoxin; PTHR10168: ; SIGNAL_PEPTIDE: Signal peptide region; IPR014025: Glutaredoxin subgroup; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR011767: Glutaredoxin active site; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1752
comp31678_c0_seq7.p1	Ec-02_000440.1	SURF1/SHY1 homolog, cytochrome c oxidase assembly protein	GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR23427: ; IPR002994: Surfeit locus 1/Shy1; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1563
comp32537_c0_seq4.p1	Ec-02_000470.1	Catalase	GO:0006979;GO:0020037;GO:0004096;GO:0004601;GO:0055114	NA	NA
comp30008_c0_seq1.p1	Ec-02_000480.1	Cytochrome b5-like heme/steroid binding domain	GO:0020037	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001433: Oxidoreductase FAD/NAD(P)-binding; IPR010255: Haem peroxidase; IPR019791: Haem peroxidase, animal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR005018: DOMON domain; SIGNAL_PEPTIDE: Signal peptide region; IPR001199: Cytochrome b5-like heme/steroid binding domain; PTHR11475: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF52343: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:3.40.50.80: ; SignalP-noTM: ; IPR006593: Cytochrome b561/ferric reductase transmembrane; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28460_c0_seq6.p1	Ec-02_000530.1	RGS domain	GO:0038032	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.10.167.10: ; IPR016137: RGS domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28150_c1_seq1.p1	Ec-02_000540.1	Ribosome biogenesis protein Nop53/GLTSCR2	n/a;n/a;n/a	NA	NA
comp31385_c0_seq3.p1	Ec-02_000580.2	Small acidic protein-like domain	GO:0003824;GO:0005488;GO:0008152	IPR028124: Small acidic protein-like domain	NA
comp21257_c0_seq1.p1	Ec-02_000590.1	predicted tubulin-tyrosin ligase	GO:0006464	IPR027750: Tubulin polyglutamylase TTLL1; SSF56059: ; IPR004344: Tubulin-tyrosine ligase/Tubulin polyglutamylase; PTHR12241:	KOG2157
comp25062_c0_seq2.p1	Ec-02_000610.1	Armadillo-like helical	GO:0005488	PF13513: HEAT-like repeat; IPR011989: Armadillo-like helical; PTHR10527: ; IPR016024: Armadillo-type fold	NA
comp30026_c0_seq2.p1	Ec-02_000620.1	YTH domain	n/a;n/a;n/a	PTHR12357: ; PTHR12357:SF15: ; IPR007275: YTH domain; Coil:	NA
comp29217_c1_seq9.p1	Ec-02_000630.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29244_c0_seq1.p1	Ec-02_000640.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824	IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C family	NA
comp34727_c0_seq1.p1	Ec-02_000650.1	Transcription factor IIIC, subunit 5	n/a;n/a;n/a	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR019136: Transcription factor IIIC, subunit 5	NA
comp30074_c0_seq1.p1	Ec-02_000660.1	SAP domain	GO:0003676;GO:0008270	IPR003034: SAP domain; IPR004087: K Homology domain; IPR004088: K Homology domain, type 1; IPR031150: BBP/SF1 family; IPR001878: Zinc finger, CCHC-type; PTHR11208: ; SSF68906:	NA
comp28962_c0_seq1.p1	Ec-02_000680.1	Tetratricopeptide-like helical domain	GO:0005515	IPR002885: Pentatricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; PTHR24015:	NA
comp18008_c0_seq1.p3	Ec-02_000700.1	Nuclear transport factor 2	GO:0005622;GO:0006810	IPR002075: Nuclear transport factor 2; PTHR12612: ; IPR018222: Nuclear transport factor 2, eukaryote; SSF54427: ; G3DSA:3.10.450.50:	NA
comp14918_c0_seq1.p1	Ec-02_000740.1	Dual specificity phosphatase, subgroup, catalytic domain	GO:0008138;GO:0006470	IPR029021: Protein-tyrosine phosphatase-like; IPR016130: Protein-tyrosine phosphatase, active site; IPR000387: Protein-tyrosine/Dual specificity phosphatase; IPR024950: Dual specificity phosphatase; IPR000340: Dual specificity phosphatase, catalytic domain; IPR020422: Dual specificity phosphatase, subgroup, catalytic domain	NA
comp31168_c0_seq3.p1	Ec-02_000830.1	Uncharacterised conserved protein UCP033563	n/a;n/a;n/a	IPR008323: Uncharacterised conserved protein UCP033563	NA
comp29849_c0_seq2.p1	Ec-02_000840.1	Tubby C-terminal-like domain	n/a;GO:0005515	IPR025659: Tubby C-terminal-like domain; IPR001609: Myosin head, motor domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR018066: Tubby, C-terminal, conserved site; Coil: ; IPR000007: Tubby, C-terminal; PTHR13140: ; IPR000048: IQ motif, EF-hand binding site	NA
comp34559_c0_seq1.p1	Ec-02_000850.1	Light harvesting complex protein	GO:0009765;GO:0016020	SIGNAL_PEPTIDE: Signal peptide region; IPR022796: Chlorophyll A-B binding protein; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023329: Chlorophyll a/b binding protein domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001344: Chlorophyll A-B binding protein, plant; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20969_c0_seq1.p1	Ec-02_000870.1	similar to 3-phosphoadenosine 5-phosphosulfate synthase 2 isoform 2	GO:0000287;GO:0004427;GO:0005737;GO:0006796	IPR015947: PUA-like domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR002891: Adenylyl-sulfate kinase; PTHR11055: ; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF52374: ; IPR025980: ATP-sulfurylase PUA-like domain; IPR024951: Sulphate adenylyltransferase catalytic domain; IPR008162: Inorganic pyrophosphatase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:3.10.400.10:	NA
comp27163_c0_seq2.p1	Ec-02_000920.1	Alpha/Beta hydrolase fold	GO:0016787	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000073: Alpha/beta hydrolase fold-1; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10992:	NA
comp31476_c0_seq1.p1	Ec-02_000930.1	Fanconi anaemia protein FANCD2	GO:0006281;GO:0005488	PTHR32086: ; IPR029448: Fanconi anaemia protein FANCD2; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold; Coil:	NA
comp30459_c0_seq48.p1	Ec-02_000950.1	VRR-NUC domain	GO:0016788	PTHR15749: ; IPR014883: VRR-NUC domain	NA
comp24644_c0_seq2.p1	Ec-02_000960.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp20790_c0_seq4.p1	Ec-02_000980.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20497_c0_seq1.p1	Ec-02_000990.1	NAD(P)-binding domain	GO:0055114;GO:0008270;GO:0016491	SSF51735: ; IPR011032: GroES (chaperonin 10)-like; IPR020843: Polyketide synthase, enoylreductase domain; IPR016040: NAD(P)-binding domain; IPR013154: Alcohol dehydrogenase GroES-like; IPR013149: Alcohol dehydrogenase, C-terminal; IPR002085: Alcohol dehydrogenase superfamily, zinc-type	NA
comp24766_c0_seq2.p1	Ec-02_001000.1	Histone deacetylase domain protein	NA	NA	NA
comp31197_c0_seq2.p1	Ec-02_001010.1	HAD-like domain	GO:0005524;GO:0006754;GO:0006810;GO:0015662;GO:0016020	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF12710: haloacid dehalogenase-like hydrolase; IPR023299: P-type ATPase, cytoplasmic domain N; IPR008250: P-type ATPase, A domain; SSF81653: ; IPR032631: P-type ATPase, N-terminal; IPR023214: HAD-like domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR032630: P-type ATPase, C-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006539: P-type ATPase, subfamily IV; SSF81665: ; IPR001757: P-type ATPase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR018303: P-type ATPase, phosphorylation site	NA
comp21128_c0_seq1.p1	Ec-02_001020.1	Succinate:CoA ligase (ADP-forming)	GO:0004775	IPR005809: Succinyl-CoA synthetase, beta subunit; IPR005811: ATP-citrate lyase/succinyl-CoA ligase; IPR017866: Succinyl-CoA synthetase, beta subunit, conserved site; SSF56059: ; IPR013816: ATP-grasp fold, subdomain 2; IPR013650: ATP-grasp fold, succinyl-CoA synthetase-type; IPR013815: ATP-grasp fold, subdomain 1; IPR016102: Succinyl-CoA synthetase-like	NA
comp31896_c1_seq1.p1	Ec-02_001070.1	ABC transporter type 1, transmembrane domain	GO:0006810;GO:0055085;GO:0005524;GO:0042626;GO:0016021;GO:0016887	IPR003439: ABC transporter-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:1.20.1560.10: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011527: ABC transporter type 1, transmembrane domain; PTHR24223: ; IPR017871: ABC transporter, conserved site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20938_c0_seq1.p1	Ec-02_001080.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp25604_c0_seq2.p1	Ec-02_001110.1	RGS domain	GO:0038032	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.10.167.10: ; IPR016137: RGS domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp51864_c0_seq1.p1	Ec-02_001130.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp12224_c0_seq1.p1	Ec-02_001140.1	Galactose-binding domain-like	GO:0006808;GO:0016564	SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; PTHR15020: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016040: NAD(P)-binding domain; IPR013857: NADH:ubiquinone oxidoreductase intermediate-associated protein 30; PF13460: NADH(P)-binding; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR008979: Galactose-binding domain-like; IPR008030: NmrA-like domain	NA
comp32893_c0_seq6.p1	Ec-02_001160.1	Pectin lyase fold	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011050: Pectin lyase fold/virulence factor; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR012334: Pectin lyase fold; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	NA
comp27366_c0_seq1.p1	Ec-02_001200.1	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25054_c0_seq2.p2	Ec-02_001230.1	Pyridoxamine kinase	NA	IPR004625: Pyridoxal phosphate (active vitamin B6) biosynthesis, pyridoxal kinase; PR01228: Eggshell protein signature; IPR029056: Ribokinase-like; IPR013749: Pyridoxamine kinase/Phosphomethylpyrimidine kinase	NA
comp32023_c0_seq8.p1	Ec-02_001250.1	Serine/threonine-protein kinase CTR1	GO:0016772	PTHR23257: ; IPR000719: Protein kinase domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR020635: Tyrosine-protein kinase, catalytic domain; PIRSF000654: ; IPR011009: Protein kinase-like domain	NA
comp33187_c0_seq4.p1	Ec-02_001270.1	TPX2	GO:0005819;GO:0005874;GO:0007067	Coil: ; IPR027330: TPX2 central domain; IPR009675: TPX2	NA
comp31997_c0_seq3.p1	Ec-02_001290.4	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp32057_c0_seq2.p1	Ec-02_001380.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0005524;GO:0006468;GO:0004672	PTHR24349: ; IPR017441: Protein kinase, ATP binding site; IPR018247: EF-Hand 1, calcium-binding site; G3DSA:3.30.200.20: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; SSF47473: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR000719: Protein kinase domain; G3DSA:1.10.510.10:	KOG0032
comp30489_c0_seq2.p1	Ec-02_001390.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	IPR015324: Ribosomal protein Rsm22, bacterial-type; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR007533: Cytochrome c oxidase assembly protein CtaG/Cox11	NA
comp26969_c0_seq1.p1	Ec-02_001400.1	COP9 signalosome complex subunit 5a	GO:0005515	IPR000555: JAB1/MPN/MOV34 metalloenzyme domain; G3DSA:3.40.140.10: ; SSF102712: ; PTHR10410:	NA
comp19801_c0_seq1.p1	Ec-02_001410.1	Jumonji domain protein	n/a;n/a;n/a	NA	NA
comp20575_c0_seq1.p1	Ec-02_001420.1	nicolin 1	n/a;n/a;n/a	PTHR31239: ; PD868899: NUCLEAR NICOLIN-1 KIDNEY RIKEN PRODUCT:NICOLIN EMBRYO CDNA ENRICHED FULL-LENGTH LIBRARY	NA
comp35742_c0_seq1.p1	Ec-02_001435.1	hypothetical protein	GO:0003735;GO:0005622;GO:0005840;GO:0006412	IPR000554: Ribosomal protein S7e	NA
comp32374_c8_seq3.p1	Ec-02_001440.1	Phospholipid/glycerol acyltransferase	GO:0016746;GO:0008152	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002123: Phospholipid/glycerol acyltransferase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF69593: ; PTHR31605: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32457_c0_seq23.p1	Ec-02_001450.1	RNA recognition motif domain	GO:0003676;GO:0000166	SSF54928: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; PTHR23003:	NA
comp24964_c0_seq1.p1	Ec-02_001460.1	mitochondrial helicase twinkle	GO:0005524;GO:0006260;GO:0043139;GO:0003697;GO:0003678	SSF56731: ; IPR003593: AAA+ ATPase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR006171: Toprim domain; IPR007694: DNA helicase, DnaB-like, C-terminal; PF13481: AAA domain; G3DSA:3.40.1360.10: ; IPR027032: Twinkle-like protein	NA
comp13049_c0_seq2.p1	Ec-02_001470.1	60S ribosomal protein L6E	GO:0003735;GO:0005622;GO:0005840;GO:0006412	IPR000915: 60S ribosomal protein L6E; IPR008991: Translation protein SH3-like domain; IPR014722: Ribosomal protein L2 domain 2	NA
comp31320_c0_seq1.p2	Ec-02_001480.1	AARP2CN	GO:0005634;GO:0042254	IPR030387: Bms1/Tsr1-type G domain; IPR012948: AARP2CN; PTHR12858: ; IPR007034: Ribosome biogenesis protein BMS1/TSR1, C-terminal	NA
comp31320_c0_seq1.p1	Ec-02_001490.1	Paired amphipathic helix	GO:0005634;GO:0006355	PTHR12346: ; IPR013194: Histone deacetylase interacting domain; IPR031693: Sin3, C-terminal; PTHR12346:SF0: ; Coil: ; IPR003822: Paired amphipathic helix	NA
comp14281_c0_seq2.p1	Ec-02_001510.1	Meiosis-specific nuclear structural protein 1	n/a;n/a;n/a	IPR026504: Meiosis-specific nuclear structural protein 1; PF13868: Tumour suppressor, Mitostatin; Coil: ; PTHR19265:	NA
comp35115_c0_seq1.p1	Ec-02_001530.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0003723;GO:0005634;GO:0006364;GO:0008033;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; G3DSA:3.30.200.20: ; PTHR10335: ; IPR000692: Fibrillarin	NA
comp19755_c0_seq1.p1	Ec-02_001540.1	agmatine deiminase	GO:0004668;GO:0047632;GO:0009446	SSF55909: ; G3DSA:3.75.10.10: ; IPR017754: Agmatine deiminase; IPR007466: Peptidyl-arginine deiminase, Porphyromonas-type; PTHR31377:	no relat
comp30047_c0_seq1.p1	Ec-02_001560.1	Ovarian tumour, otubain	n/a;n/a;n/a	IPR031084: OTU domain-containing protein 5/Otubain-like deubiquitinase 1; IPR003323: OTU domain; SSF54001: ; PTHR12419:	NA
comp30778_c0_seq4.p1	Ec-02_001570.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp31916_c0_seq4.p1	Ec-02_001580.1	Magnesium chelatase subunit D, putative chloroplast precursor	NA	G3DSA:1.10.8.80: ; IPR000523: Magnesium chelatase ChlI domain; SIGNAL_PEPTIDE: Signal peptide region; IPR011776: Magnesium chelatase, ATPase subunit D; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10338: ; PTHR10338:SF126: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002035: von Willebrand factor, type A	NA
comp33961_c0_seq1.p2	Ec-02_001590.3	EPS15 homology (EH)	GO:0005515	IPR000261: EH domain; SSF52047: ; PTHR11216: ; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR032675: Leucine-rich repeat domain, L domain-like; PTHR11216:SF61:	NA
comp20469_c0_seq1.p1	Ec-02_001620.1	conserved unknown protein	n/a;n/a;n/a	SSF57850:	NA
comp20717_c0_seq1.p1	Ec-02_001640.1	Protein kinase-like domain	GO:0004672;GO:0005524;GO:0006468;GO:0016772	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:1.10.510.10: ; PTHR24362: ; IPR011009: Protein kinase-like domain	NA
comp25729_c0_seq2.p1	Ec-02_001650.3	Hypothetical leucine rich repeat protein	GO:0005515	IPR018247: EF-Hand 1, calcium-binding site; IPR002048: EF-hand domain; IPR001611: Leucine-rich repeat; IPR032675: Leucine-rich repeat domain, L domain-like; PTHR15454:	NA
comp32779_c0_seq8.p1	Ec-02_001660.1	Lipase domain protein	GO:0003824;GO:0004806;GO:0006629	IPR002921: Fungal lipase-like domain; IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR21493: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	no relat
comp72526_c0_seq1.p1	Ec-02_001670.2	Ankyrin repeat-containing domain	n/a;n/a;n/a	PF13637: Ankyrin repeats (many copies); IPR020683: Ankyrin repeat-containing domain; Coil: ; PTHR24123: ; IPR002110: Ankyrin repeat; IPR000048: IQ motif, EF-hand binding site	NA
comp29491_c0_seq1.p1	Ec-02_001710.1	Mitochondrial substrate/solute carrier	n/a;n/a;n/a	PTHR24089: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20744_c0_seq1.p1	Ec-02_001720.1	Mitochondrial TOM complex subunit, Tom40 homolog	GO:0006820;GO:0055085;GO:0008308;GO:0005741	PTHR10802: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR027246: Eukaryotic porin/Tom40; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023614: Porin domain	KOG3296
comp12437_c0_seq1.p1	Ec-02_001740.1	ascorbate peroxidase	GO:0020037;GO:0006118;GO:0055114;GO:0006979;GO:0004601	G3DSA:1.10.520.10: ; IPR010255: Haem peroxidase; IPR002207: Plant ascorbate peroxidase; G3DSA:1.10.420.10: ; PTHR31356: ; IPR002016: Haem peroxidase, plant/fungal/bacterial	NA
comp24902_c0_seq1.p1	Ec-02_001760.1	dhm exonuclease	GO:0005622;GO:0003676;GO:0004527	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027073: 5'-3' exoribonuclease; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR004859: Putative 5-3 exonuclease; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp24902_c0_seq1.p2	Ec-02_001770.1	Dynein heavy chain	GO:0003777;GO:0007018	IPR013602: Dynein heavy chain, domain-2; IPR026980: Dynein heavy chain 6, axonemal; IPR028034: Domain of unknown function DUF4496; IPR026983: Dynein heavy chain	NA
comp30649_c0_seq3.p1	Ec-02_001930.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp27745_c0_seq3.p1	Ec-02_001940.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp26946_c0_seq1.p1	Ec-02_001950.1	Homeodomain-like	GO:0003677	IPR016827: Transcriptional adaptor 2; PTHR12374: ; SSF57850: ; IPR009057: Homeodomain-like; Coil:	NA
comp30540_c0_seq5.p1	Ec-02_001960.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29900_c1_seq1.p1	Ec-02_001970.1	Apyrase	GO:0005509;GO:0016462	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR009283: Apyrase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29150_c0_seq4.p1	Ec-02_001980.1	C2 domain	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000008: C2 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp14726_c0_seq2.p1	Ec-02_002020.1	Thioredoxin-like fold	n/a;n/a;n/a	IPR004123: mRNA splicing factor, thioredoxin-like U5 snRNP; IPR012336: Thioredoxin-like fold	NA
comp27041_c0_seq2.p1	Ec-02_002040.1	acyltransferase	GO:0016746;GO:0008152	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR10983: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002123: Phospholipid/glycerol acyltransferase; SSF69593: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1505
comp27180_c0_seq4.p1	Ec-02_002050.1	Ubiquitin-like	GO:0005515	G3DSA:3.10.20.90: ; PTHR10666: ; IPR019956: Ubiquitin; IPR019954: Ubiquitin conserved site; IPR029071: Ubiquitin-related domain; IPR000626: Ubiquitin-like; Coil:	NA
comp13142_c0_seq2.p1	Ec-02_002080.1	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20920_c0_seq1.p1	Ec-02_002090.1	EDG-8 sphingosine 1-phosphate receptor	GO:0007186;GO:0038036;GO:0016021	IPR005386: EDG-8 sphingosine 1-phosphate receptor; Coil:	NA
comp34404_c0_seq1.p1	Ec-02_002170.1	Serine incorporator/TMS membrane protein	GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR029559: Membrane protein Tms1-like; IPR005016: Serine incorporator/TMS membrane protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	NA
comp32721_c2_seq1.p1	Ec-02_002190.1	C2 domain	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000008: C2 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25279_c0_seq1.p1	Ec-02_002200.1	FNIP	n/a;n/a;n/a	IPR008615: FNIP; SSF52058: ; PTHR32134:	NA
comp33745_c0_seq1.p1	Ec-02_002210.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp26980_c1_seq1.p1	Ec-02_002220.1	Bms1, nucleolar GTPase involved in the ribosome assembly	n/a;n/a;n/a	IPR030387: Bms1/Tsr1-type G domain; PTHR12858: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR012948: AARP2CN; PTHR12858:SF2: ; IPR007034: Ribosome biogenesis protein BMS1/TSR1, C-terminal; Coil:	NA
comp21552_c0_seq2.p1	Ec-02_002270.1	Cysteinyl-tRNA Synthetase	GO:0004817;GO:0005524;GO:0005737;GO:0006423;GO:0006418;GO:0000166;GO:0006412;GO:0004812	IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; SSF52374: ; G3DSA:1.20.120.640: ; IPR015803: Cysteine-tRNA ligase; IPR024909: Cysteinyl-tRNA synthetase/mycothiol ligase; Coil: ; IPR009080: Aminoacyl-tRNA synthetase, class 1a, anticodon-binding	KOG2007
comp26528_c0_seq1.p1	Ec-02_002280.1	Dynamitin	GO:0007067;GO:0005869;GO:0007017	PF04912: Dynamitin; Coil: ; IPR028133: Dynamitin; PTHR15346:	NA
comp19705_c0_seq2.p1	Ec-02_002310.1	Helicase and acetyltransferase (GNAT) domain protein	NA	NA	NA
comp12367_c0_seq1.p1	Ec-02_002320.1	AP2/ERF domain	GO:0006355;GO:0003700	IPR016177: DNA-binding domain; IPR001471: AP2/ERF domain	NA
comp32124_c4_seq2.p2	Ec-02_002330.1	Restriction endonuclease type II-like	n/a;n/a;n/a	IPR011335: Restriction endonuclease type II-like; PF12705: PD-(D/E)XK nuclease superfamily	NA
comp30271_c1_seq2.p1	Ec-02_002430.1	Digalactosyldiacylglycerol synthase, family GT4	GO:0009058	SSF53756: ; IPR001296: Glycosyl transferase, family 1; PTHR12526: ; G3DSA:3.40.50.2000:	no relat
comp29222_c0_seq1.p1	Ec-02_002450.2	C2 domain	GO:0005515	IPR000008: C2 domain	NA
comp32965_c0_seq15.p1	Ec-02_002470.1	WD40 repeat	GO:0005515	PTHR14221: ; IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; Coil:	NA
comp31502_c0_seq1.p1	Ec-02_002560.1	Hypothetical leucine rich repeat protein	GO:0005515	G3DSA:3.80.10.10: ; SSF52058: ; PTHR23311: ; IPR001611: Leucine-rich repeat; Coil:	NA
comp28847_c0_seq2.p1	Ec-02_002570.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10281: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF09335: SNARE associated Golgi protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31977_c0_seq7.p1	Ec-02_002600.2	expressed unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; IPR024079: Metallopeptidase, catalytic domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13688: Metallo-peptidase family M12; SignalP-noTM: ; SSF55486: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28720_c0_seq3.p1	Ec-02_002670.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp27062_c0_seq1.p2	Ec-02_002700.1	Major facilitator superfamily domain	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11662: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11662:SF277: ; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27452_c0_seq1.p1	Ec-02_002710.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27013_c0_seq3.p1	Ec-02_002720.1	conserved unknown protein	n/a;n/a;n/a	PTHR33504:SF2: ; PTHR33504: ; IPR000048: IQ motif, EF-hand binding site	NA
comp31799_c0_seq1.p1	Ec-02_002730.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp25144_c0_seq1.p1	Ec-02_002740.1	RNA recognition motif domain	GO:0003676;GO:0000166	SSF54928: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; PTHR19965:	NA
comp30018_c0_seq2.p1	Ec-02_002750.1	EsV-1-7 domain protein	n/a;n/a;n/a	NA	NA
comp26636_c0_seq4.p1	Ec-02_002760.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28523_c0_seq1.p1	Ec-02_002780.1	F-box domain	GO:0005515	IPR001810: F-box domain; G3DSA:1.20.1280.50:	NA
comp26010_c0_seq1.p1	Ec-02_002790.1	Phosphatidylinositol-4-phosphate 5-kinase	GO:0016307;GO:0046488	IPR027483: Phosphatidylinositol-4-phosphate 5-kinase, C-terminal; IPR016034: Phosphatidylinositol-4-phosphate 5-kinase, core, subgroup; IPR023610: Phosphatidylinositol-4-phosphate 5-kinase; SSF56104: ; IPR002498: Phosphatidylinositol-4-phosphate 5-kinase, core; IPR027484: Phosphatidylinositol-4-phosphate 5-kinase, N-terminal domain	NA
comp12304_c0_seq1.p1	Ec-02_002820.1	predicted tubulin-tyrosin ligase	GO:0004835;GO:0006464	SSF56059: ; IPR004344: Tubulin-tyrosine ligase/Tubulin polyglutamylase; IPR027751: Probable tubulin polyglutamylase TTLL9; Coil: ; PTHR12241:	KOG2157
comp31844_c0_seq19.p1	Ec-02_002830.1	hypothetical protein	n/a;n/a;n/a	IPR011993: PH domain-like	NA
comp31253_c0_seq2.p1	Ec-02_002850.1	Sterol or diacylglycerol O-acyltransferase, partial	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004299: Membrane bound O-acyl transferase, MBOAT; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0380
comp28717_c0_seq1.p1	Ec-02_002870.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp27800_c0_seq3.p1	Ec-02_002880.1	Hypothetical leucine rich repeat protein	NA	G3DSA:3.80.10.10: ; PTHR23125: ; IPR006553: Leucine-rich repeat, cysteine-containing subtype; SSF52047: ; PF13516: Leucine Rich repeat	NA
comp33137_c0_seq13.p1	Ec-02_002940.1	Alpha-ketoglutarate-dependent dioxygenase FTO, catalytic domain	n/a;n/a;n/a	IPR015947: PUA-like domain; IPR024366: Alpha-ketoglutarate-dependent dioxygenase FTO, C-terminal; PTHR31291:SF2: ; IPR032868: Alpha-ketoglutarate-dependent dioxygenase FTO; IPR024367: Alpha-ketoglutarate-dependent dioxygenase FTO, catalytic domain; G3DSA:2.30.130.30:	NA
comp27939_c0_seq2.p1	Ec-02_003040.1	JAB1/MPN/MOV34 metalloenzyme domain	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR000555: JAB1/MPN/MOV34 metalloenzyme domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR024969: Rpn11/EIF3F C-terminal domain; PTHR10540: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29668_c0_seq2.p1	Ec-02_003050.1	Transport protein particle component (TRAPP)/ SPP30-like	NA	IPR007194: Transport protein particle (TRAPP) component; G3DSA:3.30.1380.20: ; IPR016696: TRAPP I complex, subunit 5; IPR024096: NO signalling/Golgi transport ligand-binding domain	NA
comp26280_c0_seq1.p1	Ec-02_003060.1	Diacylglycerol O-acyltransferase	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0380
comp30806_c1_seq1.p1	Ec-02_003090.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp20464_c0_seq2.p1	Ec-02_003100.1	Malate dehydrogenase	GO:0016616;GO:0003824;GO:0055114;GO:0005975	IPR010945: Malate dehydrogenase, type 2; IPR022383: Lactate/malate dehydrogenase, C-terminal; SSF51735: ; IPR016040: NAD(P)-binding domain; IPR001236: Lactate/malate dehydrogenase, N-terminal; IPR015955: Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal	KOG1496
comp26260_c0_seq1.p1	Ec-02_003120.1	S15/NS1, RNA-binding	GO:0003735;GO:0005840;GO:0006412;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR000589: Ribosomal protein S15; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR23321: ; IPR009068: S15/NS1, RNA-binding; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32722_c0_seq3.p2	Ec-02_003140.1	hypothetical protein	n/a;n/a;n/a	mobidb-lite: consensus disorder prediction	NA
comp26259_c0_seq1.p1	Ec-02_003190.1	HotDog domain	GO:0008152;GO:0016491	PTHR13078: ; IPR002539: MaoC-like domain; IPR029069: HotDog domain	NA
comp30303_c0_seq10.p1	Ec-02_003210.1	Zinc finger, RING/FYVE/PHD-type	GO:0005515;GO:0008270	IPR001841: Zinc finger, RING-type; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR22996: ; PF13920: Zinc finger, C3HC4 type (RING finger); SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29958_c0_seq1.p1	Ec-02_003270.1	AAA+ ATPase domain	GO:0005524;GO:0006810;GO:0016021;GO:0016887;GO:0042626	PTHR11384: ; PTHR11384:SF28: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR003439: ABC transporter-like; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011527: ABC transporter type 1, transmembrane domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21182_c0_seq1.p1	Ec-02_003280.1	SAP domain	GO:0005622;GO:0006139;GO:0003676;GO:0008408	SSF56672: ; G3DSA:1.20.1060.10: ; PTHR10133: ; IPR002298: DNA polymerase A; IPR002562: 3'-5' exonuclease domain; SSF68906: ; IPR003034: SAP domain; G3DSA:1.10.150.20: ; IPR012337: Ribonuclease H-like domain; IPR001098: DNA-directed DNA polymerase, family A, palm domain; Coil: ; G3DSA:3.30.70.370:	NA
comp28871_c0_seq1.p1	Ec-02_003310.1	conserved unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28810_c0_seq1.p1	Ec-02_003320.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27998_c0_seq3.p1	Ec-02_003330.1	Molybdenum cofactor sulfurase, C-terminal	GO:0030151;GO:0003824;GO:0030170	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR011037: Pyruvate kinase-like, insert domain; PTHR14237: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005303: MOSC, N-terminal beta barrel; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR005302: Molybdenum cofactor sulfurase, C-terminal; SSF141673: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32721_c4_seq8.p1	Ec-02_003340.1	Ubiquinone biosynthesis O-methyltransferase	GO:0006744;GO:0008425	PF13489: Methyltransferase domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR010233: Ubiquinone biosynthesis O-methyltransferase; SignalP-TM:	NA
comp31859_c1_seq4.p1	Ec-02_003350.1	Short-chain dehydrogenase/reductase SDR	GO:0008152;GO:0016491	SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24320: ; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29004_c0_seq1.p1	Ec-02_003360.2	CRAL-TRIO domain	n/a;n/a;n/a	IPR001251: CRAL-TRIO lipid binding domain; IPR000306: FYVE zinc finger; IPR017455: Zinc finger, FYVE-related; G3DSA:1.10.8.20: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; PTHR23324: ; IPR011074: CRAL/TRIO, N-terminal domain	NA
comp33996_c0_seq1.p1	Ec-02_003380.3	EF-hand domain pair	GO:0005509	IPR011992: EF-hand domain pair; IPR002048: EF-hand domain	NA
comp19743_c0_seq1.p1	Ec-02_003410.1	ATPase, AAA-type, core	GO:0005524	PTHR11669: ; IPR003593: AAA+ ATPase domain; IPR003959: ATPase, AAA-type, core; G3DSA:1.20.272.10: ; IPR013748: Replication factor C, C-terminal domain; IPR008921: DNA polymerase III, clamp loader complex, gamma/delta/delta subunit, C-terminal; G3DSA:1.10.8.60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp28712_c0_seq2.p1	Ec-02_003420.1	SNF2-related and helicase domain protein	GO:0003677;GO:0005524	NA	NA
comp50188_c0_seq1.p1	Ec-02_003425.1	hypothetical protein	GO:0008080	IPR000182: GNAT domain; SIGNAL_PEPTIDE: Signal peptide region; mobidb-lite: consensus disorder prediction; PTHR43617: ; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; cd04301: NAT_SF; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp17344_c1_seq1.p2	Ec-02_003430.1	Hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31211_c0_seq2.p3	Ec-02_003440.1	Nucleophile aminohydrolases, N-terminal	GO:0051603;GO:0004298;GO:0005839;GO:0006511	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001353: Proteasome, subunit alpha/beta; IPR023333: Proteasome B-type subunit; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016050: Proteasome beta-type subunit, conserved site; IPR029055: Nucleophile aminohydrolases, N-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11599:	NA
comp31211_c0_seq7.p1	Ec-02_003450.1	Centromere-associated protein NUF2	GO:0000775;GO:0007067	PTHR21650: ; Coil: ; IPR005549: Kinetochore protein Nuf2	KOG4438
comp32171_c0_seq1.p1	Ec-02_003460.1	WD40 repeat	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; PTHR13720:	NA
comp32103_c0_seq40.p2	Ec-02_003510.1	Carbohydrate kinase PfkB	n/a;n/a;n/a	IPR011611: Carbohydrate kinase PfkB; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002173: Carbohydrate/puine kinase, PfkB, conserved site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR10584: ; IPR029056: Ribokinase-like	NA
comp28320_c0_seq4.p3	Ec-02_003520.1	HotDog domain	n/a;n/a;n/a	PTHR12418: ; IPR006683: Thioesterase superfamily; IPR029069: HotDog domain	NA
comp28320_c0_seq4.p1	Ec-02_003550.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp24443_c1_seq1.p1	Ec-02_003560.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31731_c2_seq2.p1	Ec-02_003570.1	hypothetical tRNA/rRNA methyltransferase	GO:0006396;GO:0003723;GO:0008168;GO:0008173;GO:0001510	IPR029028: Alpha/beta knot methyltransferases; IPR001537: tRNA/rRNA methyltransferase, SpoU type; IPR029026: tRNA (guanine-N1-)-methyltransferase, N-terminal; PTHR12029: ; IPR016914: tRNA (cytidine/uridine-2'-O-)-methyltransferase	NA
comp28450_c0_seq4.p1	Ec-02_003580.1	WD40-repeat-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp19429_c0_seq2.p1	Ec-02_003600.1	Chromatin modification-related protein vid-21	GO:0004871;GO:0007165	IPR000014: PAS domain; Coil: ; G3DSA:3.30.450.20:	NA
comp30554_c0_seq4.p1	Ec-02_003620.1	SWIRM domain protein	GO:0005515	NA	NA
comp31074_c0_seq6.p1	Ec-02_003630.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp19758_c0_seq2.p1	Ec-02_003640.1	Uncharacterised protein family UPF0047	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR30615: ; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; IPR001602: Uncharacterised protein family UPF0047; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31332_c0_seq9.p1	Ec-02_003650.1	Ribosomal L11 methyltransferase, PrmA	GO:0005737;GO:0006479;GO:0008276	PF06325: Ribosomal protein L11 methyltransferase (PrmA); PTHR18895: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase	NA
comp28940_c0_seq2.p1	Ec-02_003660.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	PTHR12277: ; IPR029058: Alpha/Beta hydrolase fold; IPR000073: Alpha/beta hydrolase fold-1	NA
comp31895_c2_seq7.p1	Ec-02_003670.1	Tetratricopeptide-like helical domain	GO:0005515	IPR011990: Tetratricopeptide-like helical domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR11102: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF81901: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006597: Sel1-like	NA
comp30286_c0_seq8.p1	Ec-02_003680.1	expressed unknown protein	GO:0005525;GO:0005874;GO:0007017	Coil:	NA
comp25159_c0_seq2.p2	Ec-02_003740.1	GSH-dependent dehydroascorbate reductase	GO:0005515	NA	NA
comp33756_c0_seq1.p1	Ec-02_003750.1	cyclin-dependent kinase	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil: ; PTHR24056:	KOG0594
comp32107_c0_seq4.p1	Ec-02_003760.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; Coil: ; IPR002110: Ankyrin repeat; PTHR24193:	NA
comp32107_c0_seq10.p2	Ec-02_003770.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp31760_c0_seq8.p1	Ec-02_003780.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR15394:	NA
comp27118_c0_seq2.p1	Ec-02_003840.1	Mitochondrial substrate/solute carrier	GO:0005488;GO:0006810;GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR24089: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25159_c0_seq2.p1	Ec-02_003850.1	GRAM domain	n/a;n/a;n/a	IPR004182: GRAM domain; Coil: ; PTHR23319:	NA
comp28216_c0_seq4.p1	Ec-02_003890.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp30222_c0_seq1.p1	Ec-02_003900.1	Nuclear pore localisation protein NPL4	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR007717: Nuclear pore localisation protein NPL4; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR12710: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp92402_c0_seq1.p1	Ec-02_003910.1	GAF domain-like	n/a;GO:0005515	PTHR11347: ; IPR029016: GAF domain-like; IPR003018: GAF domain	NA
comp31892_c0_seq2.p1	Ec-02_003920.1	putative transmembrane protein	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002794: Protein of unknown function DUF92, TMEM19; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG4491
comp26657_c0_seq2.p1	Ec-02_003930.2	EF-hand domain pair	GO:0004672;GO:0005524;GO:0006468	PTHR24349: ; IPR018247: EF-Hand 1, calcium-binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; PTHR24349:SF23: ; IPR000719: Protein kinase domain; G3DSA:1.10.510.10:	KOG0032
comp32683_c1_seq1.p1	Ec-02_003940.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR027640: Kinesin-like protein; Coil: ; IPR001752: Kinesin motor domain	NA
comp81224_c0_seq1.p1	Ec-02_003950.1	plectin isoform 1	GO:0006118;GO:0016491	Coil:	NA
comp32074_c0_seq5.p1	Ec-02_003980.1	Phox homologous domain	GO:0035091	Coil: ; IPR001683: Phox homologous domain	NA
comp31895_c2_seq5.p1	Ec-02_003990.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp31219_c1_seq1.p1	Ec-02_004010.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0005515	SIGNAL_PEPTIDE: Signal peptide region; IPR001623: DnaJ domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR015940: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR24076: ; G3DSA:1.10.8.10: ; IPR020683: Ankyrin repeat-containing domain; Coil: ; IPR009060: UBA-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp21417_c0_seq1.p2	Ec-02_004050.1	Mitochondrial protein import TIM9.10 complex subunit, Tim10 homolog	GO:0006626;GO:0042719;GO:0045039	IPR004217: Tim10/DDP family zinc finger; IPR027247: Mitochondrial import inner membrane translocase subunit Tim10/Tim12	KOG3480
comp32686_c2_seq3.p1	Ec-02_004060.1	Major facilitator superfamily domain	GO:0016020;GO:0008168;GO:0003676;GO:0016021;GO:0032259	SSF103481: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000620: EamA domain; IPR020846: Major facilitator superfamily domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:1.20.1250.20: ; PTHR23051: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31207_c0_seq3.p1	Ec-02_004080.1	Xylosyltransferase, family GT14	GO:0008375;GO:0016020	SIGNAL_PEPTIDE: Signal peptide region; IPR003406: Glycosyl transferase, family 14; PTHR19297: ; IPR000772: Ricin B lectin domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; G3DSA:2.80.10.50: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33925_c0_seq1.p1	Ec-02_004090.1	EIF2S3, gamma subunit of the eukaryotic translation initiation factor 2	n/a;n/a;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR009001: Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal; IPR000795: Transcription factor, GTP-binding domain; G3DSA:2.40.30.10: ; IPR004161: Translation elongation factor EFTu/EF1A, domain 2; PTHR23115: ; IPR015256: Translation initiation factor 2, gamma subunit, C-terminal; PF00009: Elongation factor Tu GTP binding domain; IPR009000: Translation protein, beta-barrel domain	NA
comp12140_c0_seq1.p1	Ec-02_004100.1	COP9 signalosome, subunit CSN8	n/a;n/a;n/a	PTHR13339: ; PF10075: COP9 signalosome, subunit CSN8	NA
comp19353_c0_seq1.p1	Ec-02_004130.1	Triose-phosphate transporter domain	n/a;n/a;n/a	IPR004853: Triose-phosphate transporter domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25139_c0_seq1.p1	Ec-02_004200.1	Zinc finger, C3HC4 RING-type	GO:0046872	IPR017907: Zinc finger, RING-type, conserved site; IPR001841: Zinc finger, RING-type; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR018957: Zinc finger, C3HC4 RING-type	NA
comp25139_c0_seq1.p2	Ec-02_004210.1	Thioredoxin domain	GO:0045454	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR18929: ; IPR013766: Thioredoxin domain; IPR012336: Thioredoxin-like fold; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34025_c0_seq1.p1	Ec-02_004250.1	Phox homologous domain	GO:0035091	IPR001683: Phox homologous domain	NA
comp24255_c0_seq1.p1	Ec-02_004270.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp29784_c0_seq4.p1	Ec-02_004290.1	Triose-phosphate transporter domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF103481: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13536: Multidrug resistance efflux transporter; IPR004853: Triose-phosphate transporter domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11132: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19371_c0_seq1.p1	Ec-02_004320.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp32239_c0_seq23.p1	Ec-02_004340.1	Sulfite reductase	GO:0055114;GO:0016491	SSF56014: ; IPR006067: Nitrite/sulphite reductase 4Fe-4S domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR005117: Nitrite/Sulfite reductase ferredoxin-like domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; G3DSA:3.30.413.10: ; PTHR11493: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11493:SF48:	NA
comp32623_c2_seq2.p1	Ec-02_004350.1	BTB/POZ-like	GO:0005515	IPR003131: Potassium channel tetramerisation-type BTB domain; IPR011333: BTB/POZ fold; IPR000210: BTB/POZ-like; G3DSA:3.30.710.10: ; Coil: ; PTHR14499:	NA
comp31207_c0_seq3.p2	Ec-02_004370.1	Anthranilate Synthase	GO:0003824;GO:0004049;GO:0005950;GO:0009058	IPR010112: Anthranilate synthase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR029062: Class I glutamine amidotransferase-like; PR00097: Anthranilate synthase component II signature; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015890: Chorismate-utilising enzyme, C-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE: Signal peptide region; PR00096: Glutamine amidotransferase superfamily signature; PTHR11236: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR006805: Anthranilate synthase component I, N-terminal; IPR005801: ADC synthase; SignalP-noTM: ; PTHR11236:SF22: ; IPR017926: Glutamine amidotransferase; IPR001789: Signal transduction response regulator, receiver domain; Coil:	KOG0026
comp32370_c0_seq18.p1	Ec-02_004390.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777	IPR019821: Kinesin motor domain, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR027640: Kinesin-like protein; Coil: ; IPR001752: Kinesin motor domain	NA
comp32878_c0_seq17.p1	Ec-02_004400.1	Transmembrane protein C5orf28-like	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR026572: Transmembrane protein C5orf28-like; PTHR13628:SF1: ; IPR007087: Zinc finger, C2H2; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12408_c0_seq1.p1	Ec-02_004410.1	expressed unknown protein	n/a;n/a;n/a	Coil: ; SignalP-TM:	NA
comp31967_c0_seq7.p2	Ec-02_004430.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp31967_c0_seq3.p1	Ec-02_004440.2	expressed unknown protein	n/a;n/a;n/a	IPR011989: Armadillo-like helical; Coil:	NA
comp30584_c0_seq7.p1	Ec-02_004520.1	Major facilitator superfamily domain	n/a;GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24003: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27431_c0_seq1.p1	Ec-02_004550.4	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	NA	NA
comp32125_c0_seq2.p1	Ec-02_004560.1	WW domain	GO:0005515	IPR001202: WW domain; Coil: ; PTHR11254: ; G3DSA:2.20.70.10:	NA
comp31343_c0_seq7.p1	Ec-02_004570.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp13081_c0_seq1.p1	Ec-02_004580.1	Type III Polyketide Synthase (phloroglucinol synthase)	GO:0008415;GO:0008152;GO:0003824	IPR016038: Thiolase-like, subgroup; IPR001099: Chalcone/stilbene synthase, N-terminal; IPR016039: Thiolase-like; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR011141: Polyketide synthase, type III; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR012328: Chalcone/stilbene synthase, C-terminal; PTHR11877: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26659_c0_seq1.p1	Ec-02_004660.1	zeta-carotene desaturase, chloroplast precursor	GO:0016719;GO:0055114;GO:0016117	SIGNAL_PEPTIDE: Signal peptide region; PTHR10742: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR014103: Zeta-carotene desaturase; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002937: Amine oxidase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF51905:	NA
comp30500_c0_seq15.p1	Ec-02_004730.2	Translin	n/a;n/a;n/a	PTHR21686:SF12: ; PTHR21686: ; IPR014810: Fcf2 pre-rRNA processing; Coil:	NA
comp28352_c0_seq4.p1	Ec-02_004740.1	Translin	GO:0043565	IPR016069: Translin, C-terminal; IPR002848: Translin; IPR016068: Translin, N-terminal; SignalP-TM:	NA
comp30500_c0_seq15.p2	Ec-02_004760.1	Major facilitator superfamily domain	n/a;GO:0055085;GO:0016021;GO:0022857	IPR005829: Sugar transporter, conserved site; IPR005828: General substrate transporter; IPR003663: Sugar/inositol transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; PTHR24063: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32235_c1_seq15.p1	Ec-02_004770.1	Protein of unknown function DUF2196	n/a;n/a;n/a	IPR019240: Protein of unknown function DUF2196; SignalP-TM:	NA
comp30933_c0_seq1.p1	Ec-02_004780.1	bHLH and PAS domain protein	GO:0007165;GO:0004871;GO:0046983	NA	NA
comp48494_c0_seq1.p1	Ec-02_004790.1	hypothetical protein	GO:0016491;GO:0055114	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015151: Beta-adaptin appendage, C-terminal subdomain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11926_c0_seq1.p1	Ec-02_004800.1	ATPase, AAA-type, core	GO:0005524	PTHR11669: ; IPR003593: AAA+ ATPase domain; IPR003959: ATPase, AAA-type, core; G3DSA:1.20.272.10: ; IPR008921: DNA polymerase III, clamp loader complex, gamma/delta/delta subunit, C-terminal; IPR013748: Replication factor C, C-terminal domain; G3DSA:1.10.8.60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp21268_c0_seq1.p1	Ec-02_004810.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp29834_c0_seq1.p1	Ec-02_004820.1	SAP and inner centromere, ARK-binding domain protein	n/a;n/a;n/a	NA	NA
comp20787_c0_seq2.p1	Ec-02_004860.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13414: TPR repeat; IPR011990: Tetratricopeptide-like helical domain; PTHR12760: ; IPR013026: Tetratricopeptide repeat-containing domain	NA
comp25970_c1_seq1.p1	Ec-02_004870.1	Metacaspase	GO:0006508;GO:0004197	PTHR31773: ; IPR029030: Caspase-like domain; IPR011600: Peptidase C14, caspase domain	KOG1546
comp19384_c0_seq2.p1	Ec-02_004880.1	FAR1 DNA binding domain	n/a;n/a;n/a	IPR004330: FAR1 DNA binding domain	NA
comp29807_c0_seq3.p1	Ec-02_004890.1	P-loop containing nucleoside triphosphate hydrolase	GO:0004140;GO:0005524;GO:0015937;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001977: Dephospho-CoA kinase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR10695: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29902_c0_seq3.p1	Ec-02_004900.1	Immunoglobulin E-set	n/a;n/a;n/a	IPR014756: Immunoglobulin E-set; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR017868: Filamin/ABP280 repeat-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013783: Immunoglobulin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25741_c0_seq1.p1	Ec-02_004920.1	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0006511;GO:0036459	IPR018200: Ubiquitin specific protease, conserved site; SSF54001: ; IPR028889: Ubiquitin specific protease domain; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase; PTHR24006:	NA
comp12008_c0_seq1.p2	Ec-02_004960.1	6-Phosphogluconolactonase	GO:0017057;GO:0006098;GO:0005975	PTHR11054: ; IPR006148: Glucosamine/galactosamine-6-phosphate isomerase; SSF100950: ; G3DSA:3.40.50.1360: ; IPR005900: 6-phosphogluconolactonase, DevB-type	NA
comp12008_c0_seq1.p1	Ec-02_004970.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21287_c0_seq1.p1	Ec-02_004980.1	Snf7 family	GO:0007034	IPR005024: Snf7 family; PTHR10476:	NA
comp11828_c0_seq2.p1	Ec-02_004990.1	Ubiquitin-like	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:3.10.20.90: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015496: Ubiquilin; IPR029071: Ubiquitin-related domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000626: Ubiquitin-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp13764_c0_seq1.p2	Ec-02_005010.1	photosystem II 11 kDa protein	GO:0010207	IPR025585: Photosystem II Pbs27; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp13764_c0_seq1.p1	Ec-02_005020.1	conserved unknown protein	n/a;n/a;n/a	IPR005135: Endonuclease/exonuclease/phosphatase	NA
comp29330_c0_seq6.p1	Ec-02_005040.1	Protein of unknown function DUF3326	GO:0015078;GO:0015986;GO:0016469;GO:0016820;GO:0033178	IPR021763: Protein of unknown function DUF3326	NA
comp29295_c0_seq3.p1	Ec-02_005080.1	Insulin-induced protein family	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR025929: Insulin-induced protein family; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26599_c0_seq2.p1	Ec-02_005090.1	P-loop containing nucleoside triphosphate hydrolase	GO:0008146	SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR10605: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000863: Sulfotransferase domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24883_c0_seq2.p1	Ec-02_005110.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR31326: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30316_c0_seq4.p4	Ec-02_005130.1	putative methylated-DNA--protein-cysteine methyltransferase	GO:0003824;GO:0006281	PTHR10815:SF5: ; IPR011991: Winged helix-turn-helix DNA-binding domain; IPR001497: Methylated-DNA-[protein]-cysteine S-methyltransferase, active site; PTHR10815: ; IPR014048: Methylated-DNA-[protein]-cysteine S-methyltransferase, DNA binding	NA
comp33196_c0_seq13.p1	Ec-02_005140.1	Phox homologous domain	GO:0035091	IPR001683: Phox homologous domain; PTHR15454:	NA
comp11747_c0_seq1.p1	Ec-02_005150.1	Leucine rich repeat protein	GO:0005515	G3DSA:3.80.10.10: ; PTHR24420: ; SSF52058: ; IPR001611: Leucine-rich repeat	NA
comp31448_c0_seq1.p2	Ec-02_005170.2	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR000629: ATP-dependent RNA helicase DEAD-box, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR24031: ; IPR014001: Helicase superfamily 1/2, ATP-binding domain; PTHR24031:SF25: ; Coil: ; IPR001650: Helicase, C-terminal	KOG0334
comp13138_c0_seq2.p1	Ec-02_005190.1	Amidophosphoribosyltransferase	GO:0008152	PTHR11907:SF4: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR029057: Phosphoribosyltransferase-like; IPR005854: Amidophosphoribosyltransferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029055: Nucleophile aminohydrolases, N-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PF13522: Glutamine amidotransferase domain; IPR017932: Glutamine amidotransferase type 2 domain; PTHR11907:	KOG0572
comp30316_c0_seq4.p1	Ec-02_005220.1	conserved unknown protein	GO:0005529	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp33755_c0_seq1.p1	Ec-02_005230.1	expressed unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28451_c0_seq1.p1	Ec-02_005250.1	Armadillo-type fold	GO:0005488	IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold; Coil:	NA
comp24347_c0_seq2.p1	Ec-02_005300.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0019201	IPR020618: Adenylate kinase isoenzyme 6; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PF13238: AAA domain; PTHR12595:	NA
comp28015_c1_seq1.p1	Ec-02_005310.1	DNA binding domain, putative	GO:0003723;GO:0004826;GO:0006412	SSF55681: ; IPR009061: DNA binding domain, putative; IPR005147: tRNA synthetase, B5-domain; IPR020825: Phenylalanyl-tRNA synthetase, B3/B4; G3DSA:3.30.930.10: ; IPR004531: Phenylalanyl-tRNA synthetase, class IIc, beta subunit, archae/euk cytosolic; PTHR10947: ; IPR005146: B3/B4 tRNA-binding domain	NA
comp28451_c0_seq1.p2	Ec-02_005320.1	Mgm1 homolog, dynamin-related GTPase	GO:0005525	IPR030381: Dynamin-type guanine nucleotide-binding (G) domain; IPR022812: Dynamin superfamily; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001401: Dynamin, GTPase domain; IPR020850: GTPase effector domain, GED; Coil: ; IPR000375: Dynamin central domain; PF00350: Dynamin family	NA
comp30801_c0_seq1.p1	Ec-02_005330.1	Thioredoxin reductase	GO:0050660;GO:0055114;GO:0016491	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PR00368: FAD-dependent pyridine nucleotide reductase signature; PTHR22912: ; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.50.50.60: ; IPR012999: Pyridine nucleotide-disulphide oxidoreductase, class I, active site; IPR004099: Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain; PR00411: Pyridine nucleotide disulphide reductase class-I signature; IPR006338: Thioredoxin/glutathione reductase selenoprotein; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR016156: FAD/NAD-linked reductase, dimerisation domain; IPR001327: Pyridine nucleotide-disulphide oxidoreductase, NAD-binding domain; SSF51905: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain	KOG4716
comp25232_c0_seq1.p1	Ec-02_005340.1	SAP domain	GO:0006281;GO:0004518	IPR020848: AP endonuclease 1, conserved site; SIGNAL_PEPTIDE: Signal peptide region; IPR004808: AP endonuclease 1; IPR005135: Endonuclease/exonuclease/phosphatase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF68906: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003034: SAP domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31063_c0_seq2.p1	Ec-02_005350.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34192_c0_seq1.p1	Ec-02_005360.1	aspartic protease PM5	GO:0004190;GO:0006508	IPR021109: Aspartic peptidase domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001461: Aspartic peptidase; IPR001969: Aspartic peptidase, active site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1339
comp30933_c0_seq1.p2	Ec-02_005380.1	PITH domain	n/a;n/a;n/a	PTHR12175: ; IPR010400: PITH domain; IPR008979: Galactose-binding domain-like	NA
comp21512_c0_seq2.p2	Ec-02_005390.1	Ribosomal protein L19/L19e domain	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR027547: Ribosomal protein L19/L19e; IPR000196: Ribosomal protein L19/L19e domain; IPR023638: Ribosomal protein L19/L19e conserved site; IPR015974: Ribosomal protein L19/L19e, domain 3; IPR015972: Ribosomal protein L19/L19e, domain 1; PTHR10722: ; Coil:	NA
comp31714_c0_seq7.p4	Ec-02_005410.1	Forkhead-associated (FHA) domain	GO:0005515	IPR008984: SMAD/FHA domain; Coil: ; IPR000253: Forkhead-associated (FHA) domain	NA
comp33832_c0_seq1.p1	Ec-02_005420.1	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	n/a;n/a;n/a	IPR011256: Regulatory factor, effector binding domain; IPR025870: Glyoxalase-like domain; IPR029068: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase; IPR029442: GyrI-like small molecule binding domain	NA
comp29472_c0_seq3.p1	Ec-02_005430.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp15919_c0_seq1.p1	Ec-02_005440.1	hypothetical protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32520_c2_seq10.p1	Ec-02_005450.1	Rab-GTPase-TBC domain	GO:0005097;GO:0032313	G3DSA:1.10.8.270: ; IPR000195: Rab-GTPase-TBC domain; PTHR22957:	NA
comp57999_c0_seq1.p1	Ec-02_005460.1	MORN domain repeat containing protein	n/a;n/a;n/a	G3DSA:2.20.110.10: ; PTHR23084: ; Coil: ; SSF82185: ; IPR003409: MORN motif	NA
comp28821_c0_seq1.p1	Ec-02_005470.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp12621_c0_seq1.p1	Ec-02_005500.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR12734: ; IPR022238: Uncharacterised protein family, methyltransferase, Williams-Beuren syndrome; IPR013216: Methyltransferase type 11	NA
comp29087_c0_seq11.p1	Ec-02_005510.1	Lycopene cyclase	GO:0016705;GO:0045436;GO:0016117	IPR008671: Lycopene cyclase-type, FAD-binding; G3DSA:3.50.50.60: ; IPR010108: Lycopene cyclase, beta/epsilon; SSF51905:	NA
comp28832_c0_seq5.p2	Ec-02_005540.1	Ribosomal protein L32e	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR001515: Ribosomal protein L32e; IPR018263: Ribosomal protein L32e, conserved site; PTHR23413:	NA
comp32648_c3_seq2.p1	Ec-02_005560.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp32648_c3_seq10.p2	Ec-02_005570.1	Six-bladed beta-propeller, TolB-like	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF63829: ; Coil: ; IPR011042: Six-bladed beta-propeller, TolB-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24649_c0_seq1.p1	Ec-02_005590.1	Zinc finger, MYND-type	GO:0008270	IPR002893: Zinc finger, MYND-type; SSF144232:	NA
comp26177_c0_seq1.p1	Ec-02_005600.1	Shikimate Kinase	GO:0004765;GO:0005524	IPR000623: Shikimate kinase/Threonine synthase-like 1; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR21087: ; PR01100: Shikimate kinase family signature	NA
comp32353_c2_seq9.p2	Ec-02_005610.1	Mpv17/PMP22	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007248: Mpv17/PMP22; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA

comp27078_c0_seq3.p1	Ec-02_005620.1	hypothetical protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27078_c0_seq3.p2	Ec-02_005630.1	BolA protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; PTHR12735: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002634: BolA protein	KOG2313
comp28214_c0_seq2.p1	Ec-02_005640.1	Amino acid/polyamine transporter I	GO:0016020;GO:0003333;GO:0015171	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002293: Amino acid/polyamine transporter I; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12841_c0_seq1.p1	Ec-02_005650.1	EamA domain	GO:0016020;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR12715: ; SSF103481: ; IPR000620: EamA domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20616_c0_seq1.p1	Ec-02_005660.1	Sel1-like	n/a;n/a;n/a	PTHR11102: ; IPR011990: Tetratricopeptide-like helical domain; SSF81901: ; IPR006597: Sel1-like	NA
comp31530_c1_seq2.p1	Ec-02_005670.1	Inositol monophosphatase	GO:0046854	G3DSA:3.30.540.10: ; IPR000760: Inositol monophosphatase; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.40.190.80: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF56655: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR020583: Inositol monophosphatase, metal-binding site; IPR020552: Inositol monophosphatase, Lithium-sensitive	KOG2951
comp31530_c0_seq4.p1	Ec-02_005680.1	Hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp157205_c0_seq1.p1	Ec-02_005690.3	Domain of unknown function DUF1736	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013105: Tetratricopeptide repeat 2; IPR013618: Domain of unknown function DUF1736; PTHR23083:SF401: ; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; PTHR23083: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30268_c0_seq1.p2	Ec-02_005710.1	GTP cyclohydrolase II, RibA	GO:0003935;GO:0009231	IPR000926: GTP cyclohydrolase II, RibA; SSF142695: ; PTHR21327:	NA
comp27271_c0_seq2.p1	Ec-02_005730.2	P-loop containing nucleoside triphosphate hydrolase	GO:0000166;GO:0005524;GO:0017111	IPR003959: ATPase, AAA-type, core; IPR003593: AAA+ ATPase domain; PTHR11262:SF4: ; G3DSA:1.10.8.60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR11262:	NA
comp77156_c0_seq1.p1	Ec-02_005740.1	EF-hand domain pair	n/a;GO:0005509	IPR018247: EF-Hand 1, calcium-binding site; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; Coil: ; SSF47473:	NA
comp30291_c3_seq1.p1	Ec-02_005750.1	Peptidase C78, ubiquitin fold modifier-specific peptidase 1/ 2	n/a;n/a;n/a	PTHR13226: ; IPR012462: Peptidase C78, ubiquitin fold modifier-specific peptidase 1/ 2	NA
comp29159_c0_seq1.p1	Ec-02_005760.1	Hypothetical protein	NA	NA	NA
comp32350_c0_seq4.p1	Ec-02_005760.2	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp32850_c0_seq21.p1	Ec-02_005770.1	conserved unknown protein	GO:0005515	IPR001478: PDZ domain; G3DSA:3.15.10.10: ; Coil:	NA
comp32850_c0_seq18.p1	Ec-02_005780.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp32850_c0_seq21.p2	Ec-02_005790.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp26840_c0_seq1.p1	Ec-02_005800.1	Folate-biopterin transporter	GO:0006810;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR31585: ; G3DSA:1.20.1250.20: ; PTHR31585:SF0: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004324: Folate-biopterin transporter	NA
comp24512_c0_seq1.p1	Ec-02_005810.1	conserved unknown protein	n/a;n/a;n/a	PTHR12681: ; Coil:	NA
comp26966_c1_seq1.p1	Ec-02_005820.1	Rab7L, RAB family GTPase	GO:0005525;GO:0007264;GO:0015031	SM00173: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SM00175: ; SM00176: ; SM00174: ; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; PS51419: small GTPase Rab1 family profile.; PTHR24073:SF57: ; PR00449: Transforming protein P21 ras signature; PTHR24073:	NA
comp26726_c0_seq2.p1	Ec-02_005830.1	Beta-propeller repeat	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR010620: Beta-propeller repeat; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21136_c0_seq1.p1	Ec-02_005840.1	HD/PDEase domain	GO:0003824	SSF109604: ; IPR006674: HD domain; IPR003607: HD/PDEase domain; PTHR11373:	NA
comp29400_c0_seq1.p1	Ec-02_005850.1	Myosin head, motor domain	GO:0005524;GO:0003774;GO:0005515;GO:0016459	IPR001609: Myosin head, motor domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR13140: ; IPR000048: IQ motif, EF-hand binding site	NA
comp32730_c0_seq4.p1	Ec-02_005870.1	RNaseIII	GO:0006396;GO:0003723;GO:0004525;GO:0016075	PTHR11207: ; IPR000999: Ribonuclease III domain	KOG0701
comp33218_c0_seq13.p1	Ec-02_005880.1	Peptidase S28	GO:0008236;GO:0006508	IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR008758: Peptidase S28; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26089_c0_seq2.p1	Ec-02_005890.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30460_c0_seq1.p1	Ec-02_005900.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp30460_c1_seq1.p1	Ec-02_005910.1	glutamyl tRNA amidotransferase, subunit A, n-terminal region	GO:0016884	SIGNAL_PEPTIDE: Signal peptide region; IPR000120: Amidase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR023631: Amidase signature domain; IPR020556: Amidase, conserved site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR004412: Glutamyl-tRNA(Gln) amidotransferase A subunit; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1211
comp33065_c0_seq14.p1	Ec-02_005930.1	poly(A) binding protein	GO:0003723;GO:0000166	SSF54928: ; IPR002004: Polyadenylate-binding protein/Hyperplastic disc protein; IPR000504: RNA recognition motif domain; IPR006515: Polyadenylate binding protein, human types 1, 2, 3, 4; IPR012677: Nucleotide-binding alpha-beta plait domain; Coil: ; PTHR24011:	NA
comp31641_c0_seq6.p1	Ec-02_005950.1	Protein kinase-like domain	GO:0006468;GO:0004672;GO:0016772	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain	NA
comp24573_c0_seq2.p1	Ec-02_005960.1	flagellar associated protein, quinone reductase-like protein	GO:0045892;GO:0010181;GO:0016491	IPR010089: Flavoprotein WrbA; IPR005025: NADPH-dependent FMN reductase-like; SIGNAL_PEPTIDE: Signal peptide region; IPR008254: Flavodoxin/nitric oxide synthase; IPR029039: Flavoprotein-like; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR30546: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG3135
comp25354_c0_seq6.p1	Ec-02_005970.1	RNA recognition motif domain, eukaryote	GO:0003676	SSF54928: ; PF14259: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain); IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; IPR003954: RNA recognition motif domain, eukaryote; PTHR23139:	NA
comp25354_c0_seq2.p3	Ec-02_005970.3	RNA recognition motif domain, eukaryote	GO:0003676	PF14259: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain); IPR000504: RNA recognition motif domain; SignalP-noTM: ; IPR012677: Nucleotide-binding alpha-beta plait domain; IPR003954: RNA recognition motif domain, eukaryote; PTHR23139:	NA
comp34133_c0_seq1.p1	Ec-02_005990.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp27219_c0_seq1.p1	Ec-02_006000.1	Glycosyl transferase family 90 domain protein	NA	IPR006598: Lipopolysaccharide-modifying protein; PTHR12203: ; Coil:	NA
comp30014_c0_seq1.p1	Ec-02_006010.1	Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase	n/a;GO:0055114;GO:0004764	IPR006151: Quinate/shikimate 5-dehydrogenase/glutamyl-tRNA reductase; IPR013785: Aldolase-type TIM barrel; SSF51735: ; G3DSA:3.40.192.10: ; IPR010110: Shikimate dehydrogenase, AroM-type; SSF53223: ; PTHR21090: ; SSF51569: ; IPR016040: NAD(P)-binding domain; IPR022893: Shikimate dehydrogenase family; IPR001381: 3-dehydroquinate dehydratase type I; IPR013708: Shikimate dehydrogenase substrate binding, N-terminal	KOG0692
comp20671_c0_seq1.p1	Ec-02_006020.1	Short-chain dehydrogenase/reductase SDR	GO:0008152;GO:0016491	PTHR24322: ; SSF51735: ; IPR016040: NAD(P)-binding domain; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR; IPR013968: Polyketide synthase, ketoreductase domain	NA
comp29884_c0_seq2.p1	Ec-02_006060.1	SGNH hydrolase-type esterase domain	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR014982: GSCFA; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013830: SGNH hydrolase-type esterase domain	NA
comp13637_c0_seq1.p1	Ec-02_006070.1	PDZ domain	GO:0005515	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; IPR001478: PDZ domain; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp25954_c0_seq2.p3	Ec-02_006080.1	Beta-grasp domain	GO:0006118;GO:0009055;GO:0051536	IPR001041: 2Fe-2S ferredoxin-type domain; IPR006058: 2Fe-2S ferredoxin, iron-sulphur binding site; IPR012675: Beta-grasp domain	NA
comp25954_c0_seq2.p1	Ec-02_006090.1	Domain of unknown function DUF1767	n/a;n/a;n/a	IPR032199: Recq-mediated genome instability protein 1, C-terminal OB-fold domain; PTHR14790: ; IPR013894: RecQ mediated genome instability protein, N-terminal; Coil:	NA
comp30485_c0_seq5.p1	Ec-02_006100.1	WD40 repeat	GO:0005515	PTHR14221: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp30291_c1_seq1.p1	Ec-02_006110.1	Homeodomain-like	GO:0003677	IPR009057: Homeodomain-like; IPR006600: HTH CenpB-type DNA-binding domain; Coil:	NA
comp29312_c0_seq1.p1	Ec-02_006160.1	1-acyl-sn-glycerol-3-phosphate acyltransferase	GO:0016746;GO:0008152;GO:0008415	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10434: ; IPR002123: Phospholipid/glycerol acyltransferase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF69593: ; G3DSA:3.40.1130.10: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2848
comp27086_c0_seq1.p1	Ec-02_006170.1	Acetyltransferase (GNAT) domain protein	n/a;n/a;n/a	NA	NA
comp31014_c0_seq2.p1	Ec-02_006180.2	steroid-5-alpha-reductase	GO:0003865;GO:0008202;GO:0016020;GO:0055114;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001104: 3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal; IPR016636: 3-oxo-5-alpha-steroid 4-dehydrogenase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10556: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1638
comp32256_c0_seq16.p1	Ec-02_006190.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28329_c0_seq1.p1	Ec-02_006210.1	WD40-repeat-containing domain	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR16317: ; IPR017986: WD40-repeat-containing domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31297_c0_seq1.p1	Ec-02_006260.1	expressed unknown protein	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp29589_c0_seq1.p1	Ec-02_006280.1	NAD-dependent epimerase/dehydratase, N-terminal domain	GO:0003824;GO:0050662	IPR001509: NAD-dependent epimerase/dehydratase, N-terminal domain; SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR10366:	NA
comp26901_c0_seq1.p1	Ec-02_006300.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp11896_c0_seq2.p1	Ec-02_006310.1	Leucyl aminopeptidase	GO:0005622;GO:0005737;GO:0008235;GO:0006508;GO:0004177;GO:0019538;GO:0030145	IPR000819: Peptidase M17, leucyl aminopeptidase, C-terminal; SSF52949: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR023042: Peptidase M17, leucine aminopeptidase; PTHR11963: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR008283: Peptidase M17, leucyl aminopeptidase, N-terminal; IPR011356: Leucine aminopeptidase/peptidase B; SSF53187: ; SignalP-noTM: ; G3DSA:3.40.630.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:3.40.220.10:	KOG2597
comp30871_c0_seq1.p3	Ec-02_006320.1	Ribosomal protein S17	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR012340: Nucleic acid-binding, OB-fold; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000266: Ribosomal protein S17; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30871_c0_seq1.p1	Ec-02_006330.1	Histidine phosphatase superfamily	GO:0003824;GO:0008152	IPR013078: Histidine phosphatase superfamily, clade-1; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR23029:SF26: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001345: Phosphoglycerate/bisphosphoglycerate mutase, active site; PTHR23029: ; IPR029033: Histidine phosphatase superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32349_c1_seq94.p1	Ec-02_006340.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33018_c5_seq10.p1	Ec-02_006340.2	expressed unknown protein	n/a;n/a;n/a	IPR007527: Zinc finger, SWIM-type	NA
comp27974_c0_seq2.p1	Ec-02_006360.1	Plastid lipid-associated protein/fibrillin conserved domain	GO:0005198	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR31906: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR006843: Plastid lipid-associated protein/fibrillin conserved domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp11802_c0_seq1.p1	Ec-02_006370.1	immunophilin	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp25083_c0_seq1.p1	Ec-02_006390.1	thioredoxin-related protein	GO:0045454;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005746: Thioredoxin; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0907
comp35666_c0_seq1.p1	Ec-02_006400.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp26753_c0_seq1.p1	Ec-02_006410.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29016_c0_seq1.p1	Ec-02_006430.1	long chain acyl-CoA synthetase	GO:0008152;GO:0003824	G3DSA:3.40.50.980: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000873: AMP-dependent synthetase/ligase; G3DSA:2.30.38.10: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR020845: AMP-binding, conserved site; PTHR24096: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF56801:	KOG1256
comp32886_c1_seq9.p1	Ec-03_000060.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0005524;GO:0006468;GO:0004672	IPR017441: Protein kinase, ATP binding site; IPR030616: Aurora kinase; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PIRSF000654: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR000719: Protein kinase domain; G3DSA:1.10.510.10:	NA
comp30350_c0_seq1.p1	Ec-03_000090.4	Inner centromere protein, ARK-binding domain	n/a;n/a;n/a	IPR003034: SAP domain; IPR005635: Inner centromere protein, ARK-binding domain	NA
comp32711_c1_seq28.p1	Ec-03_000110.1	FAD-binding, type 2, subdomain 1	GO:0008762;GO:0050660;GO:0003824;GO:0055114;GO:0016491	PTHR13878: ; IPR016167: FAD-binding, type 2, subdomain 1; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR016166: FAD-binding, type 2; IPR007173: D-arabinono-1,4-lactone oxidase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016169: CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2; IPR006093: Oxygen oxidoreductase covalent FAD-binding site; IPR016164: FAD-linked oxidase-like, C-terminal; IPR006094: FAD linked oxidase, N-terminal; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28209_c0_seq2.p1	Ec-03_000210.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13371: Tetratricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF13374: Tetratricopeptide repeat; IPR011717: Tetratricopeptide TPR-4; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; Coil: ; IPR019734: Tetratricopeptide repeat; PTHR23083: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27778_c0_seq3.p1	Ec-03_000220.1	Dihydroxy-acid dehydratase, N-terminal part	GO:0003824;GO:0008152	IPR004404: Dihydroxy-acid dehydratase; IPR020558: Dihydroxy-acid/6-phosphogluconate dehydratase, conserved site; SSF143975: ; IPR000581: Dihydroxy-acid/6-phosphogluconate dehydratase; IPR015928: Aconitase/3-isopropylmalate dehydratase, swivel	KOG2448
comp14522_c0_seq1.p1	Ec-03_000400.1	Conserved oligomeric Golgi complex subunit 7	GO:0006886;GO:0017119	IPR019335: Conserved oligomeric Golgi complex subunit 7; Coil:	NA
comp29870_c0_seq2.p2	Ec-03_000410.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29870_c0_seq2.p1	Ec-03_000420.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp32050_c0_seq1.p1	Ec-03_000450.1	hypothetical protein	GO:0003677;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32851_c1_seq21.p1	Ec-03_000480.1	FAD linked oxidase	GO:0000062;GO:0003824;GO:0008152;GO:0008609;GO:0008610;GO:0008762;GO:0016491;GO:0016614;GO:0016746;GO:0050660;GO:0055114	IPR025650: Alkyldihydroxyacetonephosphate synthase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR016167: FAD-binding, type 2, subdomain 1; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016166: FAD-binding, type 2; IPR016164: FAD-linked oxidase-like, C-terminal; IPR006094: FAD linked oxidase, N-terminal; IPR014352: FERM/acyl-CoA-binding protein, 3-helical bundle; mobidb-lite: consensus disorder prediction; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR004113: FAD-linked oxidase, C-terminal; IPR002123: Phospholipid/glycerol acyltransferase; PTHR11748: ; IPR016040: NAD(P)-binding domain; IPR016169: CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2; Coil: ; IPR013120: Male sterility, NAD-binding; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31185_c1_seq3.p1	Ec-03_000530.1	conserved unknown protein	n/a;n/a;n/a	SignalP-TM:	NA
comp30343_c0_seq16.p1	Ec-03_000550.1	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	GO:0003824;GO:0030170	IPR015424: Pyridoxal phosphate-dependent transferase; IPR004839: Aminotransferase, class I/classII; PTHR11751: ; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	NA
comp30324_c0_seq5.p1	Ec-03_000560.1	Uncharacterised protein family UPF0250	NA	IPR027471: YbeD-like domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR007454: Uncharacterised protein family UPF0250	NA
comp29053_c0_seq1.p1	Ec-03_000580.2	Hydroxymethylglutaryl-CoA reductase (NADPH)	GO:0004420;GO:0055114	IPR023076: Hydroxymethylglutaryl-CoA reductase, class I/II, conserved site; IPR009029: Hydroxymethylglutaryl-CoA reductase, class I/II, substrate-binding domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023074: Hydroxymethylglutaryl-CoA reductase, class I/II, catalytic domain; IPR009023: Hydroxymethylglutaryl-CoA reductase, class I/II, NAD/NADP-binding domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023282: Hydroxymethylglutaryl-CoA reductase, N-terminal; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002202: Hydroxymethylglutaryl-CoA reductase, class I/II	NA
comp31371_c0_seq4.p1	Ec-03_000600.1	hypothetical protein	n/a;GO:0005515	Coil: ; IPR000048: IQ motif, EF-hand binding site	NA
comp12400_c0_seq1.p1	Ec-03_000660.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	IPR020683: Ankyrin repeat-containing domain; PTHR24188: ; IPR002110: Ankyrin repeat	NA
comp108709_c0_seq1.p2	Ec-03_000670.1	expressed unknown protein	GO:0008270;GO:0016491;GO:0055114	NA	NA
comp31752_c1_seq15.p1	Ec-03_000680.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777	IPR019821: Kinesin motor domain, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR027640: Kinesin-like protein; Coil: ; IPR001752: Kinesin motor domain	KOG0240
comp9706_c0_seq2.p1	Ec-03_000740.1	imm upregulated 13	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp28608_c0_seq2.p1	Ec-03_000790.1	Tricarboxylate/iron carrier	GO:0016020;GO:0055085;GO:0015075;GO:0006811	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004686: Tricarboxylate/iron carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30343_c0_seq16.p2	Ec-03_000800.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	PF12847: Methyltransferase domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR026170: FAM173 family	NA
comp12504_c0_seq1.p1	Ec-03_000820.1	conserved unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21418_c0_seq1.p1	Ec-03_000840.1	Bestrophin/UPF0187	n/a;n/a;n/a	IPR021134: Bestrophin/UPF0187; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32764_c5_seq29.p1	Ec-03_000890.1	Flavoprotein	GO:0003824	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR003382: Flavoprotein; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14359: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33776_c0_seq1.p1	Ec-03_000900.1	NADH dehydrogenase (ubiquinone)	GO:0016651;GO:0022900	IPR006885: NADH dehydrogenase ubiquinone Fe-S protein 4, mitochondrial; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.30.160.190: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG3389
comp34751_c0_seq1.p1	Ec-03_000910.1	Rrp41 is a component of the exosome 3'->5' exoribonuclease complex, a complex that degrades mRNAs.	GO:0000175;GO:0003723;GO:0006396	PTHR11953: ; IPR015847: Exoribonuclease, phosphorolytic domain 2; IPR001247: Exoribonuclease, phosphorolytic domain 1; IPR020568: Ribosomal protein S5 domain 2-type fold; IPR027408: PNPase/RNase PH domain	NA
comp33509_c0_seq1.p1	Ec-03_000920.1	CS domain	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; PTHR12356: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR008978: HSP20-like chaperone; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR007052: CS domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27547_c0_seq2.p1	Ec-03_000930.2	conserved unknown protein	GO:0005634;GO:0006355;GO:0004402;GO:0008270;GO:0003712	IPR000197: Zinc finger, TAZ-type	NA
comp32529_c0_seq12.p1	Ec-03_000960.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24077: ; IPR001623: DnaJ domain; Coil: ; IPR002110: Ankyrin repeat	NA
comp12031_c0_seq1.p1	Ec-03_000990.1	HSP20-like chaperone	n/a;n/a;n/a	PTHR22932: ; IPR008978: HSP20-like chaperone	NA
comp33946_c0_seq1.p1	Ec-03_001000.1	Single-stranded nucleic acid binding R3H	GO:0003676	IPR015880: Zinc finger, C2H2-like; IPR001841: Zinc finger, RING-type; SIGNAL_PEPTIDE: Signal peptide region; IPR001374: Single-stranded nucleic acid binding R3H; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR22938: ; IPR007087: Zinc finger, C2H2; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21141_c0_seq1.p3	Ec-03_001010.1	Uncharacterised protein family UPF0047	n/a;n/a;n/a	PTHR30615: ; IPR001602: Uncharacterised protein family UPF0047	NA
comp29699_c0_seq4.p1	Ec-03_001030.1	Chromatin associated protein KTI12	n/a;n/a;n/a	PTHR20873: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32748_c1_seq1.p1	Ec-03_001040.1	conserved unknown protein	n/a;n/a;n/a	G3DSA:1.20.5.170: ; Coil:	NA
comp55117_c0_seq1.p1	Ec-03_001050.1	Meckelin	GO:0010826;GO:0042384;GO:0036038	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR019170: Meckelin; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR21274: ; SignalP-TM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34051_c0_seq1.p1	Ec-03_001070.1	Protein-tyrosine phosphatase-like	n/a;GO:0005515	IPR029021: Protein-tyrosine phosphatase-like; IPR016130: Protein-tyrosine phosphatase, active site; PTHR12305: ; IPR029023: Tensin phosphatase, lipid phosphatase domain; IPR014020: Tensin phosphatase, C2 domain; IPR000008: C2 domain; G3DSA:2.60.40.1110:	NA
comp29710_c0_seq1.p1	Ec-03_001090.1	Phosphatidylinositol 3-/4-kinase, catalytic domain	GO:0016773	G3DSA:3.30.1010.10: ; IPR000403: Phosphatidylinositol 3-/4-kinase, catalytic domain; IPR003151: PIK-related kinase, FAT; PTHR11139: ; IPR003152: PIK-related kinase, FATC; IPR011009: Protein kinase-like domain	NA
comp32396_c0_seq3.p1	Ec-03_001100.1	Armadillo-like helical	GO:0005488	IPR012582: NUC194; IPR011989: Armadillo-like helical; PTHR11139:SF68: ; PTHR11139: ; IPR016024: Armadillo-type fold	NA
comp20979_c0_seq1.p1	Ec-03_001120.1	Two pore domain potassium channel domain	n/a;n/a;n/a	SSF81324: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.10.287.70: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013099: Two pore domain potassium channel domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11959_c0_seq1.p1	Ec-03_001140.1	Band 7 protein	n/a;n/a;n/a	SSF117892: ; IPR001972: Stomatin family; IPR001107: Band 7 protein	NA
comp19431_c0_seq1.p1	Ec-03_001150.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp20365_c0_seq1.p1	Ec-03_001170.1	DPB3 class protein with histone-like transcription factor (NF-YC subunit) and high mobility group domains	GO:0005634;GO:0003677;GO:0006355;GO:0046982	NA	NA
comp30279_c0_seq4.p1	Ec-03_001180.2	P-loop containing nucleoside triphosphate hydrolase	GO:0000166;GO:0005524;GO:0017111	PTHR23073: ; IPR003959: ATPase, AAA-type, core; IPR003593: AAA+ ATPase domain; PTHR23073:SF29: ; G3DSA:1.10.8.60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SignalP-TM:	NA
comp32006_c1_seq9.p1	Ec-03_001220.1	Elongated TPR repeat-containing domain	n/a;n/a;n/a	IPR013078: Histidine phosphatase superfamily, clade-1; IPR029033: Histidine phosphatase superfamily; IPR023114: Elongated TPR repeat-containing domain; IPR014720: Double-stranded RNA-binding domain; SSF54768:	NA
comp32384_c0_seq9.p1	Ec-03_001240.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp31568_c0_seq1.p1	Ec-03_001270.3	SANT/Myb domain	GO:0003682	PTHR10641:SF538: ; PTHR10641: ; IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; Coil: ; IPR017930: Myb domain; IPR017877: Myb-like domain	NA
comp26381_c0_seq1.p1	Ec-03_001280.1	flagellar associated protein	GO:0005524;GO:0016887	PTHR19211: ; IPR003593: AAA+ ATPase domain; IPR003439: ABC transporter-like; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; PF12848: ABC transporter; IPR017871: ABC transporter, conserved site	NA
comp25857_c0_seq1.p1	Ec-03_001310.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp28934_c0_seq1.p1	Ec-03_001320.1	expressed unknown protein	GO:0006508;GO:0008236;GO:0016020;GO:0016021	NA	NA
comp25577_c1_seq1.p1	Ec-03_001370.1	beta tubulin	GO:0003924;GO:0005525;GO:0006184;GO:0043234;GO:0051258	IPR002453: Beta tubulin; IPR000217: Tubulin; IPR003008: Tubulin/FtsZ, GTPase domain; IPR023123: Tubulin, C-terminal; IPR008280: Tubulin/FtsZ, C-terminal; IPR013838: Beta tubulin, autoregulation binding site; IPR017975: Tubulin, conserved site; Coil: ; IPR018316: Tubulin/FtsZ, 2-layer sandwich domain	KOG1375
comp18541_c0_seq1.p1	Ec-03_001380.1	Nucleoside diphosphate kinase	GO:0005524;GO:0006241;GO:0006165;GO:0004550;GO:0006228;GO:0006183	PTHR11349: ; IPR006602: Uncharacterised domain DM10; IPR001564: Nucleoside diphosphate kinase	NA
comp27363_c0_seq1.p1	Ec-03_001400.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp27788_c0_seq2.p1	Ec-03_001410.1	Arginyl-tRNA Synthetase	GO:0005524;GO:0004814;GO:0006420	IPR008909: DALR anticodon binding; IPR001412: Aminoacyl-tRNA synthetase, class I, conserved site; IPR005148: Arginyl tRNA synthetase N-terminal domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001278: Arginine-tRNA ligase; IPR009080: Aminoacyl-tRNA synthetase, class 1a, anticodon-binding; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; SSF52374: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG4426
comp27342_c0_seq2.p1	Ec-03_001420.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	GO:0016020	IPR000727: Target SNARE coiled-coil domain; G3DSA:1.20.58.70: ; IPR010989: t-SNARE; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006011: Syntaxin, N-terminal domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR19957: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0812
comp13046_c0_seq1.p1	Ec-03_001460.1	carotenoid isomerase-like protein	GO:0016117;GO:0016705;GO:0050660	PR00419: Adrenodoxin reductase family signature; PF13450: NAD(P)-binding Rossmann-like domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10668: ; G3DSA:3.50.50.60: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF51905:	NA
comp19565_c0_seq1.p1	Ec-03_001530.1	putative DNA topoisomerase III	GO:0005694;GO:0003677;GO:0003916;GO:0006265;GO:0006268	IPR013498: DNA topoisomerase, type IA, zn finger; IPR000380: DNA topoisomerase, type IA; G3DSA:3.30.65.10: ; IPR003601: DNA topoisomerase, type IA, domain 2; IPR003602: DNA topoisomerase, type IA, DNA-binding domain; IPR023406: DNA topoisomerase, type IA, active site; IPR013497: DNA topoisomerase, type IA, central; IPR013826: DNA topoisomerase, type IA, central region, subdomain 3; IPR023405: DNA topoisomerase, type IA, core domain; IPR013824: DNA topoisomerase, type IA, central region, subdomain 1; IPR006171: Toprim domain	NA
comp25869_c0_seq2.p1	Ec-03_001540.1	conserved unknown protein	n/a;n/a;n/a	IPR018714: Protein of unknown function DUF2237	NA
comp30396_c0_seq1.p1	Ec-03_001560.1	WD40-repeat-containing domain	GO:0005515	PTHR19879: ; IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR020472: G-protein beta WD-40 repeat; SSF160897: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR007582: TFIID subunit, WD40-associated region	NA
comp26771_c1_seq1.p1	Ec-03_001570.1	Putative subunit of the Anaphase Promoting Complex	GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; PF13414: TPR repeat; IPR013105: Tetratricopeptide TPR2; PTHR12558: ; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; PF12895: Anaphase-promoting complex, cyclosome, subunit 3	KOG2165
comp21484_c0_seq2.p1	Ec-03_001590.1	COX19 homolog, cytochrome c oxidase assembly protein	NA	PTHR21107: ; IPR010625: CHCH	KOG3477
comp32989_c0_seq9.p1	Ec-03_001610.5	expressed unknown protein	n/a;n/a;n/a	SignalP-TM:	NA
comp19883_c0_seq1.p1	Ec-03_001620.1	Leucyl aminopeptidase	GO:0005737;GO:0008235;GO:0004177;GO:0019538;GO:0030145	PTHR11963: ; IPR000819: Peptidase M17, leucyl aminopeptidase, C-terminal; IPR011356: Leucine aminopeptidase/peptidase B; SSF53187: ; G3DSA:3.40.630.10:	KOG2597
comp27089_c0_seq2.p1	Ec-03_001640.1	U6 snRNA-associated Sm-like protein LSm3	NA	IPR001163: Ribonucleoprotein LSM domain; PTHR13110: ; G3DSA:2.30.30.100: ; IPR006649: Ribonucleoprotein LSM domain, eukaryotic/archaea-type; IPR010920: Like-Sm (LSM) domain	NA
comp24546_c0_seq1.p1	Ec-03_001650.1	SLC41 divalent cation transporters, integral membrane domain	GO:0006812;GO:0008324	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006667: SLC41 divalent cation transporters, integral membrane domain; SSF161093: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12473_c0_seq1.p1	Ec-03_001670.1	Domain of unknown function DUF21	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR000644: CBS domain; SSF54631: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR12064: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.10.580.10: ; IPR002550: Domain of unknown function DUF21; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31895_c3_seq3.p1	Ec-03_001680.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp28713_c0_seq3.p1	Ec-03_001710.1	Tetratricopeptide-like helical domain	GO:0005515	PTHR16193: ; SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat	NA
comp33107_c2_seq3.p1	Ec-03_001760.2	hypothetical protein	n/a;n/a;n/a	PTHR11439:SF185: ; PTHR11439: ; Coil:	NA
comp29122_c0_seq2.p1	Ec-03_001790.1	LRR-GTPase of the ROCO family	GO:0005524;GO:0006355;GO:0005622;GO:0005515;GO:0008134	G3DSA:3.80.10.10: ; SSF52058: ; IPR001611: Leucine-rich repeat; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR025875: Leucine rich repeat 4; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001806: Small GTPase superfamily; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR24420: ; IPR003591: Leucine-rich repeat, typical subtype; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG4308
comp19376_c0_seq1.p2	Ec-03_001810.1	Nucleic acid-binding, OB-fold	GO:0000049	IPR012340: Nucleic acid-binding, OB-fold; PF13410: Glutathione S-transferase, C-terminal domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR010987: Glutathione S-transferase, C-terminal-like; PTHR11586: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002547: tRNA-binding domain	NA
comp30548_c0_seq9.p1	Ec-03_001850.1	Myb-like DNA-binding domain containing protein	GO:0003677;GO:0045449	PTHR10641: ; PF13921: Myb-like DNA-binding domain; IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; PTHR10641:SF513: ; Coil: ; IPR017930: Myb domain; IPR017877: Myb-like domain	NA
comp25492_c0_seq1.p1	Ec-03_001860.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28941_c0_seq3.p1	Ec-03_001880.1	NF-X1 finger and helicase domain protein, putative	GO:0006508;GO:0004197	NA	KOG1807
comp21446_c0_seq1.p1	Ec-03_001890.1	pyruvate carboxylase	GO:0003824;GO:0004736;GO:0005524	IPR013785: Aldolase-type TIM barrel; IPR005481: Carbamoyl-phosphate synthase, large subunit, N-terminal; IPR000089: Biotin/lipoyl attachment; IPR005930: Pyruvate carboxylase; IPR000891: Pyruvate carboxyltransferase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; IPR016185: Pre-ATP-grasp domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011761: ATP-grasp fold; IPR005482: Biotin carboxylase, C-terminal; IPR003379: Carboxylase, conserved domain; SSF51569: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR011053: Single hybrid motif; PTHR18866: ; IPR005479: Carbamoyl-phosphate synthetase large subunit-like, ATP-binding domain; SSF56059: ; SIGNAL_PEPTIDE: Signal peptide region; IPR013815: ATP-grasp fold, subdomain 1; SSF89000: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; G3DSA:2.40.50.100: ; IPR001882: Biotin-binding site; IPR011764: Biotin carboxylation domain; IPR009057: Homeodomain-like; IPR013816: ATP-grasp fold, subdomain 2; G3DSA:3.10.600.10: ; IPR011054: Rudiment single hybrid motif	NA
comp33863_c0_seq1.p1	Ec-03_001900.1	Light harvesting complex protein	GO:0009765;GO:0016020	SIGNAL_PEPTIDE: Signal peptide region; IPR022796: Chlorophyll A-B binding protein; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023329: Chlorophyll a/b binding protein domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001344: Chlorophyll A-B binding protein, plant; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33010_c1_seq2.p1	Ec-03_001910.1	Threonine dehydratase, catabolic	GO:0004794;GO:0006567	IPR001926: Tryptophan synthase beta subunit-like PLP-dependent enzyme; SSF55021: ; IPR005789: Threonine dehydratase, catabolic; PTHR10314: ; G3DSA:3.30.70.260: ; G3DSA:3.40.50.1100: ; SignalP-TM:	NA
comp33248_c0_seq3.p1	Ec-03_001930.1	Glycosyl transferase, family 25	GO:0009103	IPR002654: Glycosyl transferase, family 25; Coil:	NA
comp31146_c0_seq5.p1	Ec-03_001940.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp33940_c0_seq1.p1	Ec-03_001960.1	gamma carbonic anhydrase	GO:0008415;GO:0016740	PTHR13061: ; IPR011004: Trimeric LpxA-like; IPR001451: Bacterial transferase hexapeptide repeat; PF14602: Hexapeptide repeat of succinyl-transferase; G3DSA:2.160.10.10:	NA
comp33010_c5_seq24.p1	Ec-03_002010.1	SHQ1 protein	n/a;n/a;n/a	IPR007009: SHQ1 protein; PTHR12967: ; Coil: ; IPR008978: HSP20-like chaperone	NA
comp32572_c1_seq11.p1	Ec-03_002030.1	UTP--glucose-1-phosphate uridylyltransferase family	GO:0008152;GO:0070569	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002618: UTP--glucose-1-phosphate uridylyltransferase family; IPR029044: Nucleotide-diphospho-sugar transferases; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp34079_c0_seq1.p1	Ec-03_002040.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29806_c0_seq3.p1	Ec-03_002090.1	Pleckstrin homology-like domain	n/a;n/a;n/a	IPR011993: PH domain-like; Coil: ; IPR001849: Pleckstrin homology domain	NA
comp29168_c0_seq2.p1	Ec-03_002100.4	Zn(2)-C6 fungal-type DNA-binding domain containing protein	GO:0005634;GO:0006355;GO:0008270;GO:0003700	IPR001138: Zn(2)-C6 fungal-type DNA-binding domain; Coil:	NA
comp25798_c0_seq1.p2	Ec-03_002170.1	Histidine phosphatase superfamily, clade-1	GO:0006096;GO:0016868;GO:0004619	IPR013078: Histidine phosphatase superfamily, clade-1; IPR005952: Phosphoglycerate mutase 1; IPR029033: Histidine phosphatase superfamily	NA
comp28129_c0_seq2.p1	Ec-03_002180.1	Eukaryotic-type methylenetetrahydrofolate reductase	GO:0004489;GO:0006555;GO:0055114	IPR003171: Methylenetetrahydrofolate reductase; IPR004621: Eukaryotic-type methylenetetrahydrofolate reductase; PTHR21091: ; IPR029041: FAD-linked oxidoreductase-like	NA
comp20644_c0_seq1.p1	Ec-03_002190.2	Heat shock protein 70	GO:0005524	PTHR19375: ; PTHR19375:SF154: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SSF53067: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.30.420.40: ; IPR013126: Heat shock protein 70 family; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27294_c0_seq1.p1	Ec-03_002250.1	Mitochondrial substrate/solute carrier	GO:0005488;GO:0006810;GO:0016020	PTHR24089: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002067: Mitochondrial carrier protein; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31566_c0_seq5.p1	Ec-03_002260.1	Nucleic acid-binding, OB-fold	n/a;GO:0000724	IPR012340: Nucleic acid-binding, OB-fold; IPR015252: Breast cancer type 2 susceptibility protein, helical domain; IPR015187: BRCA2, oligonucleotide/oligosaccharide-binding 1; IPR002093: BRCA2 repeat; IPR015525: Breast cancer type 2 susceptibility protein; SignalP-TM:	NA
comp31432_c0_seq3.p1	Ec-03_002260.2	Nucleic acid-binding, OB-fold	n/a;n/a;n/a	IPR002093: BRCA2 repeat; SignalP-TM:	NA
comp32452_c0_seq2.p1	Ec-03_002280.1	Glycosyl transferase, family 31	GO:0016020;GO:0006486;GO:0008378	IPR005049: Protein of unknown function DUF288; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002659: Glycosyl transferase, family 31; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR31362: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31813_c0_seq3.p1	Ec-03_002320.1	Methyltransferase type 11	GO:0008152;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR013216: Methyltransferase type 11; PTHR10108:	NA
comp21390_c0_seq1.p1	Ec-03_002330.1	Mitochondrial Processing Peptidase beta subunit.	GO:0003824;GO:0046872	PTHR11851: ; IPR007863: Peptidase M16, C-terminal domain; IPR011765: Peptidase M16, N-terminal; IPR011249: Metalloenzyme, LuxS/M16 peptidase-like; IPR011237: Peptidase M16 domain	KOG0960
comp31973_c0_seq5.p1	Ec-03_002350.1	EF-hand domain pair	GO:0005509	IPR018247: EF-Hand 1, calcium-binding site; SIGNAL_PEPTIDE: Signal peptide region; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF47473: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31973_c0_seq7.p1	Ec-03_002360.2	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28481_c0_seq2.p1	Ec-03_002400.1	Cyclin-dependent kinase	NA	IPR000719: Protein kinase domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR011009: Protein kinase-like domain; PTHR24056:	KOG0600
comp21051_c0_seq2.p1	Ec-03_002420.1	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0006511;GO:0036459	PTHR24619: ; IPR001607: Zinc finger, UBP-type; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; SSF54001: ; IPR028889: Ubiquitin specific protease domain; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase	NA
comp25384_c0_seq2.p1	Ec-03_002430.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp33255_c0_seq13.p1	Ec-03_002440.1	Jumonji domain protein	n/a;n/a;n/a	IPR003347: JmjC domain; SSF51197: ; mobidb-lite: consensus disorder prediction; Coil:	NA
comp34543_c0_seq1.p1	Ec-03_002460.1	Cathepsin Z-like proteinase	GO:0008234;GO:0006508	SSF54001: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR013128: Peptidase C1A; IPR025661: Cysteine peptidase, asparagine active site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000668: Peptidase C1A, papain C-terminal; G3DSA:3.90.70.10: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1543
comp32451_c0_seq1.p1	Ec-03_002500.1	Patched	GO:0008158;GO:0016020	SSF82866: ; G3DSA:1.20.1640.10: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10796: ; IPR003392: Patched; IPR000731: Sterol-sensing domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29253_c0_seq3.p1	Ec-03_002540.1	Vesicle coat complex COPII, subunit SEC23	GO:0006886;GO:0006888;GO:0008270;GO:0030127	SSF82754: ; SSF81995: ; IPR006900: Sec23/Sec24, helical domain; IPR012990: Sec23/Sec24 beta-sandwich; G3DSA:2.60.40.1670: ; PTHR11141: ; IPR006896: Sec23/Sec24, trunk domain; IPR006895: Zinc finger, Sec23/Sec24-type; IPR029006: ADF-H/Gelsolin-like domain; IPR007123: Gelsolin-like domain; IPR002035: von Willebrand factor, type A	KOG1986
comp31458_c3_seq3.p2	Ec-03_002550.1	WW domain binding protein 11	GO:0006396	IPR019007: WW domain binding protein 11; Coil:	NA
comp31103_c0_seq1.p1	Ec-03_002580.2	NB-ARC	GO:0043531	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR002182: NB-ARC; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp12091_c0_seq1.p1	Ec-03_002620.1	Rab11D, RAB family GTPase	GO:0005622;GO:0007264;GO:0005525	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR005225: Small GTP-binding protein domain; IPR001806: Small GTPase superfamily; IPR020849: Small GTPase superfamily, Ras type; PS51419: small GTPase Rab1 family profile.; IPR003579: Small GTPase superfamily, Rab type; PTHR24073:	NA
comp26701_c0_seq3.p1	Ec-03_002630.1	Metallo-dependent phosphatase-like	n/a;GO:0016787	IPR029052: Metallo-dependent phosphatase-like; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32748_c0_seq6.p1	Ec-03_002640.1	Nucleotide-diphospho-sugar transferases	n/a;n/a;n/a	IPR002495: Glycosyl transferase, family 8; IPR029044: Nucleotide-diphospho-sugar transferases	NA
comp33138_c0_seq21.p1	Ec-03_002680.1	YHYH domain	n/a;n/a;n/a	IPR025924: YHYH domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28005_c0_seq3.p1	Ec-03_002700.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp20496_c0_seq1.p1	Ec-03_002720.1	Putative RNA methyltransferase	n/a;n/a;n/a	IPR029028: Alpha/beta knot methyltransferases; IPR012340: Nucleic acid-binding, OB-fold; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR003750: Putative RNA methyltransferase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029026: tRNA (guanine-N1-)-methyltransferase, N-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31380_c1_seq2.p1	Ec-03_002730.1	armadillo/beta-catenin-like repeat domain containing protein	GO:0005488	PTHR23316: ; IPR011989: Armadillo-like helical; IPR000225: Armadillo; IPR016024: Armadillo-type fold; Coil:	NA
comp24253_c0_seq1.p1	Ec-03_002740.1	expressed unknown protein	GO:0005509	Coil:	NA
comp26371_c0_seq1.p1	Ec-03_002770.1	conserved unknown protein	n/a;n/a;n/a	PTHR16453: ; IPR013083: Zinc finger, RING/FYVE/PHD-type	NA
comp24210_c0_seq2.p1	Ec-03_002790.1	Triose-phosphate isomerase	GO:0008152;GO:0004807	IPR013785: Aldolase-type TIM barrel; SIGNAL_PEPTIDE: Signal peptide region; IPR000652: Triosephosphate isomerase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1643
comp24743_c0_seq1.p1	Ec-03_002800.1	Oxidoreductase, FAD-binding domain	GO:0004324;GO:0006118;GO:0042651;GO:0050660;GO:0050661;GO:0055114	IPR017927: Ferredoxin reductase-type FAD-binding domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:2.40.30.10: ; SSF52343: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001433: Oxidoreductase FAD/NAD(P)-binding; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.40.50.80: ; PTHR19384:SF75: ; IPR017938: Riboflavin synthase-like beta-barrel; PTHR19384: ; IPR001709: Flavoprotein pyridine nucleotide cytochrome reductase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33010_c6_seq1.p1	Ec-03_002840.1	conserved unknown protein	GO:0005488	NA	NA
comp30904_c0_seq3.p1	Ec-03_002850.1	conserved unknown protein	GO:0005198;GO:0019028;n/a	Coil:	NA
comp34244_c0_seq1.p1	Ec-03_002860.1	Mitochondrial import protein TIM15	n/a;n/a;n/a	IPR007853: Zinc finger, DNL-type; IPR024158: Mitochondrial import protein TIM15; PTHR20922:SF13:	NA
comp29173_c0_seq1.p1	Ec-03_002870.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;GO:0018024	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR013110: Histone methylation DOT1	NA
comp29274_c0_seq2.p1	Ec-03_002920.1	Pyridoxal-dependent decarboxylase	GO:0003824;GO:0030170	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11999:SF5: ; PTHR11999: ; IPR002129: Pyridoxal phosphate-dependent decarboxylase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR015424: Pyridoxal phosphate-dependent transferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2	KOG1383
comp25275_c0_seq2.p1	Ec-03_002930.1	Short-chain dehydrogenase/reductase SDR	GO:0008152;GO:0016491	SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; PTHR24311: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31426_c1_seq3.p1	Ec-03_002950.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp26293_c0_seq1.p1	Ec-03_002970.1	RNA polymerase Rpb7, N-terminal	GO:0003899;GO:0006351	IPR012340: Nucleic acid-binding, OB-fold; PTHR12709: ; IPR005576: RNA polymerase Rpb7, N-terminal; IPR013238: RNA polymerase III, subunit Rpc25	NA
comp30679_c0_seq1.p1	Ec-03_002990.1	violaxanthin de-epoxidase-like protein of unknown function	NA	SIGNAL_PEPTIDE: Signal peptide region; IPR012674: Calycin; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011038: Calycin-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR010788: Violaxanthin de-epoxidase	NA
comp28707_c0_seq7.p1	Ec-03_003010.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0006810;GO:0016021;GO:0042626;GO:0055085	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR003439: ABC transporter-like; IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:1.20.1560.10: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR24223: ; IPR011527: ABC transporter type 1, transmembrane domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR017871: ABC transporter, conserved site	NA
comp25215_c0_seq2.p1	Ec-03_003030.1	NUDIX hydrolase domain	GO:0016787	IPR015797: NUDIX hydrolase domain-like; PTHR12992: ; IPR000086: NUDIX hydrolase domain	NA
comp32110_c0_seq13.p1	Ec-03_003050.1	Uncharacterised domain, di-copper centre	n/a;n/a;n/a	IPR008922: Uncharacterised domain, di-copper centre; IPR002227: Tyrosinase copper-binding domain; IPR000601: PKD domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11474: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20895_c0_seq1.p1	Ec-03_003060.1	Sec1-like, domain 2	GO:0006904;GO:0016192	IPR027121: Vacuolar protein sorting-associated protein 33; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; G3DSA:3.90.830.10: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001619: Sec1-like protein; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027482: Sec1-like, domain 2; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33159_c0_seq4.p1	Ec-03_003110.3	hypothetical protein	n/a;n/a;n/a	IPR007527: Zinc finger, SWIM-type	NA
comp29577_c0_seq1.p1	Ec-03_003130.1	Uncharacterised domain, di-copper centre	n/a;GO:0008152;GO:0016491	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002227: Tyrosinase copper-binding domain; IPR008922: Uncharacterised domain, di-copper centre; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp21059_c0_seq1.p1	Ec-03_003160.1	WD40-repeat-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp25274_c1_seq1.p1	Ec-03_003170.1	Peptidase S28	GO:0006508;GO:0008236	PTHR11010: ; IPR029058: Alpha/Beta hydrolase fold; IPR008758: Peptidase S28; PTHR11010:SF38:	NA
comp32248_c7_seq3.p1	Ec-03_003180.1	Patched	GO:0008158;GO:0016020	SSF82866: ; G3DSA:1.20.1640.10: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10796: ; IPR003392: Patched; IPR000731: Sterol-sensing domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30659_c0_seq6.p2	Ec-03_003210.1	putative: flagellar outer dynein arm light chain 6	GO:0005875;GO:0007017	IPR019763: Dynein light chain, type 1/2, conserved site; SSF54648: ; IPR001372: Dynein light chain, type 1/2	KOG3430
comp25004_c0_seq2.p1	Ec-03_003220.1	Patched	GO:0016020;GO:0008158;GO:0016021	G3DSA:1.20.1640.10: ; SSF82866: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10796: ; IPR003392: Patched; IPR000731: Sterol-sensing domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32669_c0_seq3.p1	Ec-03_003240.1	Pheophorbide a oxygenase	GO:0010277;GO:0055114	IPR017941: Rieske [2Fe-2S] iron-sulphur domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF55961: ; SignalP-noTM: ; IPR013626: Pheophorbide a oxygenase; PTHR21266: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27123_c0_seq1.p1	Ec-03_003260.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR014014: RNA helicase, DEAD-box type, Q motif; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; PTHR24031:	KOG0331
comp32953_c4_seq29.p1	Ec-03_003270.1	aspartate aminotransferase	GO:0003824;GO:0004069;GO:0006520;GO:0030170	IPR015424: Pyridoxal phosphate-dependent transferase; IPR004839: Aminotransferase, class I/classII; IPR004838: Aminotransferases, class-I, pyridoxal-phosphate-binding site; IPR000796: Aspartate/other aminotransferase; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	KOG1411
comp32953_c4_seq35.p1	Ec-03_003280.1	SOUL haem-binding protein	n/a;n/a;n/a	IPR011256: Regulatory factor, effector binding domain; SIGNAL_PEPTIDE: Signal peptide region; IPR006917: SOUL haem-binding protein; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR11220:SF35: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp34198_c0_seq1.p1	Ec-03_003290.1	NTP pyrophosphohydrolase MazG, putative catalytic core	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:1.10.287.1080: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14552: ; SSF101386: ; PTHR14552:SF12: ; IPR004518: NTP pyrophosphohydrolase MazG, putative catalytic core; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34457_c0_seq1.p1	Ec-03_003300.1	Thioredoxin-like protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR005746: Thioredoxin; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0910
comp32928_c0_seq16.p1	Ec-03_003340.1	Alanine transaminase	GO:0003824;GO:0030170	IPR015424: Pyridoxal phosphate-dependent transferase; IPR004839: Aminotransferase, class I/classII; PTHR11751: ; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; SignalP-TM:	KOG0258
comp33125_c0_seq5.p1	Ec-03_003410.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp26447_c0_seq2.p1	Ec-03_003420.1	aureochrome 4	GO:0004871;GO:0007165	IPR004827: Basic-leucine zipper domain; IPR001610: PAC motif; SSF57959: ; IPR000014: PAS domain; G3DSA:1.20.5.170: ; IPR000700: PAS-associated, C-terminal; G3DSA:3.30.450.20: ; PTHR24351:SF71: ; Coil: ; PTHR24351:	NA
comp28512_c0_seq5.p1	Ec-03_003430.1	Protein of unknown function DUF1042	GO:0005524;GO:0006139;GO:0019205	IPR010441: Protein of unknown function DUF1042; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR14919: ; Coil:	NA
comp20020_c0_seq1.p1	Ec-03_003460.1	SCAR-WAVE	GO:0005856;GO:0030036;GO:0003779	IPR003124: WH2 domain; IPR000095: CRIB domain; IPR028288: SCAR/WAVE family; Coil: ; PR01217: Proline rich extensin signature	no relat
comp20991_c0_seq2.p1	Ec-03_003490.1	acyl-CoA dehydrogenase	GO:0016627;GO:0008152;GO:0055114;GO:0003995	IPR013786: Acyl-CoA dehydrogenase/oxidase, N-terminal; IPR009100: Acyl-CoA dehydrogenase/oxidase, N-terminal and middle domain; IPR006091: Acyl-CoA oxidase/dehydrogenase, central domain; G3DSA:1.20.140.10: ; IPR009075: Acyl-CoA dehydrogenase/oxidase C-terminal; PTHR10909:	KOG1469
comp19541_c0_seq1.p2	Ec-03_003510.1	monocarboxylate permease, putative	GO:0003700;GO:0005634;GO:0006355;GO:0008270	NA	NA
comp28902_c0_seq1.p1	Ec-03_003520.1	Geranylgeranyl reductase	GO:0016628;GO:0003824;GO:0055114;GO:0003674;GO:0045550;GO:0016491	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; IPR011774: Geranylgeranyl reductase, plant/cyanobacteria; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; IPR010253: Geranylgeranyl reductase, plant/prokaryotic; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PR00420: Aromatic-ring hydroxylase (flavoprotein monooxygenase) signature; PTHR10617: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SSF51905: ; G3DSA:3.30.9.10: ; IPR011777: Geranylgeranyl reductase family	NA
comp28937_c0_seq3.p1	Ec-03_003530.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp32256_c0_seq11.p1	Ec-03_003540.1	Carbohydrate binding family 6	GO:0030246	PTHR19328: ; SSF50956: ; IPR022409: PKD/Chitinase domain; IPR012938: Glucose/Sorbosone dehydrogenase; SIGNAL_PEPTIDE: Signal peptide region; IPR000601: PKD domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011042: Six-bladed beta-propeller, TolB-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR19328:SF13: ; IPR011041: Soluble quinoprotein glucose/sorbosone dehydrogenase; IPR005084: Carbohydrate binding module family 6; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR008979: Galactose-binding domain-like	NA
comp32767_c0_seq6.p1	Ec-03_003560.1	Ankyrin repeat-containing domain	n/a;GO:0005515	SIGNAL_PEPTIDE: Signal peptide region; PTHR24133: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR020683: Ankyrin repeat-containing domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp33928_c0_seq1.p1	Ec-03_003570.1	Uracil phosphoribosyltransferase	GO:0003674;GO:0016763;GO:0016757;GO:0004845;GO:0009116;GO:0016740;GO:0003824	PTHR10285: ; PF14681: Uracil phosphoribosyltransferase; IPR029057: Phosphoribosyltransferase-like	NA
comp30264_c0_seq3.p1	Ec-03_003580.1	thioredoxin-like protein	GO:0045454	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005746: Thioredoxin; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0190
comp29539_c0_seq2.p1	Ec-03_003590.3	General substrate transporter	GO:0016021;GO:0022857;GO:0055085	IPR005829: Sugar transporter, conserved site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR005828: Major facilitator, sugar transporter-like; IPR003663: Sugar/inositol transporter; PTHR23500: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12871_c0_seq1.p1	Ec-03_003600.1	ThiC-associated domain	GO:0009228	SIGNAL_PEPTIDE: Signal peptide region; IPR002817: Phosphomethylpyrimidine synthase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR30557: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR025747: ThiC-associated domain; PTHR30557:SF1: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33960_c0_seq1.p1	Ec-03_003610.1	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase, chloroplast precursor	GO:0055114;GO:0016114;GO:0046429	PTHR30454: ; SSF56014: ; IPR017178: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase, atypical; IPR004588: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase, bacterial-type	NA
comp34231_c0_seq1.p1	Ec-03_003630.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32846_c0_seq20.p1	Ec-03_003640.1	Aldo/Keto Reductase	GO:0016491;GO:0055114	IPR001395: Aldo/keto reductase; IPR018170: Aldo/keto reductase, conserved site; IPR020471: Aldo/keto reductase subgroup; IPR023210: NADP-dependent oxidoreductase domain	KOG1577
comp26412_c0_seq1.p1	Ec-03_003660.1	Sec8 exocyst complex component specific domain	GO:0006904;GO:0000145;GO:0015031	IPR007191: Sec8 exocyst complex component specific domain; PTHR14146:	NA
comp32737_c1_seq3.p1	Ec-03_003720.1	hypothetical protein	n/a;n/a;n/a	PF13583: Metallo-peptidase family M12B Reprolysin-like; IPR024079: Metallopeptidase, catalytic domain; SSF55486:	NA
comp33139_c0_seq14.p1	Ec-03_003740.1	long chain acyl-coA synthetase	GO:0008152;GO:0003824	G3DSA:3.40.50.980: ; IPR020845: AMP-binding, conserved site; PTHR24096: ; IPR000873: AMP-dependent synthetase/ligase; G3DSA:2.30.38.10: ; SSF56801:	KOG1256
comp24255_c0_seq1.p2	Ec-03_003770.1	Cyclophilin-like domain	GO:0003755;GO:0006457	IPR024936: Cyclophilin-type peptidyl-prolyl cis-trans isomerase; IPR002130: Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain; IPR029000: Cyclophilin-like domain; IPR020892: Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site	NA
comp33123_c0_seq7.p1	Ec-03_003790.1	NAD(P)-binding domain	GO:0003824;GO:0005488;GO:0008152	SSF51735: ; PTHR14097: ; IPR016040: NAD(P)-binding domain; PF13460: NADH(P)-binding	NA
comp32997_c1_seq18.p1	Ec-03_003810.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30172_c0_seq1.p1	Ec-03_003830.1	Exostosin-like	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004263: Exostosin-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34380_c0_seq1.p1	Ec-03_003850.1	Indole-3-glycerol-phosphate synthase	GO:0004425	IPR013785: Aldolase-type TIM barrel; IPR011060: Ribulose-phosphate binding barrel; PTHR22854: ; IPR013798: Indole-3-glycerol phosphate synthase	KOG4201
comp11995_c0_seq1.p1	Ec-03_003870.1	putative microtubule-associated protein EB1	GO:0008017;GO:0005515	IPR027328: Microtubule-associated protein RP/EB; IPR001715: Calponin homology domain; Coil: ; IPR004953: EB1, C-terminal	KOG3000
comp32753_c1_seq2.p1	Ec-03_003910.1	DDE superfamily endonuclease, CENP-B-like	GO:0003676	IPR004875: DDE superfamily endonuclease, CENP-B-like; PTHR19303:	NA
comp32203_c1_seq12.p1	Ec-03_003920.1	Pre-mRNA-processing factor 6/Prp1/STA1	GO:0000398	SSF48452: ; IPR003107: HAT (Half-A-TPR) repeat; IPR010491: PRP1 splicing factor, N-terminal; IPR011990: Tetratricopeptide-like helical domain; IPR013105: Tetratricopeptide TPR2; PTHR11246: ; Coil: ; IPR019734: Tetratricopeptide repeat; IPR027108: Pre-mRNA-processing factor 6/Prp1/STA1	NA
comp32527_c0_seq22.p1	Ec-03_003930.1	conserved unknown protein	n/a;n/a;n/a	SSF140990: ; Coil:	NA
comp29637_c0_seq2.p1	Ec-03_003940.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32873_c1_seq31.p2	Ec-03_003950.1	Vesicle transport protein, Got1/SFT2-like	GO:0006810;GO:0016192;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR007305: Vesicle transport protein, Got1/SFT2-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011691: Vesicle transport protein, SFT2-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28752_c0_seq1.p1	Ec-03_003960.1	Coatomer protein complex, gamma sub-unit	GO:0005488	IPR013040: Coatomer, gamma subunit, appendage, Ig-like subdomain; IPR011989: Armadillo-like helical; IPR002553: Clathrin/coatomer adaptor, adaptin-like, N-terminal; IPR017106: Coatomer gamma subunit; IPR016024: Armadillo-type fold; IPR009028: Coatomer/calthrin adaptor appendage, C-terminal subdomain; IPR015873: Clathrin alpha-adaptin/coatomer adaptor, appendage, C-terminal subdomain; IPR013041: Coatomer/clathrin adaptor appendage, Ig-like subdomain	KOG1078
comp35065_c0_seq1.p1	Ec-03_003980.1	expressed unknown protein	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32261_c1_seq18.p1	Ec-03_003990.2	Protein kinase with leucine rich repeat domains	NA	IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR001611: Leucine-rich repeat; IPR032675: Leucine-rich repeat domain, L domain-like; IPR001245: Serine-threonine/tyrosine-protein kinase catalytic domain; IPR011009: Protein kinase-like domain; PTHR23257: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29792_c0_seq2.p1	Ec-03_004020.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; PF13637: Ankyrin repeats (many copies); IPR002110: Ankyrin repeat; PTHR24123:	NA
comp34835_c0_seq1.p1	Ec-03_004030.1	DNA-directed RNA polymerase, RBP11-like dimerisation domain	GO:0006351;GO:0046983	IPR011262: DNA-directed RNA polymerase, insert domain; G3DSA:3.30.1360.10: ; IPR001514: DNA-directed RNA polymerase, 30-40kDa subunit, conserved site; IPR011263: DNA-directed RNA polymerase, RpoA/D/Rpb3-type; PTHR11800: ; IPR009025: DNA-directed RNA polymerase, RBP11-like dimerisation domain	NA
comp27491_c0_seq1.p1	Ec-03_004040.1	N-acetyltransferase B complex, non-catalytic subunit	n/a;GO:0005515	SSF48452: ; IPR019183: N-acetyltransferase B complex, non-catalytic subunit; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; PTHR22767:	NA
comp30418_c0_seq1.p1	Ec-03_004090.2	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp17122_c0_seq2.p1	Ec-03_004110.1	Pheromone shutdown, TraB	n/a;n/a;n/a	IPR002816: Pheromone shutdown, TraB; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR006311: Twin-arginine translocation pathway, signal sequence; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR21530: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32129_c0_seq4.p1	Ec-03_004120.1	PIN domain-like	n/a;n/a;n/a	Coil: ; IPR029060: PIN domain-like	NA
comp27206_c0_seq1.p1	Ec-03_004150.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp33868_c0_seq1.p1	Ec-03_004160.1	CobW/HypB/UreG domain	n/a;n/a;n/a	PTHR13748:SF43: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR13748: ; IPR003495: CobW/HypB/UreG domain; IPR011629: Cobalamin (vitamin B12) biosynthesis CobW-like, C-terminal	NA
comp30098_c2_seq7.p1	Ec-03_004180.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp26532_c0_seq1.p1	Ec-03_004190.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp33215_c1_seq21.p1	Ec-03_004210.2	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type	NA
comp31707_c0_seq1.p1	Ec-03_004240.2	Cellulose synthase (UDP-forming), family GT2	NA	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF13641: Glycosyltransferase like family 2; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029044: Nucleotide-diphospho-sugar transferases; PTHR10587: ; PTHR10587:SF82: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29697_c0_seq2.p2	Ec-03_004330.1	Zinc finger, RING/FYVE/PHD-type	GO:0008270	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011016: Zinc finger, RING-CH-type; PTHR13145: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24448_c0_seq2.p1	Ec-03_004340.1	Mg2+ transporter protein, CorA-like/Zinc transport protein ZntB	GO:0016020;GO:0030001;GO:0046873;GO:0055085	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; SSF143865: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR21535: ; Coil: ; IPR002523: Mg2+ transporter protein, CorA-like/Zinc transport protein ZntB; G3DSA:3.30.460.20: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF144083: ; PTHR21535:SF33: ; G3DSA:1.20.58.340:	NA
comp28793_c0_seq4.p1	Ec-03_004350.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0000981;GO:0005634;GO:0006355;GO:0008270	IPR001138: Zn(2)-C6 fungal-type DNA-binding domain; IPR001478: PDZ domain	NA
comp32097_c0_seq3.p1	Ec-03_004370.3	Pentatricopeptide repeat	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; IPR002885: Pentatricopeptide repeat; IPR002625: Smr domain; Coil: ; PTHR24015: ; SignalP-TM:	NA
comp24729_c0_seq1.p1	Ec-03_004420.1	Alpha-(1,3)-mannosyltransferase, family GT4	GO:0009058	SSF53756: ; IPR027054: Alpha-1,3/1,6-mannosyltransferase ALG2; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; IPR001296: Glycosyl transferase, family 1; PTHR12526: ; G3DSA:3.40.50.2000: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0853
comp32415_c0_seq9.p1	Ec-03_004440.2	Peptidase S54, rhomboid domain	GO:0004252;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002610: Peptidase S54, rhomboid; PTHR22936:SF32: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR022764: Peptidase S54, rhomboid domain; SSF144091: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp37193_c0_seq1.p1	Ec-03_004450.1	conserved unknown protein	GO:0005509	IPR011989: Armadillo-like helical; IPR002048: EF-hand domain; Coil: ; PTHR23053:	NA
comp14888_c0_seq1.p1	Ec-03_004480.1	Bax inhibitor 1-related	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006214: Bax inhibitor 1-related; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21196_c0_seq1.p1	Ec-03_004490.1	von Willebrand factor, type A	n/a;n/a;n/a	IPR026126: BRISC and BRCA1-A complex member 1; PF13519: von Willebrand factor type A domain; IPR002035: von Willebrand factor, type A	NA
comp29399_c0_seq2.p1	Ec-03_004530.1	Peptidase S49, N-terminal proteobacteria	GO:0004252;GO:0008233;GO:0006508;GO:0005886	IPR029045: ClpP/crotonase-like domain; IPR002142: Peptidase S49; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR013703: Peptidase S49, N-terminal proteobacteria; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21220_c0_seq1.p1	Ec-03_004540.1	Winged helix-turn-helix DNA-binding domain	n/a;GO:0005515	IPR000717: Proteasome component (PCI) domain; IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; PTHR10855:	NA
comp26693_c0_seq1.p2	Ec-03_004550.1	Transcription elongation factor S-IIM	GO:0005634;GO:0006351;GO:0008270	IPR017890: Transcription elongation factor S-IIM; PTHR11477: ; IPR003618: Transcription elongation factor S-II, central domain; Coil: ; SSF57783: ; G3DSA:2.20.25.10:	NA
comp19968_c0_seq1.p1	Ec-03_004560.1	Sporulation-specific protein 11 homologue	GO:0003677;GO:0005694;GO:0000737	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR011991: Winged helix-turn-helix DNA-binding domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013049: Spo11/DNA topoisomerase VI, subunit A, N-terminal; G3DSA:3.40.1360.10: ; IPR002815: Spo11/DNA topoisomerase VI subunit A; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2795
comp24351_c0_seq1.p1	Ec-03_004590.1	UAA transporter	GO:0055085	SSF103481: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR10778:SF18: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013657: UAA transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10778: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp71026_c0_seq1.p2	Ec-03_004600.3	conserved unknown protein	n/a;n/a;n/a	PTHR15977: ; Coil: ; IPR019734: Tetratricopeptide repeat	NA
comp20387_c0_seq1.p1	Ec-03_004610.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020683: Ankyrin repeat-containing domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31756_c1_seq3.p1	Ec-03_004620.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0005634;GO:0000981;GO:0006355;GO:0008270	IPR001138: Zn(2)-C6 fungal-type DNA-binding domain; Coil:	NA
comp31358_c0_seq2.p1	Ec-03_004630.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp27015_c0_seq1.p2	Ec-03_004640.3	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp53409_c0_seq1.p1	Ec-03_004680.1	Pyrroline-5-carboxylate reductase, catalytic, N-terminal	GO:0006561;GO:0008152;GO:0003824;GO:0005488;GO:0055114;GO:0004735	IPR028939: Pyrroline-5-carboxylate reductase, catalytic, N-terminal; SSF51735: ; IPR016040: NAD(P)-binding domain; IPR000304: Pyrroline-5-carboxylate reductase	NA
comp32957_c0_seq7.p1	Ec-03_004710.1	Calcium release-activated calcium channel protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR012446: Calcium release-activated calcium channel protein; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34821_c0_seq1.p1	Ec-03_004720.1	1-(5-phosphoribosyl)-5- ((5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase	GO:0003949;GO:0000105	IPR013785: Aldolase-type TIM barrel; IPR006062: Histidine biosynthesis; IPR011060: Ribulose-phosphate binding barrel; IPR011858: Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase, eukaryotic	KOG3055
comp19676_c0_seq1.p1	Ec-03_004730.3	Domain of unknown function DUF4341	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR30574:SF1: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR30574:	NA
comp31815_c0_seq4.p1	Ec-03_004760.2	Sodium/hydrogen exchanger family	NA	IPR018422: Cation/H+ exchanger, CPA1 family; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10110:SF86: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006153: Cation/H+ exchanger; IPR018490: Cyclic nucleotide-binding-like; Coil: ; IPR014710: RmlC-like jelly roll fold; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA

comp28803_c0_seq4.p1	Ec-03_004770.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR012961: ATP-dependent RNA helicase Ski2, C-terminal; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR11752: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32920_c1_seq24.p1	Ec-03_004780.1	class-V aminotransferase	GO:0003824;GO:0030170	IPR015424: Pyridoxal phosphate-dependent transferase; PTHR11601: ; IPR000192: Aminotransferase class V domain; Coil: ; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	KOG1549
comp27722_c0_seq2.p1	Ec-03_004790.1	Glutaredoxin glutaredoxin/malate transporter fusion protein	NA	IPR025508: Domain of unknown function DUF4395; IPR002109: Glutaredoxin; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR014025: Glutaredoxin subgroup; IPR004695: Voltage-dependent anion channel; IPR012312: Haemerythrin-like; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.120.520: ; Coil: ; IPR012336: Thioredoxin-like fold; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1752
comp17841_c0_seq1.p1	Ec-03_004840.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32368_c0_seq1.p1	Ec-03_004850.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29863_c0_seq1.p1	Ec-03_004860.1	P-loop containing nucleoside triphosphate hydrolase	GO:0000166;GO:0017111	IPR003593: AAA+ ATPase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR003840: DNA helicase; IPR010285: DNA helicase Pif1-like	NA
comp12165_c0_seq1.p1	Ec-03_004890.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp20715_c0_seq1.p1	Ec-03_004910.1	Ribonuclease T2-like	GO:0003723;GO:0033897	PTHR11240:SF22: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR018188: Ribonuclease T2, active site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001568: Ribonuclease T2-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30700_c0_seq6.p1	Ec-03_004920.1	Ankyrin repeat-containing domain	n/a;GO:0005515	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR24188: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020683: Ankyrin repeat-containing domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp28047_c0_seq2.p1	Ec-03_004930.1	expressed unknown protein	GO:0003677;GO:0006281	NA	NA
comp25443_c1_seq1.p1	Ec-03_004950.1	S-adenosyl-L-methionine-dependent methyltransferases-like	GO:0008152;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR013216: Methyltransferase type 11; PTHR10108:	NA
comp30430_c0_seq2.p1	Ec-03_004960.1	Rab32A, RAB family GTPase	GO:0005525;GO:0007264	IPR002041: Ran GTPase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; IPR003579: Small GTPase superfamily, Rab type; IPR020849: Small GTPase superfamily, Ras type; PS51419: small GTPase Rab1 family profile.; PTHR24073:SF100: ; PR00449: Transforming protein P21 ras signature; PTHR24073:	NA
comp29026_c1_seq1.p1	Ec-03_004970.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp31673_c0_seq1.p1	Ec-03_004990.1	hypothetical protein	GO:0000166;GO:0005515	Coil:	NA
comp27454_c2_seq1.p1	Ec-03_005010.1	expressed unknown protein	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; IPR002885: Pentatricopeptide repeat; PTHR24015: ; IPR000048: IQ motif, EF-hand binding site	NA
comp29272_c0_seq1.p1	Ec-03_005030.1	Alpha-(1,3)-fucosyltransferase, family GT10	GO:0006486;GO:0008417;GO:0016020	IPR001503: Glycosyl transferase family 10; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF53756: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR031481: Fucosyltransferase, N-terminal	NA
comp28438_c0_seq3.p1	Ec-03_005110.1	Domain of unknown function DUF4033	n/a;n/a;n/a	IPR025114: Domain of unknown function DUF4033; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26113_c0_seq2.p1	Ec-03_005170.1	Putative subunit of the Anaphase Promoting Complex	GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; PF13414: TPR repeat; IPR011990: Tetratricopeptide-like helical domain; PTHR12558: ; IPR007192: Cdc23; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat	KOG1155
comp18810_c0_seq1.p1	Ec-03_005180.1	Prefoldin	GO:0006457;n/a;GO:0016272;GO:0051082	IPR002777: Prefoldin beta-like; IPR009053: Prefoldin; Coil: ; PTHR21431:	NA
comp32605_c1_seq7.p1	Ec-03_005190.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR006549: HAD-superfamily hydrolase,subfamily IIIA; IPR013954: Polynucleotide kinase 3 phosphatase; PTHR12083: ; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023214: HAD-like domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13671: AAA domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR006551: Polynucleotide 3'-phosphatase	NA
comp31966_c2_seq8.p1	Ec-03_005250.1	Formylglycine-dependent sulfatase	GO:0003824;GO:0008152	IPR000917: Sulfatase, N-terminal; G3DSA:3.30.1120.10: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR017849: Alkaline phosphatase-like, alpha/beta/alpha; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10342: ; PTHR10342:SF22: ; IPR017850: Alkaline-phosphatase-like, core domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3867
comp32652_c2_seq2.p1	Ec-03_005260.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0016301;GO:0001906	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR010488: Zeta toxin domain	NA
comp34371_c0_seq1.p1	Ec-03_005270.1	Protein of unknown function DUF583	n/a;n/a;n/a	IPR007607: Protein of unknown function DUF583; Coil:	NA
comp29532_c0_seq2.p1	Ec-03_005290.2	Histone hairpin binding protein	NA	IPR026502: Histone RNA stem-loop-binding protein SLBP1/SLBP2; Coil: ; IPR029344: Histone RNA hairpin-binding protein, RNA-binding domain	NA
comp30830_c0_seq5.p1	Ec-03_005330.1	Nucleotide-diphospho-sugar transferases	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13704: Glycosyl transferase family 2; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR029044: Nucleotide-diphospho-sugar transferases; PTHR21461: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21587_c0_seq1.p1	Ec-03_005340.1	RNAse P, Rpr2/Rpp21 subunit	n/a;n/a;n/a	IPR007175: RNAse P, Rpr2/Rpp21 subunit	NA
comp32764_c2_seq1.p1	Ec-03_005350.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32234_c0_seq2.p1	Ec-04_000030.1	Imp2 homolog, Inner Membrane Peptidase complex subunit 2	GO:0006508;GO:0008236;GO:0009003;GO:0016020;GO:0016021	IPR019759: Peptidase S24/S26A/S26B; IPR015927: Peptidase S24/S26A/S26B/S26C; IPR000223: Peptidase S26A, signal peptidase I; IPR028360: Peptidase S24/S26, beta-ribbon domain	NA
comp20413_c0_seq1.p2	Ec-04_000040.1	WW domain	GO:0005515	PTHR21737: ; IPR001202: WW domain; G3DSA:2.20.70.10:	NA
comp20413_c0_seq1.p1	Ec-04_000060.1	Cyclophilin-like domain	n/a;GO:0005515	IPR024936: Cyclophilin-type peptidyl-prolyl cis-trans isomerase; IPR002130: Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR029000: Cyclophilin-like domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR020892: Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site	NA
comp33222_c0_seq5.p1	Ec-04_000070.1	Amino acid/polyamine transporter I	GO:0016020;GO:0003333;GO:0015171	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002293: Amino acid/polyamine transporter I; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32219_c0_seq4.p2	Ec-04_000130.1	similar to WD repeat domain 36	GO:0005515	IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR007319: Small-subunit processome, Utp21; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR13889:	NA
comp34481_c0_seq1.p1	Ec-04_000140.1	SWR1-complex protein 4/DNA methyltransferase 1-associated protein 1	GO:0035267;GO:0006338;GO:0006281;GO:0043968;GO:0043967	IPR027109: SWR1-complex protein 4/DNA methyltransferase 1-associated protein 1; Coil:	NA
comp32219_c0_seq21.p1	Ec-04_000240.1	Target of rapamycin 1	GO:0005515	G3DSA:3.30.1010.10: ; IPR000403: Phosphatidylinositol 3-/4-kinase, catalytic domain; IPR011990: Tetratricopeptide-like helical domain; IPR011989: Armadillo-like helical; IPR009076: Rapamycin-binding domain; IPR024585: Domain of unknown function DUF3385, target of rapamycin protein; IPR011009: Protein kinase-like domain; IPR003151: PIK-related kinase, FAT; IPR016024: Armadillo-type fold; IPR014009: PIK-related kinase; PTHR11139: ; Coil: ; IPR003152: PIK-related kinase, FATC; IPR018936: Phosphatidylinositol 3/4-kinase, conserved site	KOG0891
comp23504_c2_seq1.p1	Ec-04_000280.1	Galactokinase	GO:0004335;GO:0005524;GO:0006012;GO:0046835	PTHR10457: ; IPR006203: GHMP kinase, ATP-binding, conserved site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006204: GHMP kinase N-terminal domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR000705: Galactokinase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006206: Mevalonate/galactokinase; IPR019741: Galactokinase, conserved site; IPR019539: Galactokinase galactose-binding domain; IPR020568: Ribosomal protein S5 domain 2-type fold; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup; IPR013750: GHMP kinase, C-terminal domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11358_c0_seq2.p1	Ec-04_000330.1	beta(1,4)-N-acetylglucosaminyltransferase	GO:0030259;GO:0016758;GO:0030246;GO:0005975	SSF53756: ; PTHR12867: ; Coil: ; IPR007235: Glycosyl transferase, family 28, C-terminal; G3DSA:3.40.50.2000:	KOG3349
comp21462_c0_seq1.p3	Ec-04_000360.1	NADH-ubiquinone reductase complex 1 MLRQ subunit	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR010530: NADH-ubiquinone reductase complex 1 MLRQ subunit; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28736_c0_seq2.p1	Ec-04_000420.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp20761_c0_seq1.p1	Ec-04_000440.1	similar to lysophospholipase II	GO:0016787	IPR029058: Alpha/Beta hydrolase fold; IPR003140: Phospholipase/carboxylesterase/thioesterase; PTHR10655:	KOG2112
comp13442_c0_seq1.p1	Ec-04_000450.1	TALE homeobox domain transcription factor	GO:0003677;GO:0006355;GO:0045449	NA	NA
comp31429_c0_seq9.p1	Ec-04_000460.1	Hypothetical leucine rich repeat protein	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.80.10.10: ; PTHR24420: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF52058: ; IPR001611: Leucine-rich repeat; IPR011646: KAP P-loop; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25310_c0_seq1.p1	Ec-04_000510.1	conserved unknown protein	n/a;n/a;n/a	mobidb-lite: consensus disorder prediction; Coil:	NA
comp12177_c0_seq1.p1	Ec-04_000520.1	divalent cation transporter, carboxyterminus	GO:0006812;GO:0008324	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006667: SLC41 divalent cation transporters, integral membrane domain; IPR000644: CBS domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF161093: ; PTHR11911: ; SIGNAL_PEPTIDE: Signal peptide region; SSF54631: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:3.10.580.10: ; SignalP-noTM: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32287_c0_seq9.p1	Ec-04_000540.1	C2 domain	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF101447: ; Coil: ; IPR000008: C2 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26980_c0_seq2.p1	Ec-04_000560.1	Hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30921_c0_seq2.p1	Ec-04_000570.1	cak1	NA	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; PTHR24056:	NA
comp30976_c0_seq2.p1	Ec-04_000580.1	Dbl homology (DH) domain	GO:0005089;GO:0035023	SSF50729: ; IPR001331: Guanine-nucleotide dissociation stimulator, CDC24, conserved site; IPR011993: Pleckstrin homology-like domain; IPR000219: Dbl homology (DH) domain; PTHR12673: ; IPR001849: Pleckstrin homology domain	NA
comp11314_c0_seq2.p1	Ec-04_000590.1	Tricarboxylate/iron carrier	GO:0016020;GO:0055085;GO:0015075;GO:0006811	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR004686: Tricarboxylate/iron carrier; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24920_c0_seq1.p1	Ec-04_000610.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0006470	IPR000222: PPM-type phosphatase, divalent cation binding; IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C	NA
comp30724_c1_seq1.p1	Ec-04_000620.1	Photosystem II PsbP, oxygen evolving complex	GO:0005509;GO:0009523;GO:0009654;GO:0015979;GO:0019898	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR016123: Mog1/PsbP, alpha/beta/alpha sandwich; IPR006311: Twin-arginine translocation pathway, signal sequence; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002683: Photosystem II PsbP, oxygen evolving complex; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29712_c0_seq2.p2	Ec-04_000630.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24031: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR014014: RNA helicase, DEAD-box type, Q motif; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0342
comp29712_c0_seq2.p1	Ec-04_000655.1	hypothetical protein	NA	Coil: ; G3DSA:1.10.110.10:	NA
comp12461_c0_seq1.p1	Ec-04_000660.1	DUF71 domain	n/a;n/a;n/a	IPR002761: DUF71 domain; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; SSF52402: ; Coil: ; PTHR21037:	NA
comp20959_c0_seq1.p1	Ec-04_000680.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;GO:0008168;GO:0003676;GO:0032259	IPR024576: Ribosomal RNA methyltransferase Spb1, domain of unknown function DUF3381; IPR028589: AdoMet-dependent rRNA methyltransferase, Spb1; IPR012920: Ribosomal RNA methyltransferase, Spb1, C-terminal; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR015507: Ribosomal RNA large subunit methyltransferase E; Coil: ; IPR002877: Ribosomal RNA methyltransferase FtsJ domain	NA
comp32026_c0_seq1.p1	Ec-04_000720.3	DNA polymerase, Y-family, little finger domain	GO:0003684;GO:0006281	SSF56672: ; IPR017961: DNA polymerase, Y-family, little finger domain; G3DSA:3.30.70.270: ; G3DSA:1.10.150.20: ; IPR001126: UmuC domain; PTHR11076:SF12: ; PTHR11076: ; IPR001357: BRCT domain	NA
comp30569_c1_seq5.p1	Ec-04_000730.1	Tyrosinase copper-binding domain	GO:0008152;GO:0016491	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR008922: Uncharacterised domain, di-copper centre; IPR002227: Tyrosinase copper-binding domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32026_c1_seq2.p1	Ec-04_000740.1	WD40 repeat	GO:0005515	PTHR22850: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; mobidb-lite: consensus disorder prediction; PTHR22850:SF160: ; IPR020472: G-protein beta WD-40 repeat	NA
comp19498_c0_seq1.p1	Ec-04_000760.1	Inositol monophosphatase	GO:0046854	G3DSA:3.30.540.10: ; IPR020550: Inositol monophosphatase, conserved site; IPR000760: Inositol monophosphatase; SSF56655: ; G3DSA:3.40.190.80: ; IPR020583: Inositol monophosphatase, metal-binding site	NA
comp12355_c0_seq1.p1	Ec-04_000790.1	Uncharacterised domain, di-copper centre	n/a;GO:0008152;GO:0016491	IPR002227: Tyrosinase copper-binding domain; IPR008922: Uncharacterised domain, di-copper centre; PTHR11474:	NA
comp28531_c0_seq3.p1	Ec-04_000810.1	SF-assemblin	GO:0005200	IPR008374: SF-assemblin; Coil: ; PF06705: SF-assemblin/beta giardin	NA
comp24404_c0_seq1.p1	Ec-04_000860.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR000629: ATP-dependent RNA helicase DEAD-box, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; PTHR24031:	NA
comp27039_c0_seq2.p1	Ec-04_000870.1	conserved unknown protein	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp25071_c0_seq1.p1	Ec-04_000890.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24158: ; IPR002110: Ankyrin repeat	NA
comp29608_c0_seq1.p1	Ec-04_000900.5	SMC2 (STRUCTURAL MAINTENANCE OF CHROMOSOMES 2)	GO:0005515;GO:0005524;GO:0005694;GO:0051276	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR003395: RecF/RecN/SMC, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR18937: ; G3DSA:1.20.1000.10: ; G3DSA:1.20.5.170: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; mobidb-lite: consensus disorder prediction; IPR024704: Structural maintenance of chromosomes protein; G3DSA:3.40.50.300: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:1.20.120.330: ; IPR010935: SMCs flexible hinge; Coil: ; PTHR18937:SF315: ; IPR027120: Smc2, ATP-binding cassette domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29967_c0_seq5.p1	Ec-04_000910.1	Dna2	GO:0017108;GO:0033567;GO:0043142	PTHR10887: ; IPR026851: Dna2; IPR014808: DNA replication factor Dna2, N-terminal	NA
comp30070_c0_seq2.p1	Ec-04_000940.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; PTHR22904:	NA
comp14496_c0_seq1.p1	Ec-04_000950.1	Protein kinase-like domain	GO:0016772	IPR004147: UbiB domain; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.90.1200.10: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011009: Protein kinase-like domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR10566: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28618_c0_seq2.p1	Ec-04_000980.1	expressed unknown protein	NA	NA	NA
comp27091_c0_seq3.p1	Ec-04_001010.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27091_c0_seq4.p1	Ec-04_001020.1	Beta-lactamase-like	n/a;GO:0004416;GO:0008270;GO:0006750	IPR001279: Beta-lactamase-like; Coil: ; PTHR11935: ; IPR017782: Hydroxyacylglutathione hydrolase	NA
comp12036_c0_seq2.p1	Ec-04_001030.2	Flavoprotein-like	GO:0006118;GO:0009055;GO:0016491;GO:0055114	IPR017927: Ferredoxin reductase-type FAD-binding domain; IPR001094: Flavodoxin-like; IPR029039: Flavoprotein-like domain; IPR008254: Flavodoxin/nitric oxide synthase; G3DSA:2.40.30.10: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001433: Oxidoreductase FAD/NAD(P)-binding; PTHR19384: ; IPR028879: NADPH-dependent diflavin oxidoreductase 1; IPR023173: NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3; IPR003097: FAD-binding, type 1; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR001709: Flavoprotein pyridine nucleotide cytochrome reductase; PTHR19384:SF10: ; SIGNAL_PEPTIDE: Signal peptide region; SSF52343: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; G3DSA:3.40.50.80: ; SignalP-noTM: ; IPR017938: Riboflavin synthase-like beta-barrel	NA
comp25494_c0_seq1.p1	Ec-04_001060.1	Periplasmic binding protein-like I	n/a;n/a;n/a	PTHR18966: ; G3DSA:1.10.287.70: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR028082: Periplasmic binding protein-like I; G3DSA:3.40.190.10: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001638: Solute-binding protein family 3/N-terminal domain of MltF; IPR001320: Ionotropic glutamate receptor; IPR001508: Ionotropic glutamate receptor, metazoa; IPR001828: Receptor, ligand binding region; G3DSA:3.40.50.2300: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF53850:	NA
comp11791_c0_seq1.p2	Ec-04_001080.1	Serine Carboxypeptidase-like	GO:0006508;GO:0004185	IPR029058: Alpha/Beta hydrolase fold; IPR001563: Peptidase S10, serine carboxypeptidase; IPR018202: Peptidase S10, serine carboxypeptidase, active site	KOG1282
comp32924_c0_seq1.p1	Ec-04_001090.2	hypothetical protein	NA	NA	NA
comp32924_c0_seq4.p1	Ec-04_001090.3	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; mobidb-lite: consensus disorder prediction; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29928_c0_seq2.p2	Ec-04_001110.1	RNA polymerase I associated factor, A49-like	GO:0005634;GO:0003677;GO:0006351;GO:0003899	PTHR14440: ; IPR009668: RNA polymerase I associated factor, A49-like; Coil:	NA
comp19697_c0_seq1.p1	Ec-04_001120.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32572_c1_seq10.p1	Ec-04_001130.1	UDP-glucose 6-dehydrogenase	GO:0016616;GO:0055114	IPR001732: UDP-glucose/GDP-mannose dehydrogenase, N-terminal; IPR028356: UDP-glucose 6-dehydrogenase, eukaryotic type; SSF51735: ; IPR008927: 6-phosphogluconate dehydrogenase C-terminal domain-like; IPR016040: NAD(P)-binding domain; IPR014027: UDP-glucose/GDP-mannose dehydrogenase, C-terminal; IPR014026: UDP-glucose/GDP-mannose dehydrogenase, dimerisation; G3DSA:1.20.5.100: ; IPR017476: UDP-glucose/GDP-mannose dehydrogenase	KOG2666
comp29006_c0_seq3.p2	Ec-04_001140.1	Nucleoside diphosphate kinase	GO:0005524;GO:0006241;GO:0006165;GO:0004550;GO:0006228;GO:0006183	SIGNAL_PEPTIDE: Signal peptide region; IPR001564: Nucleoside diphosphate kinase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11349: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29006_c0_seq3.p1	Ec-04_001150.1	Heat Shock transcription factor	GO:0005634;GO:0006355;GO:0043565;GO:0003700	NA	NA
comp27215_c0_seq4.p1	Ec-04_001180.1	conserved unknown protein	GO:0005515;GO:0006461;GO:0006886;GO:0008565;GO:0016192;GO:0030131	NA	NA
comp27215_c0_seq4.p2	Ec-04_001190.1	SEC-C motif	n/a;n/a;n/a	SSF103642: ; IPR003323: OTU domain; SSF54001: ; PTHR12419: ; IPR004027: SEC-C motif; G3DSA:3.10.450.50: ; Coil:	NA
comp12879_c0_seq1.p3	Ec-04_001200.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32839_c1_seq6.p1	Ec-04_001210.1	dolichyldiphosphatase	GO:0016020;GO:0003824	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR11247: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000326: Phosphatidic acid phosphatase type 2/haloperoxidase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3146
comp26590_c0_seq2.p1	Ec-04_001220.1	Rab-GTPase-TBC domain	GO:0005097;GO:0032313;GO:0035091	G3DSA:1.10.8.270: ; IPR000195: Rab-GTPase-TBC domain; PTHR22957: ; IPR001683: Phox homologous domain	NA
comp11791_c0_seq1.p1	Ec-04_001260.1	Tubular mastigoneme-related protein	n/a;n/a;n/a	PTHR24035: ; SIGNAL_PEPTIDE: Signal peptide region; IPR000742: Epidermal growth factor-like domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013032: EGF-like, conserved site; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; G3DSA:2.170.300.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp35754_c0_seq1.p1	Ec-04_001270.1	expressed unknown protein	n/a;n/a;n/a	G3DSA:1.25.10.20: ; mobidb-lite: consensus disorder prediction	NA
comp30936_c0_seq2.p1	Ec-04_001280.1	AMP-binding enzyme C-terminal domain	GO:0003824;GO:0008152	PTHR24095:SF169: ; PTHR24095: ; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.40.50.980: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000873: AMP-dependent synthetase/ligase; G3DSA:2.30.38.10: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.30.300.30: ; IPR020845: AMP-binding, conserved site; IPR025110: AMP-binding enzyme C-terminal domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF56801:	NA
comp30936_c0_seq8.p1	Ec-04_001300.1	conserved unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27332_c0_seq1.p1	Ec-04_001310.1	expressed unknown protein	n/a;n/a;n/a	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31590_c0_seq9.p1	Ec-04_001330.1	Zinc finger, RING/FYVE/PHD-type	GO:0004842;GO:0008152;GO:0016491;GO:0016567;GO:0055114	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; IPR003613: U box domain; cd16655: RING-Ubox_WDSUB1_like; PTHR24068:SF115: ; mobidb-lite: consensus disorder prediction; SSF57850: ; SM00212: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR000608: Ubiquitin-conjugating enzyme E2; Coil: ; IPR002035: von Willebrand factor, type A; PTHR24068:	NA
comp27176_c0_seq3.p1	Ec-04_001420.1	Hypothetical protein	n/a;n/a;n/a	PTHR32134:SF11: ; IPR008615: FNIP; PTHR32134: ; IPR032675: Leucine-rich repeat domain, L domain-like	NA
comp27483_c0_seq1.p1	Ec-04_001470.1	pleiotropic drug resistance transporter	GO:0005524;GO:0016887;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR003439: ABC transporter-like; IPR027417: P-loop containing nucleoside triphosphate hydrolase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013525: ABC-2 type transporter; IPR017871: ABC transporter, conserved site; PTHR19241:	NA
comp11821_c0_seq1.p1	Ec-04_001480.1	Ribosomal protein L21e	GO:0003735;GO:0005622;GO:0005840;GO:0006412	IPR008991: Translation protein SH3-like domain; PTHR20981:SF6: ; IPR001147: Ribosomal protein L21e; IPR018259: Ribosomal protein L21e, conserved site	NA
comp19424_c0_seq1.p1	Ec-04_001490.1	GS1-like protein	NA	PTHR18901: ; IPR006439: HAD hydrolase, subfamily IA; IPR023214: HAD-like domain	NA
comp24439_c0_seq1.p1	Ec-04_001500.1	Heat shock protein 40	GO:0006457;GO:0005524;GO:0031072;GO:0009408;GO:0051082	IPR008971: HSP40/DnaJ peptide-binding; IPR002939: Chaperone DnaJ, C-terminal; IPR001623: DnaJ domain; IPR001305: Heat shock protein DnaJ, cysteine-rich domain; IPR018253: DnaJ domain, conserved site; PTHR24076: ; IPR012724: Chaperone DnaJ; G3DSA:2.60.260.20:	KOG0715
comp33284_c0_seq1.p1	Ec-04_001520.1	Zinc finger and SET domain protein	GO:0005515	NA	NA
comp29847_c0_seq4.p1	Ec-04_001540.1	Pseudouridine synthase, RluD	GO:0003723;GO:0001522;GO:0009451;GO:0009982	IPR020103: Pseudouridine synthase, catalytic domain; SSF55174: ; IPR006145: Pseudouridine synthase, RsuA/RluB/C/D/E/F; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002942: RNA-binding S4 domain; IPR006224: Pseudouridine synthase, RluC/RluD, conserved site; IPR006225: Pseudouridine synthase, RluC/RluD; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10436: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12105_c0_seq1.p3	Ec-04_001570.2	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp33616_c0_seq1.p1	Ec-04_001610.1	Na+/H+ exchanger	GO:0006814;GO:0006885;GO:0015385;GO:0016021;GO:0055085	IPR018422: Cation/H+ exchanger, CPA1 family; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR004709: Na+/H+ exchanger; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006153: Cation/H+ exchanger; Coil: ; PTHR10110:SF114: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31505_c0_seq8.p1	Ec-04_001620.1	Similar to two-pore calcium channel [Arabidopsis thaliana]. Fragment	GO:0016020;GO:0005216;GO:0006811	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10037: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; mobidb-lite: consensus disorder prediction; IPR028801: Two pore calcium channel protein 1; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2301
comp11888_c0_seq1.p1	Ec-04_001690.1	Ubiquitin-conjugating enzyme/RWD-like	GO:0019787;GO:0043687;GO:0051246	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR24067: ; SM00212: Ubiquitin-conjugating enzyme E2, catalytic domain homologues; SignalP-noTM: ; IPR000608: Ubiquitin-conjugating enzyme E2; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33551_c0_seq1.p1	Ec-04_001700.1	SAP domain	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SSF68906: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003034: SAP domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31057_c0_seq5.p1	Ec-04_001710.1	Rab3 GTPase-activating protein catalytic subunit	GO:0005097	IPR026147: Rab3 GTPase-activating protein catalytic subunit	NA
comp25229_c0_seq1.p1	Ec-04_001720.1	peptidyl prolyl cis/trans isomerase like	GO:0016853	PTHR10657: ; IPR001763: Rhodanese-like domain; G3DSA:3.10.50.40: ; SSF54534: ; SIGNAL_PEPTIDE: Signal peptide region; IPR023058: Peptidyl-prolyl cis-trans isomerase, PpiC-type, conserved site; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000297: Peptidyl-prolyl cis-trans isomerase, PpiC-type; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28435_c1_seq5.p1	Ec-04_001740.1	Histidine kinase-like ATPase	n/a;n/a;n/a	PF13589: Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase; cd00075: HATPase_c; PTHR22640:SF3: ; PTHR22640: ; mobidb-lite: consensus disorder prediction; IPR003594: Histidine kinase-like ATPase, C-terminal domain	NA
comp11748_c0_seq1.p1	Ec-04_001790.1	Ankyrin repeat-containing domain	n/a;GO:0005515	PTHR16036: ; IPR020683: Ankyrin repeat-containing domain; Coil: ; IPR002110: Ankyrin repeat	NA
comp30882_c0_seq1.p1	Ec-04_001810.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR013105: Tetratricopeptide TPR2; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; PTHR23083:	NA
comp32269_c3_seq9.p2	Ec-04_001820.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32269_c3_seq9.p1	Ec-04_001830.1	BCNT-C domain	n/a;n/a;n/a	IPR011421: BCNT-C domain	NA
comp30562_c0_seq2.p1	Ec-04_001850.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp34303_c0_seq1.p1	Ec-04_001860.1	conserved unknown protein	n/a;n/a;n/a	mobidb-lite: consensus disorder prediction; PTHR39290:	NA
comp48404_c0_seq1.p1	Ec-04_001865.1	hypothetical protein	NA	mobidb-lite: consensus disorder prediction; Coil:	NA
comp19991_c0_seq1.p1	Ec-04_001870.1	WD40 repeat	GO:0005515	PTHR19856: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; SSF63829: ; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily	NA
comp31573_c0_seq3.p1	Ec-04_001880.1	RmlC-like jelly roll fold	n/a;n/a;n/a	IPR000595: Cyclic nucleotide-binding domain; PTHR10217: ; G3DSA:1.10.287.70: ; IPR003938: Potassium channel, voltage-dependent, EAG/ELK/ERG; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF81324: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018490: Cyclic nucleotide-binding-like; IPR005821: Ion transport domain; G3DSA:1.10.287.630: ; Coil: ; IPR014710: RmlC-like jelly roll fold; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31646_c0_seq1.p1	Ec-04_001970.4	Armadillo-type fold	GO:0005488	PTHR17695:SF11: ; IPR011989: Armadillo-like helical; PTHR17695: ; IPR011430: Down-regulated-in-metastasis protein; IPR016024: Armadillo-type fold; Coil:	NA
comp31646_c0_seq1.p2	Ec-04_001970.5	Armadillo-type fold	GO:0005488	PTHR17695:SF11: ; IPR011989: Armadillo-like helical; PTHR17695: ; IPR011430: Down-regulated-in-metastasis protein; IPR016024: Armadillo-type fold; Coil:	NA
comp19822_c0_seq1.p1	Ec-04_001980.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30836_c0_seq6.p1	Ec-04_001990.5	WD40 repeat	GO:0005515	SIGNAL_PEPTIDE: Signal peptide region; IPR001680: WD40 repeat; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22847: ; SignalP-noTM: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24669_c1_seq1.p1	Ec-04_002000.1	Nuclear pore protein 84/107	GO:0006810;GO:0005643	IPR007252: Nuclear pore protein 84/107; Coil:	NA
comp20569_c0_seq2.p1	Ec-04_002010.2	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	GO:0003755;GO:0006457	IPR024936: Cyclophilin-type peptidyl-prolyl cis-trans isomerase; PTHR11071:SF152: ; IPR002130: Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain; IPR029000: Cyclophilin-like domain; IPR020892: Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site; Coil:	NA
comp12209_c0_seq1.p1	Ec-04_002020.1	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR16038:SF4: ; PTHR16038: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp24135_c0_seq1.p1	Ec-04_002030.1	F-box domain	GO:0005515	IPR001810: F-box domain; G3DSA:3.80.10.10: ; G3DSA:1.20.1280.50: ; PTHR24106: ; SSF52047: ; PF13516: Leucine Rich repeat	NA
comp30100_c0_seq4.p1	Ec-04_002040.1	Hypothetical leucine rich repeat protein	GO:0005515	SM00364: Leucine-rich repeats, bacterial type; IPR003591: Leucine-rich repeat, typical subtype; PR00019: Leucine-rich repeat signature; IPR001611: Leucine-rich repeat; SM00365: Leucine-rich repeat, SDS22-like subfamily; IPR032675: Leucine-rich repeat domain, L domain-like; PTHR23155:	NA
comp32062_c0_seq6.p1	Ec-04_002050.1	Armadillo-like helical	GO:0001539;GO:0016020;GO:0003774;GO:0006935;GO:0005488	NA	NA
comp32062_c2_seq2.p1	Ec-04_002050.3	Armadillo-like helical	GO:0001539;GO:0003774;GO:0006935;GO:0016020	PTHR11139:SF1: ; PTHR11139: ; IPR016024: Armadillo-type fold; Coil:	NA
comp27634_c0_seq1.p1	Ec-04_002060.1	Phosphatidylinositol 3-/4-kinase, catalytic domain	GO:0016773	NA	NA
comp30941_c1_seq6.p1	Ec-04_002080.2	Cobalamin (vitamin B12) biosynthesis CobW-like, C-terminal	n/a;n/a;n/a	PTHR13748:SF4: ; PTHR13748: ; Coil: ; IPR011629: Cobalamin (vitamin B12) biosynthesis CobW-like, C-terminal	NA
comp31959_c0_seq12.p1	Ec-04_002090.1	Major facilitator superfamily domain	n/a;GO:0055085;GO:0016021;GO:0022857	IPR005829: Sugar transporter, conserved site; IPR005828: General substrate transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; PTHR24064: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24621_c0_seq1.p1	Ec-04_002180.1	Short-chain dehydrogenase/reductase	GO:0008152;GO:0016491	PTHR24322: ; SSF51735: ; IPR020904: Short-chain dehydrogenase/reductase, conserved site; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0725
comp32758_c0_seq5.p1	Ec-04_002190.1	Beta-glucosidase, family GH30	GO:0003824;GO:0043169;GO:0005975	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000772: Ricin B lectin domain; IPR017853: Glycoside hydrolase superfamily; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:2.80.10.50: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001139: Glycoside hydrolase, family 30; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013781: Glycoside hydrolase, catalytic domain	KOG2566
comp23746_c0_seq1.p1	Ec-04_002200.1	putative 8-amino-7-oxononanoate synthase	GO:0003824;GO:0030170	IPR015424: Pyridoxal phosphate-dependent transferase; IPR004839: Aminotransferase, class I/classII; PTHR13693: ; Coil: ; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	NA
comp29027_c0_seq3.p1	Ec-04_002210.3	hypothetical protein	NA	Coil:	NA
comp31505_c0_seq8.p2	Ec-04_002220.1	EF-hand domain pair	n/a;n/a;n/a	IPR018247: EF-Hand 1, calcium-binding site; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR023393: START-like domain; PTHR12901: ; SSF47473: ; SSF55961: ; IPR005031: Streptomyces cyclase/dehydrase	NA
comp32292_c1_seq5.p1	Ec-04_002230.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp27099_c0_seq2.p1	Ec-04_002240.1	Histone H3	GO:0003677;GO:0000786	NA	NA
comp33970_c0_seq1.p1	Ec-04_002250.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20489_c0_seq1.p1	Ec-04_002260.1	WD40/YVTN repeat-like-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; PTHR19857: ; IPR020472: G-protein beta WD-40 repeat	NA
comp30187_c0_seq2.p1	Ec-04_002280.1	Peroxiredoxin family protein	GO:0016209;GO:0016491;GO:0055114	IPR000866: Alkyl hydroperoxide reductase subunit C/ Thiol specific antioxidant; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR10681: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp19686_c2_seq1.p1	Ec-04_002290.1	UbiB domain	n/a;n/a;n/a	IPR004147: UbiB domain; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.90.1200.10: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011009: Protein kinase-like domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; PTHR10566: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20423_c0_seq1.p1	Ec-04_002380.1	expressed unknown protein	GO:0005488	IPR011989: Armadillo-like helical; mobidb-lite: consensus disorder prediction	NA
comp22435_c1_seq3.p1	Ec-04_002390.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp25236_c0_seq2.p1	Ec-04_002420.1	RED-like, N-terminal	GO:0005634	IPR012916: RED-like, N-terminal; PTHR12765:	NA
comp19354_c0_seq2.p1	Ec-04_002430.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30196_c0_seq6.p1	Ec-04_002450.1	Small nuclear ribonucleoprotein-associated protein D3	GO:0030529;GO:0016071	IPR001163: Ribonucleoprotein LSM domain; G3DSA:2.30.30.100: ; IPR010920: Like-Sm (LSM) domain; IPR027141: Like-Sm (LSM) domain containing protein, LSm4/SmD1/SmD3; IPR006649: Ribonucleoprotein LSM domain, eukaryotic/archaea-type	NA
comp34462_c0_seq1.p1	Ec-04_002460.1	Winged helix-turn-helix DNA-binding domain	n/a;n/a;n/a	SSF48452: ; IPR011991: Winged helix-turn-helix DNA-binding domain; IPR000717: Proteasome component (PCI) domain; SSF46785: ; IPR011990: Tetratricopeptide-like helical domain; PTHR10678: ; Coil: ; IPR013143: PCI/PINT associated module	NA
comp30545_c2_seq3.p1	Ec-04_002480.1	Armadillo-like helical	NA	G3DSA:3.30.1010.10: ; IPR000403: Phosphatidylinositol 3-/4-kinase, catalytic domain; IPR011989: Armadillo-like helical; IPR011009: Protein kinase-like domain; IPR003151: PIK-related kinase, FAT; Coil: ; PTHR11139: ; IPR014009: PIK-related kinase; IPR016024: Armadillo-type fold; IPR003152: PIK-related kinase, FATC	NA
comp29751_c0_seq2.p1	Ec-04_002590.1	UDP-Glc/Gal endoplasmic reticulum nucleotide sugar transporter	GO:0055085	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF103481: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013657: UAA transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10778: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp15700_c0_seq1.p1	Ec-04_002600.1	Thioredoxin-like fold	GO:0008152;GO:0016740;n/a	IPR013783: Immunoglobulin-like fold; PTHR13871: ; IPR003961: Fibronectin type III; IPR012336: Thioredoxin-like fold	NA
comp30538_c0_seq1.p1	Ec-04_002610.1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG	n/a;n/a;n/a	PTHR31223: ; IPR031100: LOG family; G3DSA:3.40.50.450: ; SSF102405:	NA
comp31044_c0_seq5.p1	Ec-04_002630.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	G3DSA:3.40.50.300: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; mobidb-lite: consensus disorder prediction; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24523_c0_seq1.p1	Ec-04_002660.1	Hypothetical leucine rich repeat protein	GO:0005515	PTHR24365: ; IPR001611: Leucine-rich repeat; SM00365: Leucine-rich repeat, SDS22-like subfamily; IPR032675: Leucine-rich repeat domain, L domain-like; Coil:	NA
comp31044_c0_seq4.p1	Ec-04_002680.1	Hypothetical leucine rich repeat protein	NA	PTHR24106: ; SSF52047: ; IPR032675: Leucine-rich repeat domain, L domain-like; IPR003590: Leucine-rich repeat, ribonuclease inhibitor subtype	NA
comp24431_c0_seq4.p1	Ec-04_002700.1	CDP-alcohol phosphatidyltransferase	GO:0016020;GO:0008654;GO:0016780	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14269: ; IPR000462: CDP-alcohol phosphatidyltransferase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1617
comp24301_c0_seq1.p1	Ec-04_002710.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp28315_c0_seq1.p1	Ec-04_002720.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR24089: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002067: Mitochondrial carrier protein; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27098_c0_seq1.p1	Ec-04_002730.1	Bud13	n/a;n/a;n/a	PTHR31809: ; IPR018609: Bud13	NA
comp27098_c0_seq5.p4	Ec-04_002740.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp27098_c0_seq5.p1	Ec-04_002750.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp11749_c0_seq1.p1	Ec-04_002760.1	mRNA capping enzyme	GO:0006397;GO:0006370;GO:0004484	IPR012340: Nucleic acid-binding, OB-fold; IPR001339: mRNA capping enzyme; PTHR10367: ; G3DSA:3.30.470.30: ; IPR004206: mRNA capping enzyme, beta subunit, structural domain; IPR023577: CYTH-like domain; IPR013846: mRNA capping enzyme, C-terminal; SSF56091:	NA
comp33195_c0_seq8.p1	Ec-04_002770.1	Peptidase A22B, signal peptide peptidase	GO:0004190;GO:0016021	IPR003137: PA domain; SSF52025: ; G3DSA:3.50.30.30: ; IPR007369: Peptidase A22B, signal peptide peptidase	NA
comp12345_c0_seq2.p1	Ec-04_002790.1	spermidine/spermine synthase	GO:0003824;GO:0004766;GO:0006595;GO:0016768	PF01564: Spermine/spermidine synthase; PTHR11558: ; G3DSA:2.30.140.10: ; PTHR11558:SF26: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR001045: Spermidine/spermine synthases; IPR030374: Polyamine biosynthesis domain	KOG1562
comp24702_c0_seq1.p1	Ec-04_002810.1	Phytoene synthase; chloroplast precursor	GO:0009058;GO:0016740	IPR019845: Squalene/phytoene synthase, conserved site; IPR008949: Isoprenoid synthase domain; PTHR31480: ; IPR002060: Squalene/phytoene synthase	NA
comp24855_c0_seq1.p1	Ec-04_002820.1	Ribosomal protein L22/L17	GO:0005840;GO:0015934;GO:0006412;GO:0003735	NA	NA
comp32169_c0_seq5.p1	Ec-04_002830.1	Bromodomain	GO:0003677;GO:0005515;GO:0005634;GO:0008270	IPR003889: FY-rich, C-terminal; IPR001965: Zinc finger, PHD-type; IPR003888: FY-rich, N-terminal; PTHR22880:SF5: ; IPR001876: Zinc finger, RanBP2-type; IPR001487: Bromodomain; PTHR22880: ; IPR028942: WHIM1 domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; Coil: ; IPR011011: Zinc finger, FYVE/PHD-type; IPR028935: WHIM3 domain; IPR002857: Zinc finger, CXXC-type; IPR019787: Zinc finger, PHD-finger	NA
comp32169_c0_seq4.p1	Ec-04_002830.2	Bromodomain	GO:0005515	IPR003889: FY-rich, C-terminal; IPR003888: FY-rich, N-terminal	NA
comp24292_c0_seq1.p1	Ec-04_002850.1	folate/biopterin transporter	GO:0006810;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020846: Major facilitator superfamily domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR31585: ; IPR004324: Folate-biopterin transporter; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29920_c0_seq5.p2	Ec-04_002860.1	Domain of unknown function DUF2233	n/a;n/a;n/a	IPR026876: Fn3 associated repeat; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR018711: Domain of unknown function DUF2233; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29920_c0_seq5.p3	Ec-04_002870.1	Manganese/iron superoxide dismutase, N-terminal	GO:0006801;GO:0004784;GO:0055114;GO:0046872	IPR019831: Manganese/iron superoxide dismutase, N-terminal; G3DSA:1.10.287.990: ; IPR001189: Manganese/iron superoxide dismutase; IPR019832: Manganese/iron superoxide dismutase, C-terminal; IPR019833: Manganese/iron superoxide dismutase, binding site	KOG0876
comp29920_c0_seq5.p1	Ec-04_002890.1	Sterile alpha motif/pointed domain	GO:0003676;GO:0003723;GO:0005515;n/a	PS50084: Type-1 KH domain profile.; IPR013761: Sterile alpha motif/pointed domain; IPR011990: Tetratricopeptide-like helical domain; IPR001660: Sterile alpha motif domain; G3DSA:1.10.150.50: ; IPR004087: K Homology domain; IPR004088: K Homology domain, type 1; cd00105: KH-I; IPR013083: Zinc finger, RING/FYVE/PHD-type; PF13920: Zinc finger, C3HC4 type (RING finger); PTHR10288:SF199: ; Coil: ; PTHR10288:	NA
comp20115_c0_seq1.p1	Ec-04_002950.1	importin alpha	GO:0005488	PTHR23316: ; IPR011989: Armadillo-like helical; IPR000225: Armadillo; IPR016024: Armadillo-type fold; PF13646: HEAT repeats	NA
comp21066_c0_seq1.p1	Ec-04_002960.1	Alpha-(1,2)-mannosyltransferase, family GT4	GO:0009058	SSF53756: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; mobidb-lite: consensus disorder prediction; IPR001296: Glycosyl transferase, family 1; PTHR12526: ; PTHR12526:SF431: ; G3DSA:3.40.50.2000: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR031814: ALG11 mannosyltransferase, N-terminal; cd03806: GT1_ALG11_like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1387
comp28768_c0_seq1.p1	Ec-04_002970.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020;GO:0055085	PTHR24089: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; IPR023395: Mitochondrial carrier domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp12891_c0_seq1.p1	Ec-04_003000.1	Rieske [2Fe-2S] iron-sulphur domain	GO:0051537;GO:0055114;GO:0016491	IPR017941: Rieske [2Fe-2S] iron-sulphur domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PF13806: Rieske-like [2Fe-2S] domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27956_c0_seq5.p1	Ec-04_003010.1	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	GO:0003755	NA	NA
comp28764_c0_seq1.p1	Ec-04_003020.1	Vacuolar sorting protein 39/Transforming growth factor beta receptor-associated domain 2	n/a;n/a;n/a	IPR007810: Pep3/Vps18/deep orange; PTHR23323:SF26: ; PTHR23323: ; SSF101908: ; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR015943: WD40/YVTN repeat-like-containing domain; Coil: ; IPR019453: Vacuolar sorting protein 39/Transforming growth factor beta receptor-associated domain 2	NA
comp33751_c0_seq1.p1	Ec-04_003030.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF101447: ; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25293_c0_seq2.p1	Ec-04_003040.1	GRIP	GO:0005515;GO:0000042	IPR000237: GRIP; Coil: ; PTHR23157:	NA
comp20411_c0_seq1.p2	Ec-04_003050.1	Histone-like transcription factor, NF-YB subunit	GO:0046982;GO:0043565;GO:0005622	NA	NA
comp30984_c0_seq4.p1	Ec-04_003070.1	Armadillo-like helical	GO:0005515;GO:0005488	NA	NA
comp32243_c1_seq3.p1	Ec-04_003080.1	WD40-repeat-containing domain	GO:0005515	IPR019775: WD40 repeat, conserved site; IPR012972: NLE; IPR001680: WD40 repeat; PTHR19855: ; IPR020472: G-protein beta WD-40 repeat; IPR017986: WD40-repeat-containing domain; IPR028599: WD repeat WDR12/Ytm1; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp35438_c0_seq1.p1	Ec-04_003090.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp22172_c0_seq1.p1	Ec-04_003100.1	conserved unknown protein	GO:0005515	IPR003137: Protease-associated domain, PA; IPR013783: Immunoglobulin-like fold; SSF52025: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR003961: Fibronectin type III; G3DSA:3.50.30.30:	NA
comp11712_c0_seq1.p1	Ec-04_003120.1	F-box domain	GO:0005515	IPR001810: F-box domain; G3DSA:1.20.1280.50: ; PTHR12874:	NA
comp19789_c0_seq1.p1	Ec-04_003130.1	Adenosine deaminase/editase	GO:0003723;GO:0004000;GO:0006396	PTHR10910:SF122: ; PTHR10910: ; IPR002466: Adenosine deaminase/editase; mobidb-lite: consensus disorder prediction	NA
comp32472_c0_seq1.p1	Ec-04_003150.1	conserved unknown protein	GO:0005515	IPR000409: BEACH domain; IPR019775: WD40 repeat, conserved site; IPR011989: Armadillo-like helical; G3DSA:2.60.120.200: ; G3DSA:2.30.29.40: ; IPR001680: WD40 repeat; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR13743: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017986: WD40-repeat-containing domain; IPR011993: PH domain-like; IPR015943: WD40/YVTN repeat-like-containing domain; Coil: ; IPR023362: PH-BEACH domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28300_c2_seq2.p1	Ec-04_003170.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	SSF54928: ; PTHR24012: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000504: RNA recognition motif domain; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR012677: Nucleotide-binding alpha-beta plait domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp34532_c0_seq1.p1	Ec-04_003180.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp14105_c0_seq1.p1	Ec-04_003200.1	Sterile alpha motif/pointed domain	n/a;n/a;n/a	IPR013761: Sterile alpha motif/pointed domain; IPR001660: Sterile alpha motif domain; IPR021129: Sterile alpha motif, type 1	NA
comp32725_c0_seq1.p1	Ec-04_003210.1	Acyltransferase 3	GO:0016747	PTHR11161: ; IPR002656: Acyltransferase 3; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30384_c0_seq3.p1	Ec-04_003240.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	NA	NA
comp26630_c0_seq1.p2	Ec-04_003250.1	GINS complex, subunit Psf3	n/a;n/a;n/a	SSF160059: ; IPR010492: GINS complex, subunit Psf3; Coil: ; SSF158573:	NA
comp26630_c0_seq1.p1	Ec-04_003260.1	Inorganic pyrophosphatase	GO:0000287;GO:0004427;GO:0005737;GO:0006796	IPR008162: Inorganic pyrophosphatase	NA
comp13087_c0_seq1.p1	Ec-04_003270.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	IPR029058: Alpha/Beta hydrolase fold; IPR010765: Protein of unknown function DUF1350	NA
comp24587_c0_seq2.p1	Ec-04_003290.3	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12858_c0_seq1.p1	Ec-04_003300.1	Rhodanese-like domain	n/a;n/a;n/a	IPR001763: Rhodanese-like domain; PTHR12231: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33869_c0_seq1.p1	Ec-04_003320.1	Coatomer protein complex, beta sub-unit Vesicle coat complex COPI, beta subunit	GO:0016192;GO:0006886;GO:0030117;GO:0005515;GO:0006461	IPR011710: Coatomer beta subunit, C-terminal; IPR011989: Armadillo-like helical; IPR016460: Coatomer beta subunit (COPB1); IPR016024: Armadillo-type fold; IPR029446: Coatomer beta subunit, appendage platform domain; IPR002553: Clathrin/coatomer adaptor, adaptin-like, N-terminal	KOG1058
comp30620_c1_seq1.p1	Ec-04_003330.1	Zinc finger, RING/FYVE/PHD-type	GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000306: FYVE zinc finger; IPR017455: Zinc finger, FYVE-related; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12406_c0_seq1.p1	Ec-04_003360.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003677;GO:0005634;GO:0006260	PF13177: DNA polymerase III, delta subunit; PTHR11669: ; G3DSA:1.20.272.10: ; IPR013748: Replication factor C, C-terminal domain; IPR008921: DNA polymerase III, clamp loader complex, gamma/delta/delta subunit, C-terminal; G3DSA:1.10.8.60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp32157_c0_seq16.p1	Ec-04_003370.1	SANT/Myb domain	GO:0003682	NA	NA
comp30802_c0_seq2.p1	Ec-04_003410.1	YihA4, YihA/EngB-like GTPase	GO:0000917;GO:0005525	SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006073: GTP binding domain; SignalP-noTM: ; IPR019987: GTP-binding protein, ribosome biogenesis, YsxC; IPR030393: EngB-type guanine nucleotide-binding (G) domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11649:	NA
comp21520_c0_seq1.p2	Ec-04_003430.1	Ribosomal protein L10/L12	GO:0005840;GO:0005622;GO:0006414;GO:0003735	IPR027534: Ribosomal protein L12 family; PF00428: 60s Acidic ribosomal protein; PTHR21141:	NA
comp26065_c0_seq3.p1	Ec-04_003450.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	PTHR13748:SF4: ; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR003495: CobW/HypB/UreG domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR13748: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR011629: Cobalamin (vitamin B12) biosynthesis CobW-like, C-terminal	NA
comp20454_c0_seq1.p1	Ec-04_003460.1	1-aminocyclopropane-1-carboxylate synthase	GO:0003824;GO:0006555;GO:0030170;GO:0016847	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR004839: Aminotransferase, class I/classII; IPR015424: Pyridoxal phosphate-dependent transferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004838: Aminotransferases, class-I, pyridoxal-phosphate-binding site; PR00753: 1-aminocyclopropane-1-carboxylate synthase signature; PTHR11751: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2	KOG0256
comp24369_c0_seq1.p1	Ec-04_003520.1	Cation efflux protein cytoplasmic domain	GO:0006812;GO:0008324;GO:0016020;GO:0055085;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027469: Cation efflux protein transmembrane domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF160240: ; IPR002524: Cation efflux protein; IPR027470: Cation efflux protein, cytoplasmic domain; PTHR11562:SF18: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF161111: ; SignalP-noTM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32569_c0_seq5.p1	Ec-04_003540.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000863: Sulfotransferase domain; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26097_c0_seq1.p1	Ec-04_003550.1	RAN, Ras superfamily GTPase	GO:0005622;GO:0007264;GO:0005525	IPR002041: Ran GTPase; PTHR24071: ; IPR005225: Small GTP-binding protein domain; IPR001806: Small GTPase superfamily; IPR003579: Small GTPase superfamily, Rab type; IPR020849: Small GTPase superfamily, Ras type; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type	NA
comp33775_c0_seq1.p1	Ec-04_003560.1	Ribosome recycling factor	GO:0006412	IPR023584: Ribosome recycling factor domain; G3DSA:3.40.91.10: ; mobidb-lite: consensus disorder prediction; PTHR20982:SF9: ; SignalP-TM: ; IPR002661: Ribosome recycling factor	NA
comp31603_c0_seq2.p1	Ec-04_003570.1	similar to chromodomain helicase DNA binding protein 4 isoform 5	n/a;n/a;n/a	IPR009463: Domain of unknown function DUF1087; G3DSA:2.40.50.40: ; IPR001965: Zinc finger, PHD-type; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR000953: Chromo/chromo shadow domain; IPR000330: SNF2-related, N-terminal domain; IPR023780: Chromo domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR016197: Chromo domain-like; IPR014001: Helicase superfamily 1/2, ATP-binding domain; PTHR10799: ; Coil: ; IPR001650: Helicase, C-terminal; IPR011011: Zinc finger, FYVE/PHD-type; IPR019787: Zinc finger, PHD-finger	NA
comp31762_c0_seq1.p1	Ec-04_003620.1	ENTH domain protein	n/a;n/a;n/a	PTHR12276: ; PTHR12276:SF79: ; IPR013809: ENTH domain; IPR008942: ENTH/VHS	NA
comp28317_c0_seq1.p1	Ec-04_003630.1	Sugar/inositol transporter	GO:0016020;GO:0055085;GO:0016021;GO:0022891;GO:0022857	IPR005829: Sugar transporter, conserved site; IPR005828: General substrate transporter; IPR003663: Sugar/inositol transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; PTHR24063: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27110_c0_seq1.p1	Ec-04_003640.1	Digalactosyldiacylglycerol synthase, family GT4	GO:0009058	SSF53756: ; PTHR12526: ; G3DSA:3.40.50.2000: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13692: Glycosyl transferases group 1; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	no relat
comp30446_c0_seq1.p1	Ec-04_003680.1	BRCT domain	GO:0005622	PTHR13561: ; mobidb-lite: consensus disorder prediction; PTHR13561:SF37: ; IPR001357: BRCT domain	NA
comp30446_c0_seq1.p2	Ec-04_003690.1	mannitol 1-phosphate dehydrogenase	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	n
comp11773_c0_seq1.p1	Ec-04_003700.1	Haloacid dehalogenase-like hydrolase	GO:0003824;GO:0008152	SIGNAL_PEPTIDE: Signal peptide region; PTHR18901: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023214: HAD-like domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp13445_c0_seq1.p1	Ec-04_003710.1	Armadillo-type fold	GO:0005488	IPR000357: HEAT; IPR011989: Armadillo-like helical; IPR000225: Armadillo; PTHR23314: ; IPR016024: Armadillo-type fold	NA
comp20580_c0_seq2.p1	Ec-04_003740.1	Glycoside hydrolase family 31	GO:0004553;GO:0005975	NA	NA
comp24262_c0_seq1.p3	Ec-04_003750.1	WD40-repeat-containing domain	GO:0005515	PTHR15728:SF0: ; PTHR15728: ; IPR015943: WD40/YVTN repeat-like-containing domain; SSF101898:	NA
comp31585_c1_seq1.p1	Ec-04_003770.1	Exonuclease, RNase T/DNA polymerase III	GO:0003676;n/a	SSF54001: ; mobidb-lite: consensus disorder prediction; IPR013520: Exonuclease, RNase T/DNA polymerase III; IPR028881: PAN2 domain; PTHR15728: ; G3DSA:3.90.70.10: ; IPR012337: Ribonuclease H-like domain; Coil: ; cd06143: PAN2_exo	NA
comp26203_c0_seq1.p1	Ec-04_003780.1	Hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; mobidb-lite: consensus disorder prediction; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32145_c2_seq2.p1	Ec-04_003800.1	Subunit of the Anaphase Promoting Complex	GO:0006511;GO:0031461;GO:0031625	IPR011991: Winged helix-turn-helix DNA-binding domain; G3DSA:1.20.1310.10: ; IPR016158: Cullin homology; IPR014786: Anaphase-promoting complex subunit 2, C-terminal; mobidb-lite: consensus disorder prediction; IPR001373: Cullin, N-terminal; PTHR11932: ; Coil: ; G3DSA:4.10.1030.10: ; PTHR11932:SF96:	KOG2165
comp33154_c1_seq12.p1	Ec-04_003810.1	putative phosphatidylinositol 3-kinase	GO:0016773;GO:0008270	G3DSA:3.30.1010.10: ; IPR000403: Phosphatidylinositol 3-/4-kinase, catalytic domain; IPR001263: Phosphoinositide 3-kinase, accessory (PIK) domain; IPR011009: Protein kinase-like domain; IPR000306: FYVE zinc finger; IPR017455: Zinc finger, FYVE-related; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR015433: Phosphatidylinositol Kinase; IPR016024: Armadillo-type fold; Coil: ; IPR011011: Zinc finger, FYVE/PHD-type; IPR018936: Phosphatidylinositol 3/4-kinase, conserved site	NA
comp32145_c2_seq16.p1	Ec-04_003820.1	RNA polymerase sigma-70 like domain	GO:0003677;GO:0003700;GO:0006352;GO:0006355;GO:0016987	IPR013325: RNA polymerase sigma factor, region 2; IPR011991: Winged helix-turn-helix DNA-binding domain; PTHR30603: ; IPR007624: RNA polymerase sigma-70 region 3; G3DSA:1.10.601.10: ; SIGNAL_PEPTIDE: Signal peptide region; IPR014284: RNA polymerase sigma-70 like domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR013324: RNA polymerase sigma factor, region 3/4; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR000943: RNA polymerase sigma-70; IPR007627: RNA polymerase sigma-70 region 2	NA
comp21240_c0_seq1.p3	Ec-04_003880.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21240_c0_seq1.p1	Ec-04_003890.1	EF-hand domain pair	n/a;n/a;n/a	IPR018247: EF-Hand 1, calcium-binding site; PTHR10891: ; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; Coil: ; SSF47473:	KOG0028
comp32167_c0_seq3.p1	Ec-04_003900.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0031072	IPR008971: HSP40/DnaJ peptide-binding; SIGNAL_PEPTIDE: Signal peptide region; IPR001623: DnaJ domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR018253: DnaJ domain, conserved site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR24077: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:2.60.260.20:	NA
comp26152_c0_seq4.p1	Ec-04_003910.1	Zinc finger, RING-type	GO:0005515;GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003111: Peptidase S16, lon N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017907: Zinc finger, RING-type, conserved site; IPR015947: PUA-like domain; SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR23327: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29609_c0_seq3.p1	Ec-04_003920.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp33044_c0_seq1.p1	Ec-04_003960.2	peptidase S8 and S53	GO:0004289;GO:0006508	SIGNAL_PEPTIDE: Signal peptide region; G3DSA:2.60.120.380: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000209: Peptidase S8/S53 domain; IPR015500: Peptidase S8, subtilisin-related; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10795:SF157: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023828: Peptidase S8, subtilisin, Ser-active site	KOG1153
comp12956_c0_seq1.p1	Ec-04_003970.1	Peptidase S54, rhomboid domain	GO:0004252;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF144091: ; IPR022764: Peptidase S54, rhomboid domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26140_c0_seq1.p1	Ec-04_003980.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32682_c0_seq6.p1	Ec-04_003990.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19943_c0_seq2.p1	Ec-04_004000.1	expressed unknown protein	n/a;n/a;n/a	IPR007033: RAB6-interacting golgin; Coil:	NA
comp29119_c0_seq2.p1	Ec-04_004010.3	Protein of unknown function DUF4291	GO:0004867	IPR025633: Protein of unknown function DUF4291	NA
comp31950_c0_seq19.p1	Ec-04_004030.1	Transmembrane protein 107	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029248: Transmembrane protein 107; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11977_c0_seq1.p1	Ec-04_004040.1	Sterol delta-7 reductase	GO:0009918;GO:0016020;GO:0016628;GO:0047598;GO:0055114	IPR018083: Sterol reductase, conserved site; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR21257:SF40: ; IPR001171: Ergosterol biosynthesis ERG4/ERG24; PTHR21257: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26261_c0_seq1.p1	Ec-04_004050.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp33891_c0_seq1.p1	Ec-04_004060.1	expressed unknown protein	n/a;n/a;n/a	mobidb-lite: consensus disorder prediction	NA
comp26866_c0_seq1.p1	Ec-04_004070.1	Mpv17/PMP22	GO:0016021	IPR007248: Mpv17/PMP22; mobidb-lite: consensus disorder prediction; PTHR11266:SF61: ; Coil:	NA
comp25978_c0_seq1.p1	Ec-04_004080.1	Ran binding domain	GO:0046907;GO:0006139;GO:0003676;GO:0008408	IPR000156: Ran binding domain; SSF50729: ; IPR011993: Pleckstrin homology-like domain; PTHR13620: ; IPR012337: Ribonuclease H-like domain; IPR002562: 3'-5' exonuclease domain	NA
comp27304_c1_seq1.p1	Ec-04_004090.1	Related to G-protein coupled receptors	GO:0016021	PTHR21229:SF2: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR009637: Transmembrane receptor, eukaryota; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20971_c0_seq1.p1	Ec-04_004090.3	Related to G-protein coupled receptors	GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25080_c0_seq1.p1	Ec-04_004100.1	LRAT-like domain	n/a;n/a;n/a	IPR007053: LRAT-like domain	NA
comp20207_c0_seq2.p1	Ec-04_004110.1	Ferredoxin	GO:0005515	IPR001041: 2Fe-2S ferredoxin-type domain; SIGNAL_PEPTIDE: Signal peptide region; IPR001478: PDZ domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012675: Beta-grasp domain; PTHR23426: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28064_c0_seq1.p1	Ec-04_004120.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR029021: Protein-tyrosine phosphatase-like; IPR020683: Ankyrin repeat-containing domain; IPR000340: Dual specificity phosphatase, catalytic domain; PTHR24198: ; IPR002110: Ankyrin repeat	NA
comp34484_c0_seq1.p1	Ec-04_004160.1	Galactose-binding domain-like	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR12175: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR010400: PITH domain; IPR008979: Galactose-binding domain-like	NA
comp34002_c0_seq1.p1	Ec-04_004180.1	Galactokinase (Galactose kinase)	n/a;n/a;n/a	PTHR10457: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR006204: GHMP kinase N-terminal domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR000705: Galactokinase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006206: Mevalonate/galactokinase; IPR019741: Galactokinase, conserved site; SignalP-noTM: ; IPR019539: Galactokinase galactose-binding domain; IPR020568: Ribosomal protein S5 domain 2-type fold; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013750: GHMP kinase, C-terminal domain	NA
comp24413_c1_seq1.p1	Ec-04_004190.1	eukaryotic translation initiation factor 2B alpha subunit	GO:0044237	IPR000649: Initiation factor 2B-related; SSF100950: ; Coil: ; PTHR10233: ; G3DSA:3.40.50.10470:	NA
comp33066_c0_seq27.p1	Ec-04_004230.1	WD40-repeat-containing domain	GO:0005515	PTHR14920: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR14920:SF1: ; IPR024977: Anaphase-promoting complex subunit 4, WD40 domain	NA
comp30404_c0_seq2.p1	Ec-04_004260.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0005515;GO:0006470;GO:0043169	IPR000222: PPM-type phosphatase, divalent cation binding; IPR020683: Ankyrin repeat-containing domain; IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C family; IPR002110: Ankyrin repeat	NA
comp12508_c0_seq1.p1	Ec-04_004270.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; mobidb-lite: consensus disorder prediction; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:3.40.50.300: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26031_c0_seq1.p1	Ec-04_004300.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp31340_c0_seq2.p1	Ec-04_004310.1	AAA+ ATPase domain	GO:0005622	IPR013725: DNA replication factor RFC1, C-terminal; IPR003959: ATPase, AAA-type, core; PTHR11107: ; G3DSA:1.20.272.10: ; IPR008921: DNA polymerase III, clamp loader complex, gamma/delta/delta subunit, C-terminal; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003593: AAA+ ATPase domain; G3DSA:1.10.8.60: ; IPR012178: Replication factor C subunit 1; IPR001357: BRCT domain	NA
comp28708_c1_seq1.p1	Ec-04_004360.1	conserved unknown protein	n/a;n/a;n/a	IPR011989: Armadillo-like helical; Coil: ; G3DSA:1.10.110.10:	NA
comp30673_c0_seq2.p1	Ec-04_004370.1	Exosome-associated factor Rrp47/DNA strand repair C1D	n/a;n/a;n/a	IPR007146: Sas10/Utp3/C1D; IPR011082: Exosome-associated factor Rrp47/DNA strand repair C1D	NA

comp30909_c0_seq1.p1	Ec-04_004440.1	expressed unknown protein	n/a;n/a;n/a
comp32346_c0_seq4.p1	Ec-04_004490.1	Protein kinase-like domain	GO:0016772
comp11687_c0_seq1.p1	Ec-04_004540.1	expressed unknown protein	n/a;n/a;n/a
comp34215_c0_seq1.p1	Ec-04_004560.1	methionine aminopeptidase	GO:0004177;GO:0004239;GO:0006508;GO:0008235
comp25674_c0_seq2.p1	Ec-04_004570.1	Ribonuclease P, Rpp40	n/a;n/a;n/a
comp33036_c0_seq14.p1	Ec-04_004580.1	hypothetical protein	n/a;n/a;n/a
comp20001_c0_seq1.p1	Ec-04_004590.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777
comp31683_c1_seq1.p1	Ec-04_004610.1	Glycosyltransferase family 28	GO:0008152;GO:0016758
comp30808_c0_seq2.p1	Ec-04_004660.1	Hypothetical protein	n/a;n/a;n/a
comp12495_c0_seq1.p1	Ec-04_004670.1	Armadillo-type fold	GO:0000502;GO:0005488;GO:0030234;GO:0042176
comp20182_c0_seq1.p1	Ec-04_004710.1	Fructose-bisphosphatase	GO:0005975;GO:0042132;GO:0042578
comp34246_c0_seq1.p1	Ec-04_004730.1	Sister chromatid cohesion protein Dcc1	GO:0005215;GO:0005488;GO:0006810
comp3248_c0_seq1.p1	Ec-04_004740.1	EF-hand domain pair	GO:0005509
comp17159_c0_seq1.p1	Ec-04_004750.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824
comp32737_c0_seq1.p1	Ec-04_004760.1	expressed unknown protein	n/a;n/a;n/a
comp20309_c0_seq1.p1	Ec-04_004770.1	kinesin motor protein-related	GO:0007018;GO:0005524;GO:0008017;GO:0005875;GO:0003777
comp12029_c0_seq1.p1	Ec-04_004800.1	expressed unknown protein	n/a;n/a;n/a
comp12393_c0_seq1.p1	Ec-04_004810.1	SH3 domain	GO:0005543;GO:0005515
comp24298_c0_seq1.p2	Ec-04_004810.2	SH3 domain	GO:0005515
comp31043_c0_seq2.p1	Ec-04_004820.1	GAF domain-like	n/a;n/a;n/a
comp26297_c0_seq2.p1	Ec-04_004830.1	conserved unknown protein	n/a;n/a;n/a
comp30410_c0_seq2.p1	Ec-04_004840.1	Pleckstrin homology-like domain	GO:0005515;n/a
comp20182_c0_seq1.p2	Ec-04_004930.1	NAD(P)-binding domain	GO:0055114;GO:0008270;GO:0016491
comp11906_c0_seq1.p1	Ec-04_004940.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008168
comp26489_c0_seq1.p1	Ec-04_004960.1	Glutamine cyclotransferase	GO:0005515
comp12507_c0_seq1.p1	Ec-04_004980.1	SAC domain	GO:0042578
comp26568_c0_seq1.p1	Ec-04_004990.1	Leucine rich repeat protein	GO:0005515
comp31219_c2_seq1.p1	Ec-04_005010.1	Peptidase S16, lon N-terminal	GO:0004176;GO:0006508
comp31219_c2_seq2.p1	Ec-04_005010.2	Peptidase S16, lon N-terminal	GO:0004176;GO:0006508
comp33260_c2_seq15.p1	Ec-04_005040.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005515;GO:0007051;n/a
comp20214_c0_seq1.p1	Ec-04_005050.1	expressed unknown protein	n/a;n/a;n/a
comp34276_c0_seq1.p1	Ec-04_005070.1	oxidoreductase, short chain dehydrogenase	GO:0008152;GO:0016491
comp29212_c0_seq2.p1	Ec-04_005090.1	Pseudouridine-5'-phosphate glycosidase	GO:0016798
comp29953_c0_seq5.p2	Ec-04_005100.1	hypothetical protein	n/a;n/a;n/a
comp29953_c0_seq8.p1	Ec-04_005130.1	Monooxygenase, FAD-binding	GO:0008152;GO:0016491
comp19483_c0_seq2.p1	Ec-04_005150.1	expressed unknown protein	n/a;n/a;n/a
comp32801_c1_seq9.p1	Ec-04_005180.1	hypothetical protein	n/a;n/a;n/a
comp32801_c1_seq6.p1	Ec-04_005240.1	Cyclin T	GO:0006355;GO:0000079;GO:0019901
comp30775_c0_seq13.p1	Ec-04_005270.1	Sodium/calcium exchanger membrane region	GO:0016021;GO:0055085
comp24234_c0_seq4.p1	Ec-04_005280.1	Protein of unknown function DUF501	n/a;n/a;n/a
comp33734_c0_seq1.p1	Ec-04_005290.1	Sulfotransferase	GO:0008146
comp29786_c0_seq3.p1	Ec-04_005610.1	Translation elongation factor EF1B/ribosomal protein S6	GO:0005840;GO:0005622;GO:0006412;GO:0003735;GO:0019843
comp29786_c0_seq5.p3	Ec-04_005300.1	Duplicated hybrid motif	n/a;n/a;n/a
comp21606_c0_seq2.p2	Ec-04_005320.1	Maf-like protein	GO:0005737
comp24452_c0_seq1.p1	Ec-04_005330.1	conserved unknown protein	n/a;n/a;n/a
comp33417_c0_seq1.p1	Ec-04_005340.1	Tetrapyrrole methylase	GO:0008152;GO:0008168
comp32990_c0_seq5.p1	Ec-04_005350.1	Cyclophilin-like domain	GO:0003755;n/a
comp32194_c0_seq14.p1	Ec-04_005360.1	K Homology domain, type 1	GO:0003676;GO:0003723
comp26634_c0_seq2.p1	Ec-04_005430.1	Peptidase C48, SUMO/Sentrin/Ubl1	GO:0008234;GO:0006508
comp25517_c0_seq3.p1	Ec-04_005440.1	Nucleic acid-binding, OB-fold	GO:0003723;GO:0004540
comp32058_c1_seq2.p1	Ec-04_005450.1	M-phase phosphoprotein 6	n/a;n/a;n/a
comp32058_c0_seq1.p1	Ec-04_005460.1	Cation/H+ exchanger	GO:0006812;GO:0015299;GO:0016021;GO:0055085
comp33102_c3_seq5.p1	Ec-04_005460.3	Cation/H+ exchanger	GO:0006812;GO:0015299;GO:0016021;GO:0055085
comp33001_c0_seq25.p1	Ec-04_005490.1	Membralin	GO:0008152;GO:0016791
comp24817_c0_seq1.p1	Ec-04_005530.3	OTU-like cysteine protease family protein	NA
comp26540_c0_seq1.p1	Ec-04_005560.1	Adaptin ear-binding coat-associated protein 1 NECAP-1	GO:0016020;GO:0006897
comp35270_c0_seq1.p1	Ec-04_005590.1	PROCT domain	GO:0000398;GO:0003723;GO:0005515;GO:0005681;GO:0017070;GO:0030623
comp25998_c0_seq1.p1	Ec-04_005600.1	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	GO:0006457;GO:0003755
comp28905_c0_seq2.p1	Ec-04_005660.1	Pre-mRNA-splicing factor 3	n/a;GO:0000398;GO:0046540
comp28905_c0_seq2.p3	Ec-04_005670.1	Nucleolar protein 12	n/a;n/a;n/a
comp34639_c0_seq1.p1	Ec-04_005680.1	Ubiquinone biosynthesis protein Coq4	GO:0006744
comp29005_c0_seq8.p1	Ec-04_005690.1	ABC transporter type 1, transmembrane domain	GO:0006810;GO:0055085;GO:0005524;GO:0042626;GO:0016021;GO:0016887
comp12278_c0_seq1.p1	Ec-04_005710.1	Tetratricopeptide-like helical domain	GO:0005515
comp32431_c1_seq3.p1	Ec-04_005740.1	CBP-type histone acetylase, zinc finger and Bromodomain protein	GO:0005515
comp32431_c1_seq2.p1	Ec-04_005765.1	hypothetical protein	GO:0005515
comp27653_c0_seq2.p1	Ec-04_005770.1	Domain of unknown function DUF4033	n/a;n/a;n/a
comp32827_c0_seq34.p1	Ec-04_005780.1	Amine oxidase	GO:0016491;GO:0055114
comp21140_c0_seq1.p1	Ec-04_005790.1	heme oxygenase 1	n/a;n/a;n/a
comp30218_c0_seq1.p1	Ec-04_005800.1	Hypothetical leucine rich repeat protein	NA
comp29875_c0_seq8.p1	Ec-04_005820.1	O-GlcNAc transferase, C-terminal	n/a;n/a;n/a
comp20792_c0_seq1.p1	Ec-04_005830.1	Tetratricopeptide-like helical domain	GO:0005515
comp31664_c1_seq3.p1	Ec-04_005880.2	Peptidase S54, rhomboid	GO:0004252;GO:0006508;GO:0016021
comp28235_c0_seq1.p1	Ec-04_005890.1	DNA-directed DNA polymerase, family A, palm domain	GO:0003677;GO:0003887;GO:0006260
comp28235_c0_seq3.p2	Ec-04_005890.2	DNA-directed DNA polymerase, family A, palm domain	GO:0003677;GO:0003887;GO:0006260
comp12438_c0_seq1.p1	Ec-04_005960.1	Transcription factor 25	n/a;n/a;n/a
comp31714_c0_seq9.p2	Ec-04_005970.1	Phosphatidylinositol N-acetylglucosaminyltransferase subunit Y	n/a;n/a;n/a
comp33752_c0_seq1.p1	Ec-04_006100.2	imm downregulated 26	GO:0005975;GO:0016857
comp11692_c0_seq1.p1	Ec-04_006110.1	Dimeric alpha-beta barrel	GO:0004252;GO:0004289;GO:0006508
comp34503_c0_seq1.p1	Ec-04_006120.1	Vitamin K-dependent gamma-carboxylase	GO:0008488;GO:0017187
comp12154_c0_seq1.p1	Ec-04_006130.1	Lysosomal cystine transporter	n/a;n/a;n/a
comp34592_c0_seq1.p1	Ec-04_006150.1	hypothetical protein	NA
comp28829_c0_seq1.p1	Ec-04_006180.1	Fimbrin	GO:0005515
comp57996_c0_seq1.p1	Ec-04_006190.1	conserved unknown protein	n/a;n/a;n/a
comp21621_c1_seq1.p1	Ec-04_006200.2	EF-hand domain pair	n/a;n/a;n/a
comp27322_c0_seq1.p1	Ec-04_006210.1	Nuclear transport factor 2	GO:0006810;GO:0005622;GO:0000166
comp31149_c0_seq1.p1	Ec-04_006230.1	Major facilitator superfamily domain	n/a;n/a;n/a
comp31072_c0_seq1.p1	Ec-04_006240.1	expressed unknown protein	n/a;n/a;n/a
comp31844_c0_seq21.p1	Ec-04_006260.1	MORN motif	n/a;n/a;n/a
comp29558_c1_seq2.p1	Ec-04_006270.4	Dbl homology (DH) domain	GO:0005089;GO:0035023
comp34163_c0_seq1.p1	Ec-04_006280.1	Mss4-like	n/a;n/a;n/a
comp28277_c0_seq4.p1	Ec-04_006290.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0090124;GO:0032776;GO:0003677;GO:0015667;GO:0008170;GO:0006306
comp11826_c0_seq1.p1	Ec-04_006300.1	D-3-phosphoglycerate dehydrogenase	GO:0004617;GO:0008152;GO:0016597
comp33793_c0_seq1.p1	Ec-04_006310.1	conserved unknown protein	n/a;n/a;n/a
comp13088_c0_seq1.p1	Ec-04_006320.1	WD40 repeat	GO:0005515
comp28932_c0_seq1.p1	Ec-04_006330.1	SNF2 family protein	GO:0003677;GO:0005524
comp47201_c0_seq1.p1	Ec-04_006340.1	Hypothetical protein	n/a;n/a;n/a
comp31551_c0_seq3.p1	Ec-04_006350.1	Tetratricopeptide-like helical domain	GO:0005515
comp32062_c0_seq18.p1	Ec-04_006360.1	UDP-galactose transporter	GO:0015780;GO:0005338;GO:0016021
comp12541_c0_seq1.p1	Ec-04_006380.1	DNA-directed RNA polymerase III, subunit Rpc31	n/a;GO:0006359
comp26370_c0_seq2.p2	Ec-04_006390.1	Rrp43 is a component of the exosome 3'->5' exoribonuclease complex, a complex that degrades mRNAs.	GO:0000175;GO:0003723;GO:0006396
comp26370_c0_seq1.p1	Ec-04_006400.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a
comp19374_c0_seq1.p1	Ec-04_006410.1	iron-sulfur assembly protein	GO:0051536;GO:0016226;GO:0005198
comp20632_c0_seq1.p1	Ec-04_006430.1	Sec1-like protein	GO:0006904;GO:0016192
comp13021_c0_seq1.p1	Ec-04_006440.1	Tetratricopeptide-like helical domain	GO:0005515
comp12954_c0_seq1.p1	Ec-04_006450.1	UBX domain	GO:0005515
comp27960_c0_seq7.p1	Ec-04_006460.1	conserved unknown protein	GO:0031419;GO:0000166;GO:0008998;GO:0055114
comp32299_c3_seq31.p1	Ec-04_006480.1	Protein of unknown function DUF947	n/a;n/a;n/a
comp3255_c0_seq1.p1	Ec-04_006490.1	conserved unknown protein	n/a;n/a;n/a
comp20583_c0_seq2.p1	Ec-04_006500.1	HORMA domain protein	GO:0007067
comp25774_c0_seq2.p1	Ec-04_006510.1	DEAD box helicase	n/a;n/a;n/a
comp19455_c0_seq1.p1	Ec-04_006520.1	DEAD box helicase	GO:0005524;GO:0016818
comp27878_c0_seq2.p1	Ec-04_006530.1	WD40/YVTN repeat-like-containing domain	GO:0005515
comp28573_c0_seq1.p1	Ec-04_006540.1	CAAX amino terminal protease	GO:0016020
comp27613_c0_seq2.p1	Ec-04_006560.1	AMP deaminase	GO:0032264;GO:0003876
comp29641_c0_seq2.p1	Ec-05_000090.3	Hypothetical protein	n/a;n/a;n/a
comp12347_c0_seq1.p1	Ec-05_000240.1	BFD-like [2Fe-2S]-binding domain	GO:0050660;GO:0055114;GO:0016491
comp24418_c0_seq3.p1	Ec-05_000250.1	NAD(P)-binding domain	GO:0003824;GO:0005488;GO:0008152
comp26023_c0_seq1.p1	Ec-05_000260.3	Histidine phosphatase superfamily, clade-2	GO:0003993
comp32750_c0_seq17.p1	Ec-05_000270.1	proteasome subunit beta 2	GO:0051603;GO:0004298;GO:0005839
comp32489_c0_seq1.p1	Ec-05_000290.1	Glycoside hydrolase-type carbohydrate-binding, subgroup	GO:0003824;GO:0005975;GO:0030246
comp32828_c0_seq3.p1	Ec-05_000330.3	Hypothetical protein	n/a;n/a;n/a
comp32904_c0_seq40.p1	Ec-05_000360.1	expressed unknown protein	n/a;n/a;n/a
comp32961_c0_seq9.p1	Ec-05_000520.1	hypothetical protein	n/a;n/a;n/a
comp31407_c0_seq1.p1	Ec-05_000630.1	Manganese/iron superoxide dismutase, C-terminal	GO:0006801;GO:0004784;GO:0055114;GO:0046872
comp28126_c0_seq3.p1	Ec-05_000660.1	Protein of unknown function DUF3007	n/a;n/a;n/a
comp30301_c0_seq2.p1	Ec-05_000670.2	Hypothetical protein	n/a;n/a;n/a
comp25057_c0_seq2.p1	Ec-05_000680.1	Ankyrin repeat-containing domain	n/a;n/a;n/a
comp33287_c0_seq9.p1	Ec-05_000750.1	expressed unknown protein	n/a;n/a;n/a
comp28487_c0_seq3.p1	Ec-05_000780.1	Ankyrin repeat	GO:0005515
comp26914_c1_seq1.p1	Ec-05_000820.1	F-box domain	GO:0005515
comp20954_c0_seq2.p1	Ec-05_000840.1	Cycloeucalenol cycloisomerase	n/a;n/a;n/a
comp33152_c1_seq1.p1	Ec-05_000850.1	SET domain protein	GO:0005515
comp31079_c0_seq1.p2	Ec-05_000900.1	Autophagy-related, C-terminal	n/a;n/a;n/a
comp31079_c0_seq1.p1	Ec-05_000910.1	Vacuolar protein sorting-associated protein 13	n/a;n/a;n/a
comp32264_c1_seq5.p1	Ec-05_000930.1	Zinc finger, RING/FYVE/PHD-type	GO:0008270;GO:0005488
comp34784_c0_seq1.p1	Ec-05_000940.1	expressed unknown protein	n/a;n/a;n/a
comp28927_c0_seq3.p1	Ec-05_000950.1	5'-nucleotidase	NA
comp21539_c0_seq1.p1	Ec-05_001020.1	NUDIX hydrolase	GO:0016787
comp32243_c2_seq10.p1	Ec-05_001030.1	P-loop containing nucleoside triphosphate hydrolase	n/a;GO:0005524
comp20327_c0_seq2.p1	Ec-05_001040.2	Outer Plastid Envelope Protein 16-like	GO:0005743;GO:0008565;GO:0015031
comp32946_c0_seq4.p1	Ec-05_001050.1	Putative 5-3 exonuclease	GO:0003676;GO:0004527
comp32946_c2_seq12.p1	Ec-05_001060.1	5'-3' exoribonuclease	n/a;n/a;n/a
comp29565_c0_seq1.p1	Ec-05_001090.1	hypothetical protein	n/a;n/a;n/a
comp27817_c0_seq2.p1	Ec-05_001110.1	Rab8B, RAB family GTPase	GO:0007264;GO:0005622;GO:0005525
comp30592_c0_seq2.p2	Ec-05_001120.3	conserved unknown protein	n/a;n/a;n/a
comp30592_c0_seq2.p1	Ec-05_001130.1	Sec7 and Pleckstrin homology domain protein	GO:0032012;GO:0005086
comp31975_c0_seq1.p1	Ec-05_001140.1	Acyl-CoA-binding protein, ACBP	GO:0000062
comp32453_c0_seq2.p3	Ec-05_001160.1	expressed unknown protein	n/a;n/a;n/a
comp29986_c0_seq1.p1	Ec-05_001170.2	Protein phosphatase 2C (PP2C)-like domain	GO:0003824
comp32946_c2_seq9.p1	Ec-05_001190.1	conserved unknown protein	n/a;n/a;n/a
comp31170_c0_seq2.p1	Ec-05_001200.1	hypothetical protein	n/a;n/a;n/a
comp32163_c1_seq3.p1	Ec-05_001230.1	Armadillo-like helical	GO:0005488
comp28683_c0_seq5.p2	Ec-05_001240.1	Small protein B	GO:0003723;GO:0006412
comp12395_c0_seq2.p1	Ec-05_001290.1	Mitochondrial 18kDa protein	GO:0004089;GO:0008270;GO:0015976
comp26627_c0_seq3.p1	Ec-05_001420.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0000981;GO:0005634;GO:0006355;GO:0008270
comp34255_c0_seq1.p1	Ec-05_001430.1	K Homology domain, type 1	GO:0003723
comp28504_c0_seq5.p1	Ec-05_001440.1	Rubisco LSMT, substrate-binding domain	GO:0005634
comp25007_c0_seq2.p1	Ec-05_001450.1	mono-or diacylglycerol acyltransferase type 2	GO:0016747
comp26069_c0_seq3.p1	Ec-05_001475.1	hypothetical protein	GO:0005515
comp35294_c0_seq1.p1	Ec-05_001510.1	thylakoid lumen 15.0 kDa protein	n/a;n/a;n/a
comp31544_c0_seq20.p1	Ec-05_001560.1	Phosphotyrosine protein phosphatase I superfamily	GO:0004725;GO:0006470;n/a
comp20843_c0_seq1.p1	Ec-05_001580.1	Condensin complex subunit 2/barren	GO:0000796;GO:0007076
comp19957_c0_seq2.p1	Ec-05_001700.1	Domain of unknown function DUF305	n/a;n/a;n/a
comp32439_c0_seq6.p1	Ec-05_001710.1	conserved unknown protein	n/a;n/a;n/a
comp31669_c0_seq6.p1	Ec-05_001730.1	Glutamate cysteine ligase	GO:0004357;GO:0006750
comp33074_c3_seq16.p1	Ec-05_001740.1	phosphatidate cytidylyltransferase	GO:0016020;GO:0016772
comp32840_c2_seq29.p2	Ec-05_001760.1	Peptide methionine sulfoxide reductase	GO:0006457;GO:0006979;GO:0016671;GO:0030091
comp29929_c0_seq1.p1	Ec-05_001770.1	Membrane protein,Tapt1/CMV receptor	n/a;n/a;n/a
comp20082_c0_seq2.p1	Ec-05_001780.1	Ribosomal protein L23	GO:0005840;GO:0005622;GO:0006412;GO:0003735
comp29171_c0_seq1.p1	Ec-05_001790.1	mitochondrial phosphate carrier protein	GO:0016020;GO:0005488;GO:0006810
comp22338_c0_seq1.p1	Ec-05_001810.2	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270
comp28822_c0_seq4.p1	Ec-05_001820.1	expressed unknown protein	n/a;n/a;n/a
comp26748_c0_seq1.p1	Ec-05_001860.1	TBCC domain-containing 1 protein (TBCCd1)	NA
comp34292_c0_seq1.p1	Ec-05_001880.1	Chalcone Isomerase-like	GO:0016872
comp25609_c0_seq3.p1	Ec-05_001890.1	GPA1, alpha subunit of a heterotrimeric G protein	GO:0007186;GO:0007165;GO:0003924;GO:0031683;GO:0019001;GO:0004871
comp27671_c0_seq4.p1	Ec-05_001910.1	Acyltransferase 3	GO:0016747
comp28666_c0_seq1.p1	Ec-05_001920.1	conserved unknown protein	n/a;n/a;n/a
comp30698_c0_seq1.p1	Ec-05_001980.1	Peptidyl-prolyl cis-trans isomerase, FKBP-type	GO:0006457
comp25457_c0_seq1.p2	Ec-05_001990.1	Protein Disulfide Isomerase (putive Transglutaminase bifunctional protein)	GO:0045454
comp32408_c3_seq5.p1	Ec-05_002000.1	Oligomerisation domain	n/a;n/a;n/a
comp34762_c0_seq1.p2	Ec-05_002070.1	COX4 neighbour	NA
comp27758_c0_seq1.p1	Ec-05_002080.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp26827_c0_seq1.p1	Ec-05_002090.1	SPRY domain	GO:0005515
comp31611_c1_seq1.p1	Ec-05_002100.1	weakly similar to brefeldin A-sensitive Golgi protein-like	GO:0007030;GO:0015031;GO:0016020
comp30688_c0_seq3.p1	Ec-05_002130.2	nischarin/ IRAS/ imidazoline receptor	GO:0005515
comp12293_c0_seq1.p1	Ec-05_002180.1	UTP--glucose-1-phosphate uridylyltransferase family	GO:0008152;GO:0070569
comp12376_c0_seq1.p1	Ec-05_002190.1	Eukaryotic rRNA processing	n/a;n/a;n/a
comp48701_c0_seq1.p1	Ec-05_002210.3	Bardet-Biedl syndrome 2	n/a;n/a;n/a
comp33245_c9_seq5.p1	Ec-05_002220.1	XAP5 protein	GO:0005634
comp26761_c0_seq1.p1	Ec-05_002230.1	RAP domain	n/a;n/a;n/a
comp31881_c1_seq1.p2	Ec-05_002240.1	Quinoprotein alcohol dehydrogenase-like superfamily	n/a;n/a;n/a
comp31881_c1_seq1.p1	Ec-05_002250.1	Cellulose synthase (UDP-forming), family GT2	NA
comp31739_c0_seq5.p1	Ec-05_002260.1	Nucleotide-diphospho-sugar transferases	n/a;n/a;n/a
comp24635_c0_seq1.p1	Ec-05_002360.1	Peptidase M50	GO:0004222;GO:0006508
comp28830_c0_seq2.p1	Ec-05_002370.1	DWNN domain	GO:0005634;GO:0008270
comp25140_c0_seq1.p1	Ec-05_002370.2	DWNN domain	GO:0005634;GO:0008270
comp32850_c1_seq4.p1	Ec-05_002420.1	Mpv17/PMP22	GO:0016021
comp11924_c0_seq1.p1	Ec-05_002440.1	similarities to vacuolar protein sorting-associated protein	NA
comp31682_c0_seq3.p1	Ec-05_002450.1	Vacuolar protein sorting-associated protein 13 domain	GO:0008104
comp31682_c1_seq8.p1	Ec-05_002460.1	hypothetical protein	n/a;n/a;n/a
comp31475_c1_seq1.p1	Ec-05_002520.4	Similar to Isochorismate Synthase	GO:0004601;GO:0006118;GO:0006979;GO:0008909;GO:0009058;GO:0020037
comp31581_c0_seq1.p1	Ec-05_002530.1	Domain of unknown function DUF676, lipase-like	n/a;n/a;n/a
comp34557_c0_seq1.p1	Ec-05_002550.1	Primosome PriB/single-strand DNA-binding	GO:0003697
comp30452_c0_seq3.p1	Ec-05_002560.1	Cyclic nucleotide-binding-like	n/a;n/a;n/a
comp27336_c0_seq1.p1	Ec-05_002600.1	putative nuclear LIM interactor-interacting protein	NA
comp27274_c0_seq4.p1	Ec-05_002620.1	UNC-50	n/a;n/a;n/a
comp24559_c0_seq3.p1	Ec-05_002630.2	Pleckstrin homology-like domain	GO:0004437;GO:0016311;GO:0016791;GO:0046839
comp28925_c0_seq7.p1	Ec-05_002630.3	Pleckstrin homology-like domain	GO:0004437;GO:0016311;GO:0016791;GO:0046839
comp25266_c0_seq1.p1	Ec-05_002640.1	Casein kinase II, regulatory subunit	GO:0005956;GO:0019887
comp29304_c0_seq2.p1	Ec-05_002680.1	Trehalose 6-phosphate synthase, family GT20 / Trehalose 6-phosphate phosphatase	GO:0003824;GO:0005992
comp29570_c0_seq5.p1	Ec-05_002690.1	Di-trans-poly-cis-decaprenylcistransferase	GO:0008152;GO:0016765;GO:0016740
comp31966_c1_seq8.p1	Ec-05_002730.2	Helicase superfamily 1/2, ATP-binding domain	GO:0003677;GO:0005524
comp31966_c0_seq1.p1	Ec-05_002750.1	Zinc finger, PHD-type	GO:0005515;GO:0008270
comp32798_c0_seq13.p1	Ec-05_002760.1	Yippee/Mis18	n/a;n/a;n/a
comp33778_c0_seq1.p1	Ec-05_002790.1	RmlD-like substrate binding domain	GO:0003824;GO:0005488;GO:0008152
comp19771_c0_seq1.p1	Ec-05_002800.1	Golgi apparatus membrane protein TVP15	n/a;n/a;n/a
comp81611_c0_seq1.p1	Ec-05_002810.3	Peptidase C2, calpain, catalytic domain	GO:0004198;GO:0005622;GO:0006508
comp30674_c0_seq4.p2	Ec-05_002820.1	expressed unknown protein	n/a;n/a;n/a
comp26166_c0_seq1.p1	Ec-05_002830.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp24578_c0_seq1.p1	Ec-05_002840.1	Potassium channel tetramerisation-type BTB domain	GO:0051260
comp26488_c0_seq2.p1	Ec-05_002850.1	expressed unknown protein	n/a;n/a;n/a
comp30740_c1_seq21.p1	Ec-05_002860.1	RNA polymerase sigma factor, region 2	GO:0003677;GO:0003700;GO:0006352;GO:0006355;GO:0016987
comp32566_c1_seq17.p1	Ec-05_002890.1	Pseudouridine synthase, RsuA/RluB/C/D/E/F	GO:0003723;GO:0001522;GO:0016866;GO:0009451;GO:0009982
comp28095_c0_seq1.p1	Ec-05_002900.1	Glycolipid 2-alpha-mannosyltransferase,family GT15	GO:0016020;GO:0006486;GO:0000030
comp31699_c0_seq8.p1	Ec-05_002910.2	WW domain	GO:0005515
comp31876_c0_seq4.p1	Ec-05_002920.1	WW domain	GO:0005515
comp22091_c1_seq2.p1	Ec-05_002990.1	Suppressor of forked	GO:0006397;GO:0005634
comp31602_c0_seq5.p1	Ec-05_003000.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a
comp32954_c2_seq13.p1	Ec-05_003010.1	Inositol-tetrakisphosphate 1-kinase	GO:0000287;GO:0052725;GO:0005524;GO:0005622;GO:0047325;GO:0032957;GO:0052726
comp29554_c0_seq1.p1	Ec-05_003020.1	Domain of unknown function DUF547	n/a;n/a;n/a
comp33761_c0_seq1.p1	Ec-05_003040.1	Putative Glutathione S-transferase	GO:0005515
comp32581_c0_seq10.p3	Ec-05_003050.1	Peptide methionine sulphoxide reductase MsrA	GO:0055114;GO:0008113
comp32581_c0_seq10.p1	Ec-05_003080.2	Peptidase S8, subtilisin-related	n/a;n/a;n/a
comp20369_c0_seq2.p1	Ec-05_003090.1	Peptidase C48, SUMO/Sentrin/Ubl1	GO:0006508;GO:0008234
comp25661_c0_seq5.p1	Ec-05_003110.1	heat shock protein 33	GO:0006457;GO:0005737;GO:0051082
comp30360_c0_seq3.p1	Ec-05_003120.1	Zinc finger, TAZ-type	GO:0005634;GO:0006355;GO:0004402;GO:0008270;GO:0003712
comp28494_c0_seq8.p1	Ec-05_003130.2	Nucleotide-binding alpha-beta plait domain	GO:0000166
comp12019_c0_seq1.p1	Ec-05_003160.1	Imidazole glycerol phosphate synthase, glutamine amidotransferase subunit	GO:0016763;GO:0016833;GO:0009382;GO:0000105;GO:0000107
comp30099_c0_seq3.p1	Ec-05_003240.2	DNA binding HTH domain, Psq-type	GO:0003677
comp14332_c0_seq2.p1	Ec-05_003250.3	hypothetical protein	n/a;n/a;n/a
comp29454_c0_seq1.p1	Ec-05_003300.1	Putative subunit of the Anaphase Promoting Complex	GO:0005515
comp13128_c0_seq1.p1	Ec-05_003310.1	FAD dependent oxidoreductase	GO:0016491;GO:0055114
comp32617_c2_seq23.p1	Ec-05_003390.1	Ribosomal protein L7Ae/L8/Nhp2 family	GO:0042254;GO:0030529
comp28393_c0_seq2.p1	Ec-05_003400.1	Protein of unknown function DUF599	n/a;n/a;n/a
comp30322_c0_seq5.p1	Ec-05_003410.1	Rrp44 is a component of the exosome 3'->5' exoribonuclease complex, a complex that degrades mRNAs.	GO:0003723;GO:0004540
comp32284_c0_seq4.p1	Ec-05_003420.2	conserved unknown protein	n/a;n/a;n/a
comp32421_c0_seq2.p1	Ec-05_003430.1	Hypothetical protein	n/a;n/a;n/a
comp32963_c1_seq2.p1	Ec-05_003450.1	malonyl-CoA:ACP transacylase	GO:0008152;GO:0003824;GO:0005488
comp33056_c0_seq1.p1	Ec-05_003480.1	expressed unknown protein	n/a;n/a;n/a
comp29305_c0_seq2.p1	Ec-05_003500.1	Zinc finger and SET domain protein	GO:0005634;GO:0005515;GO:0008270;GO:0018024
comp12815_c0_seq1.p1	Ec-05_003510.1	hypothetical protein	n/a;n/a;n/a
comp33929_c0_seq1.p1	Ec-05_003560.1	conserved unknown protein	n/a;n/a;n/a
comp31287_c0_seq2.p1	Ec-05_003580.2	Thioredoxin-like fold	n/a;n/a;n/a
comp28846_c1_seq1.p1	Ec-05_003590.1	Pentatricopeptide repeat	n/a;n/a;n/a
comp28828_c0_seq1.p1	Ec-05_003600.3	conserved unknown protein	n/a;n/a;n/a
comp20455_c0_seq1.p1	Ec-05_003630.1	Protein of unknown function DUF2358	n/a;n/a;n/a
comp26763_c0_seq1.p1	Ec-05_003640.1	L-aspartate oxidase	GO:0006118;GO:0055114;GO:0016491
comp11866_c0_seq1.p1	Ec-05_003660.1	Protein of unknown function DUF3727	n/a;n/a;n/a
comp12428_c0_seq1.p1	Ec-05_003670.1	conserved unknown protein	GO:0055114;GO:0016491
comp32693_c0_seq7.p1	Ec-05_003690.1	Phox/Bem1p	GO:0005515
comp31492_c0_seq5.p1	Ec-05_003730.1	Butirosin biosynthesis, BtrG-like	n/a;n/a;n/a
comp32133_c2_seq16.p1	Ec-05_003750.1	Tetratricopeptide-like helical domain	GO:0005515
comp33021_c0_seq18.p1	Ec-05_003760.2	hypothetical protein	n/a;n/a;n/a
comp31781_c0_seq7.p1	Ec-05_003790.1	Hypothetical protein	n/a;n/a;n/a
comp24594_c0_seq3.p1	Ec-05_003800.1	Protein tyrosine phosphatase	GO:0004725;GO:0006470
comp33071_c0_seq7.p1	Ec-05_003830.1	Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	GO:0004672;GO:0005524;GO:0006468
comp28439_c1_seq3.p2	Ec-05_003840.1	expressed unknown protein	n/a;n/a;n/a
comp24092_c0_seq2.p1	Ec-05_003850.1	Rab-GTPase-TBC domain	GO:0005097;GO:0032313
comp32970_c0_seq3.p1	Ec-05_003890.1	Histone deacetylase domain protein	n/a;n/a;n/a
comp20870_c0_seq2.p2	Ec-05_003900.1	60S ribosomal protein L30	GO:0005840;GO:0006412;GO:0005622;GO:0003735
comp32312_c2_seq16.p1	Ec-05_003910.1	Histone deacetylase domain protein	n/a;n/a;n/a
comp32312_c2_seq6.p1	Ec-05_003940.1	hypothetical protein	n/a;n/a;n/a
comp34080_c0_seq1.p1	Ec-05_003960.1	Conserved oligomeric Golgi complex, subunit 3	GO:0016020;GO:0005801;GO:0006886
comp20714_c1_seq2.p1	Ec-05_003970.1	Domain of unknown function DUF2013	n/a;n/a;n/a
comp14098_c0_seq2.p1	Ec-05_003980.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0005634;GO:0000981;GO:0006355;GO:0008270
comp21165_c0_seq1.p1	Ec-05_004030.1	Non-structural maintenance of chromosome element 4, C-terminal	n/a;n/a;n/a

comp22034_c0_seq2.p1	Ec-05_004040.1	Glutaredoxin	n/a;n/a;n/a	IPR002109: Glutaredoxin; IPR012336: Thioredoxin-like fold; IPR004480: Monothiol glutaredoxin-related	KOG1752
comp30617_c0_seq2.p1	Ec-05_004060.1	Pyruvate/Phosphoenolpyruvate kinase-like domain	GO:0003824	IPR015813: Pyruvate/Phosphoenolpyruvate kinase-like domain; IPR011206: Citrate lyase beta subunit-like; IPR005000: HpcH/HpaI aldolase/citrate lyase domain; SignalP-TM: ; PTHR32308:SF0:	NA
comp33166_c0_seq12.p1	Ec-05_004070.1	putative nosD copper-binding protein	n/a;n/a;n/a	IPR011050: Pectin lyase fold/virulence factor; PF13229: Right handed beta helix region; IPR006626: Parallel beta-helix repeat; IPR012334: Pectin lyase fold	NA
comp28232_c0_seq2.p1	Ec-05_004090.1	RNA polymerase Rpb2, OB-fold	GO:0003677;GO:0006351;GO:0003899	IPR015712: DNA-directed RNA polymerase, subunit 2; SSF64484: ; IPR007120: DNA-directed RNA polymerase, subunit 2, domain 6; IPR014724: RNA polymerase Rpb2, OB-fold; IPR007641: RNA polymerase Rpb2, domain 7; IPR007121: RNA polymerase, beta subunit, conserved site	NA
comp33577_c0_seq1.p1	Ec-05_004100.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp33015_c0_seq2.p1	Ec-05_004110.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp29357_c0_seq2.p1	Ec-05_004120.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28818_c0_seq1.p1	Ec-05_004160.1	Uncharacterised domain UPF0126	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR005115: Uncharacterised domain UPF0126; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR30506:	NA
comp46268_c0_seq1.p1	Ec-05_004180.2	hypothetical protein	n/a;n/a;n/a	IPR000048: IQ motif, EF-hand binding site	NA
comp91952_c0_seq1.p1	Ec-05_004190.1	Armadillo-type fold	GO:0005488	IPR016024: Armadillo-type fold; PTHR21207: ; IPR019399: Parkin co-regulated protein	NA
comp4412_c0_seq1.p1	Ec-05_004200.1	EF-hand domain pair	n/a;n/a;n/a	PTHR10891:SF531: ; IPR018247: EF-Hand 1, calcium-binding site; PTHR10891: ; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR000008: C2 domain	NA
comp29530_c0_seq3.p1	Ec-05_004210.1	Dihydrofolate reductase-like domain	GO:0009231;GO:0008703;GO:0055114	PTHR11079: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR024072: Dihydrofolate reductase-like domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR002734: Bacterial bifunctional deaminase-reductase, C-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28863_c0_seq1.p1	Ec-05_004230.1	Homeodomain-like	GO:0003677	IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; PTHR12802: ; IPR017930: Myb domain; IPR006447: Myb domain, plants	NA
comp29783_c0_seq5.p1	Ec-05_004270.1	Thiaminase II	n/a;n/a;n/a	IPR016084: Haem oxygenase-like, multi-helical; PTHR20858: ; IPR004305: Thiaminase-2/PQQC; IPR023214: HAD-like domain	NA
comp27220_c0_seq2.p1	Ec-05_004280.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; PTHR23083:	NA
comp30599_c0_seq2.p1	Ec-05_004290.1	ATG2 Autophagy-related protein homolog	NA	IPR015412: Autophagy-related, C-terminal; IPR026849: Autophagy-related protein 2; IPR026854: Vacuolar protein sorting-associated protein 13A N-terminal domain	NA
comp32921_c1_seq3.p2	Ec-05_004300.1	Nucleotide-sugar transporter	GO:0015780;GO:0005351;GO:0005338;GO:0000139;GO:0008643;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004689: UDP-galactose transporter; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF103481: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007271: Nucleotide-sugar transporter; IPR021189: UDP/CMP-sugar transporter; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32921_c1_seq17.p1	Ec-05_004310.1	conserved unknown protein	n/a;n/a;n/a	Coil: ; PTHR14594:	NA
comp18417_c0_seq1.p1	Ec-05_004320.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25016_c0_seq4.p1	Ec-05_004330.1	Haloacid dehalogenase-like hydrolase	NA	PTHR18901: ; IPR006439: HAD hydrolase, subfamily IA; IPR023214: HAD-like domain	NA
comp12387_c0_seq1.p1	Ec-05_004340.1	Methyltransferase type 11	GO:0008152;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR013216: Methyltransferase type 11; PTHR10108:	NA
comp29991_c0_seq4.p1	Ec-05_004360.1	Pyridoxal phosphate-dependent transferase	n/a;n/a;n/a	IPR015424: Pyridoxal phosphate-dependent transferase; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	NA
comp28131_c0_seq1.p1	Ec-05_004380.1	Rab28, Ras superfamily GTPase	GO:0007264;GO:0005525;GO:0015031	IPR002041: Ran GTPase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; IPR003579: Small GTPase superfamily, Rab type; PS51419: small GTPase Rab1 family profile.; IPR020849: Small GTPase superfamily, Ras type; PTHR24073:	NA
comp13041_c0_seq1.p1	Ec-05_004390.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	GO:0016020;GO:0016192;GO:0005515	IPR000727: Target SNARE coiled-coil domain; IPR010989: t-SNARE; G3DSA:1.20.5.110: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF58038: ; G3DSA:1.20.58.90: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR12380: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3202
comp31028_c1_seq7.p1	Ec-05_004410.1	UDP-glucuronosyl/UDP-glucosyltransferase	GO:0008152;GO:0016758	SSF53756: ; IPR002213: UDP-glucuronosyl/UDP-glucosyltransferase; G3DSA:3.40.50.2000:	NA
comp31028_c1_seq8.p2	Ec-05_004410.3	UDP-glucuronosyl/UDP-glucosyltransferase	GO:0008152;GO:0016758	SSF53756: ; G3DSA:3.40.50.2000:	NA
comp32135_c1_seq3.p1	Ec-05_004420.1	Synaptobrevin	GO:0016192;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR010908: Longin domain; IPR001388: Synaptobrevin; SSF58038: ; PTHR21136: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011012: Longin-like domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30769_c0_seq4.p1	Ec-05_004430.3	Tetratricopeptide-like helical domain	GO:0005515	PTHR10098: ; IPR001440: Tetratricopeptide repeat 1; IPR011990: Tetratricopeptide-like helical domain; IPR019734: Tetratricopeptide repeat	NA
comp30177_c0_seq3.p1	Ec-05_004440.1	Cell division protein kinase 2	NA	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; PTHR24056:	NA
comp70484_c0_seq1.p1	Ec-05_004480.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp34027_c0_seq1.p1	Ec-05_004490.1	Ubiquitin-like	GO:0005515	PTHR10677:SF3: ; G3DSA:3.10.20.90: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR029071: Ubiquitin-related domain; IPR015496: Ubiquilin; IPR000626: Ubiquitin domain; Coil:	NA
comp25816_c0_seq2.p1	Ec-05_004500.2	Arf GTPase activating protein	GO:0008060;GO:0008270;GO:0032312	IPR001164: Arf GTPase activating protein; SSF57863: ; PTHR23180:	NA
comp20321_c1_seq2.p1	Ec-05_004520.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20189_c0_seq1.p1	Ec-05_004550.1	expressed unknown protein	n/a;n/a;n/a	IPR018625: Protein Pet100; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32654_c1_seq3.p1	Ec-05_004560.2	tubulin	GO:0003924;GO:0005525;GO:0043234;GO:0051258	IPR002967: Delta tubulin; IPR017975: Tubulin, conserved site; IPR000217: Tubulin; IPR003008: Tubulin/FtsZ, GTPase domain; IPR023123: Tubulin, C-terminal; IPR008280: Tubulin/FtsZ, C-terminal	NA
comp32654_c1_seq3.p2	Ec-05_004570.1	PUA domain	GO:0003723	IPR015947: PUA-like domain; IPR002478: PUA domain; IPR016437: Translation-associated RNA-binding, predicted; IPR015266: Domain of unknown function DUF1947; IPR004521: Uncharacterised domain CHP00451	NA
comp24728_c0_seq1.p1	Ec-05_004590.1	conserved unknown protein	n/a;n/a;n/a	PTHR32134:	NA
comp19331_c0_seq1.p1	Ec-05_004620.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0005634;GO:0000981;GO:0006355;GO:0046872;GO:0008270	IPR001138: Zn(2)-C6 fungal-type DNA-binding domain; IPR007087: Zinc finger, C2H2	NA
comp33164_c0_seq35.p1	Ec-05_004630.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp12295_c0_seq2.p1	Ec-05_004650.1	Uncharacterised protein family FPL	NA	PTHR21481: ; IPR019155: Uncharacterised protein family FPL	NA
comp31727_c0_seq1.p1	Ec-05_004670.1	NAD(P)-binding domain	GO:0003824;GO:0005488;GO:0006813;GO:0008152;GO:0015269;GO:0016020	IPR016040: NAD(P)-binding domain	NA
comp31727_c2_seq2.p1	Ec-05_004680.1	Two pore domain potassium channel domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF81324: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10027: ; G3DSA:1.10.287.70: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013099: Two pore domain potassium channel domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28112_c0_seq1.p1	Ec-05_004720.1	CD225/Dispanin family	GO:0009607;GO:0016021	PTHR14948: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR007593: CD225/Dispanin family; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14948:SF25: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29170_c0_seq3.p1	Ec-05_004720.3	CD225/Dispanin family	GO:0009607;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR14948: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14948:SF25: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR007593: CD225/Dispanin family; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29721_c0_seq1.p1	Ec-05_004730.1	Transcription initiation factor IID, 18kDa subunit	GO:0046982;GO:0006366	IPR003195: Transcription initiation factor IID, 18kDa subunit; IPR009072: Histone-fold	NA
comp28222_c0_seq6.p1	Ec-05_004740.1	Histidine phosphatase superfamily, clade-2	GO:0003993	IPR029033: Histidine phosphatase superfamily; IPR000560: Histidine phosphatase superfamily, clade-2; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11567: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28667_c0_seq1.p1	Ec-05_004750.1	mRNA splicing factor, Cwf21	GO:0000166;n/a	SSF54928: ; IPR000061: SWAP/Surp; IPR000504: RNA recognition motif domain; IPR006569: CID domain; PTHR23140: ; IPR012677: Nucleotide-binding alpha-beta plait domain; Coil: ; IPR013170: mRNA splicing factor, Cwf21	NA
comp29350_c0_seq2.p1	Ec-05_004780.1	conserved unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29021_c0_seq2.p1	Ec-05_004800.1	Exportin-1/Importin-beta-like	GO:0005488	NA	NA
comp69411_c0_seq1.p1	Ec-05_004830.1	Cytochrome b5	GO:0020037	PTHR21281: ; IPR001199: Cytochrome b5-like heme/steroid binding domain	KOG0537
comp21315_c0_seq2.p2	Ec-05_004840.1	conserved unknown protein	GO:0015035;GO:0009055;n/a;GO:0045454	IPR002109: Glutaredoxin	NA
comp29520_c0_seq1.p1	Ec-05_004870.1	Thioredoxin-like fold	n/a;n/a;n/a	PTHR23322: ; PTHR23322:SF6: ; G3DSA:3.10.20.90: ; IPR006577: UAS; PF13899: Thioredoxin-like; G3DSA:1.10.8.10: ; IPR001012: UBX domain; IPR029071: Ubiquitin-related domain; PF14555: UBA-like domain; IPR009060: UBA-like; IPR012336: Thioredoxin-like fold	NA
comp19368_c0_seq1.p1	Ec-05_004880.3	Nucleotide-binding alpha-beta plait domain	GO:0000166	IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; Coil:	NA
comp20404_c0_seq2.p1	Ec-05_004890.1	Enkurin domain-containing protein 1	n/a;n/a;n/a	IPR027710: Enkurin domain-containing protein 1; IPR027012: Enkurin domain; PTHR21490:	NA
comp31107_c1_seq5.p1	Ec-05_004900.3	Hypothetical leucine rich repeat protein	GO:0005515	SSF52047: ; IPR006553: Leucine-rich repeat, cysteine-containing subtype; IPR032675: Leucine-rich repeat domain, L domain-like; PTHR24006:	NA
comp12697_c0_seq1.p1	Ec-05_004910.1	Alternative oxidase	GO:0009916;GO:0055114	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PTHR31803:SF10: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002680: Alternative oxidase; PTHR31803: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28742_c1_seq1.p1	Ec-05_004940.1	Ferric reductase transmembrane component-like domain	GO:0009055;GO:0005506;GO:0050660;GO:0016021;GO:0006118;GO:0055114;GO:0016491	IPR017927: Ferredoxin reductase-type FAD-binding domain; SFLDG01169: NADPH oxidase subgroup (NOX); TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; G3DSA:2.40.30.10: ; PTHR11972: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013121: Ferric reductase, NAD binding domain; IPR001221: Phenol hydroxylase reductase; SFLDS00052: Ferric Reductase Domain; IPR013130: Ferric reductase transmembrane component-like domain; SSF52343: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:3.40.50.80: ; IPR013112: FAD-binding 8; IPR017938: Riboflavin synthase-like beta-barrel; cd06186: NOX_Duox_like_FAD_NADP; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24137_c0_seq1.p1	Ec-05_004950.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24362: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31884_c0_seq3.p1	Ec-05_004970.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0006457;GO:0031072;GO:0051082	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR24076: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001623: DnaJ domain; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24488_c0_seq3.p1	Ec-05_005100.1	hypothetical protein	GO:0008152	NA	NA
comp31155_c0_seq3.p1	Ec-05_005020.1	PEFG, plastid translation elongation factor EF-G	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; G3DSA:2.40.30.10: ; IPR000795: Transcription factor, GTP-binding domain; SignalP-TM: ; IPR005517: Translation elongation factor EFG/EF2, domain IV; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005225: Small GTP-binding protein domain; IPR004161: Translation elongation factor EFTu/EF1A, domain 2; IPR031157: Tr-type G domain, conserved site; IPR020568: Ribosomal protein S5 domain 2-type fold; PF00009: Elongation factor Tu GTP binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR009000: Translation protein, beta-barrel domain; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; G3DSA:3.30.70.870: ; PTHR23115: ; IPR000640: Translation elongation factor EFG, V domain; SignalP-noTM: ; IPR004540: Translation elongation factor EFG/EF2; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup; IPR009022: Elongation factor G, III-V domain	NA
comp21161_c0_seq1.p1	Ec-05_005050.1	YjgF/Yer057p/UK114 family	n/a;n/a;n/a	IPR002761: DUF71 domain; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; IPR030662: Diphthine--ammonia ligase/Uncharacterised protein MJ0570; IPR006175: YjgF/YER057c/UK114 family; SSF52402: ; IPR013813: Endoribonuclease L-PSP/chorismate mutase-like; G3DSA:3.90.1490.10:	NA
comp32364_c0_seq4.p1	Ec-05_005060.1	threonine--tRNA ligase	GO:0004812;GO:0004829;GO:0005524;GO:0006412;GO:0006435	IPR018163: Threonyl/alanyl tRNA synthetase, class II-like, putative editing domain; IPR002314: Aminoacyl-tRNA synthetase, class II (G/ H/ P/ S), conserved domain; PTHR11451: ; G3DSA:3.30.54.20: ; IPR012675: Beta-grasp domain; IPR006195: Aminoacyl-tRNA synthetase, class II; IPR012947: Threonyl/alanyl tRNA synthetase, SAD; SSF55681: ; IPR012676: TGS-like; G3DSA:3.30.980.10: ; IPR004095: TGS; IPR004154: Anticodon-binding; G3DSA:3.30.930.10:	KOG1637
comp32950_c0_seq33.p1	Ec-05_005120.1	Phosducin, thioredoxin-like domain	n/a;n/a;n/a	IPR024253: Phosducin, thioredoxin-like domain; PTHR21148: ; IPR012336: Thioredoxin-like fold	NA
comp32276_c1_seq7.p1	Ec-05_005150.1	probable high CO2 inducible periplasmic protein	NA	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011643: High-CO2 inducible periplasmic; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20196_c0_seq1.p1	Ec-05_005180.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp21238_c0_seq1.p1	Ec-05_005190.1	Biotin/lipoate A/B protein ligase family	GO:0003824;GO:0006464	SSF55681: ; PTHR12561: ; IPR004143: Biotinyl protein ligase (BPL) and lipoyl protein ligase (LPL), catalytic domain; G3DSA:3.90.1550.10:	NA
comp30111_c0_seq1.p2	Ec-05_005220.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp12986_c0_seq2.p1	Ec-05_005230.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp24364_c0_seq1.p1	Ec-05_005280.1	Uracil-DNA glycosylase-like	n/a;n/a;n/a	IPR002043: Uracil-DNA glycosylase; IPR018085: Uracil-DNA glycosylase, active site; SM00987: UreE urease accessory protein, C-terminal domain; IPR005122: Uracil-DNA glycosylase-like	NA
comp29217_c0_seq1.p1	Ec-05_005330.1	G-patch domain	GO:0003676	IPR000467: G-patch domain; Coil: ; PTHR23340:	NA
comp32411_c1_seq9.p2	Ec-05_005340.1	AAA+ ATPase domain	GO:0000166;GO:0005524;GO:0017111	IPR003593: AAA+ ATPase domain; IPR003959: ATPase, AAA-type, core; PTHR23075: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR021911: ATPase family AAA domain-containing protein 3, domain of unknown function DUF3523; Coil:	NA
comp32411_c1_seq9.p1	Ec-05_005350.1	conserved unknown protein	n/a;n/a;n/a	PTHR12202: ; Coil:	NA
comp30031_c0_seq4.p1	Ec-05_005400.1	DRTGG	n/a;n/a;n/a	IPR010766: DRTGG; IPR028979: HPr(Ser) kinase/phosphorylase, N-terminal domain-like; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR21343: ; PF13500: AAA domain	NA
comp21034_c0_seq2.p1	Ec-05_005410.1	Peptidase S9A, N-terminal domain	GO:0004252;GO:0006508;GO:0070008	IPR001375: Peptidase S9, prolyl oligopeptidase, catalytic domain; IPR029058: Alpha/Beta hydrolase fold; IPR023302: Peptidase S9A, N-terminal domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF50993: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002470: Peptidase S9A, prolyl oligopeptidase	NA
comp29715_c0_seq3.p1	Ec-05_005440.1	RNA recognition motif domain	GO:0003676	SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF54928: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000504: RNA recognition motif domain; PF14259: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain); IPR012677: Nucleotide-binding alpha-beta plait domain; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR24011:	NA
comp31011_c0_seq5.p1	Ec-05_005470.1	Voltage-dependent channel, four helix bundle domain	GO:0005216;GO:0006811;GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005821: Ion transport domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027359: Voltage-dependent channel, four helix bundle domain; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20452_c0_seq1.p1	Ec-05_005480.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19452_c0_seq1.p1	Ec-05_005510.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020	PTHR24089: ; IPR002067: Mitochondrial carrier protein; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier	NA
comp33723_c0_seq1.p2	Ec-05_005520.1	Sin3 associated polypeptide p18	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR010516: Sin3 associated polypeptide p18; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27298_c0_seq2.p1	Ec-05_005550.1	Proteasome maturation factor UMP1	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR008012: Proteasome maturation factor UMP1; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp24146_c0_seq3.p1	Ec-05_005560.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33161_c0_seq1.p1	Ec-05_005570.1	SPRY domain	GO:0005515	IPR027713: Protein Ssh4-like; IPR001810: F-box domain; G3DSA:1.20.1280.50: ; IPR001870: B30.2/SPRY domain; PTHR12864: ; IPR013320: Concanavalin A-like lectin/glucanase domain; IPR003877: SPRY domain	NA
comp32188_c0_seq25.p1	Ec-05_005580.1	PIH1 family	n/a;n/a;n/a	IPR012981: PIH1 family	NA
comp26989_c0_seq2.p1	Ec-05_005680.1	Leukotriene-A(4) hydrolase	GO:0005488	PTHR11533:SF174: ; IPR014782: Peptidase M1, membrane alanine aminopeptidase, N-terminal; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001930: Peptidase M1, alanine aminopeptidase/leukotriene A4 hydrolase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015211: Peptidase M1, leukotriene A4 hydrolase, aminopeptidase C-terminal; G3DSA:1.10.390.10: ; SSF55486: ; IPR016024: Armadillo-type fold; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF63737:	NA
comp25169_c0_seq1.p1	Ec-05_005700.1	Mitochondrial inner membrane protein Mitofilin	GO:0031305;n/a	PTHR15415: ; Coil: ; IPR019133: Mitochondrial inner membrane protein Mitofilin; SignalP-TM:	NA
comp21841_c0_seq2.p1	Ec-05_005710.1	Potassium channel, calcium-activated, BK, alpha subunit	GO:0006813;GO:0015269;GO:0016020	PTHR10027: ; G3DSA:1.10.287.70: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR024939: Calcium-activated potassium channel Slo; SSF81324: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005821: Ion transport domain; IPR016040: NAD(P)-binding domain; IPR003929: Potassium channel, calcium-activated, BK, alpha subunit; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp90069_c0_seq1.p1	Ec-05_005720.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp35145_c0_seq1.p1	Ec-05_005740.1	NADH dehydrogenase (ubiquinone)	GO:0016020;GO:0009055;GO:0008137	PF05071: NADH ubiquinone oxidoreductase subunit NDUFA12; IPR007763: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	KOG3382
comp28256_c0_seq1.p1	Ec-05_005750.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31338_c0_seq34.p3	Ec-05_005760.1	Protein of unknown function DUF2046	n/a;n/a;n/a	IPR019152: Protein of unknown function DUF2046; Coil:	NA
comp17345_c0_seq1.p1	Ec-05_005770.1	ENTH domain	n/a;n/a;n/a	IPR013809: ENTH domain; Coil: ; PTHR21514: ; IPR008942: ENTH/VHS	NA
comp43914_c0_seq1.p1	Ec-05_005780.1	EF-hand domain pair	GO:0005509	IPR018247: EF-Hand 1, calcium-binding site; SIGNAL_PEPTIDE: Signal peptide region; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF47473: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp51965_c0_seq1.p1	Ec-05_005800.1	conserved unknown protein	n/a;n/a;n/a	SSF48452: ; Coil:	NA
comp16389_c0_seq1.p1	Ec-05_005840.2	MutS protein homolog 5	GO:0005524;GO:0006298;GO:0030983	PTHR11361:SF20: ; IPR007861: DNA mismatch repair protein MutS, clamp; IPR007696: DNA mismatch repair protein MutS, core; IPR000432: DNA mismatch repair protein MutS, C-terminal; PTHR11361: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase	KOG0221
comp11693_c0_seq1.p1	Ec-05_005860.1	Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdomain	GO:0006886;GO:0016192;GO:0030131	IPR008152: Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdomain; IPR003164: Clathrin adaptor, alpha-adaptin, appendage, C-terminal subdomain; IPR015873: Clathrin alpha-adaptin/coatomer adaptor, appendage, C-terminal subdomain; IPR009028: Coatomer/calthrin adaptor appendage, C-terminal subdomain; IPR013038: Clathrin adaptor, alpha-adaptin, appendage; PTHR22780: ; IPR013041: Coatomer/clathrin adaptor appendage, Ig-like subdomain	NA
comp14108_c0_seq1.p1	Ec-05_005870.1	Coatomer protein complex, alpha sub-unit	GO:0005488;GO:0016192;GO:0006886;GO:0030117	IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold; PTHR22780: ; IPR002553: Clathrin/coatomer adaptor, adaptin-like, N-terminal	KOG1077
comp34119_c0_seq1.p1	Ec-05_005880.1	ATPase, V1 complex, subunit F	GO:0034220	IPR005772: ATPase, V1 complex, subunit F, eukaryotic; IPR008218: ATPase, V1 complex, subunit F	NA
comp11853_c0_seq1.p1	Ec-05_005900.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13432: Tetratricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; Coil: ; IPR019734: Tetratricopeptide repeat; PTHR22904:	NA
comp32683_c3_seq8.p1	Ec-05_005910.1	Transcription factor IIIC, 90kDa subunit, N-terminal	n/a;n/a;n/a	IPR024761: Transcription factor IIIC, 90kDa subunit, N-terminal; Coil:	NA
comp17316_c0_seq1.p1	Ec-05_005930.1	hypothetical protein	n/a;n/a;n/a	Coil: ; SignalP-TM:	NA
comp28343_c0_seq2.p1	Ec-05_005940.1	CDC48 domain 2-like	GO:0007031;GO:0005524;GO:0005777;GO:0005515	IPR029067: CDC48 domain 2-like; IPR003959: ATPase, AAA-type, core; IPR003960: ATPase, AAA-type, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR23077: ; IPR003593: AAA+ ATPase domain; G3DSA:1.10.8.60: ; Coil: ; IPR025653: Peroxisome biogenesis factor 1; IPR015342: Peroxisome biogenesis factor 1, N-terminal	NA
comp29762_c0_seq2.p1	Ec-05_005950.1	Acidic fibroblast growth factor binding (FIBP) domain protein	GO:0017134	PTHR13223:SF2: ; IPR008614: Acidic fibroblast growth factor intracellular-binding protein	NA
comp29762_c0_seq2.p2	Ec-05_005950.3	Acidic fibroblast growth factor binding (FIBP) domain protein	GO:0017134	PTHR13223:SF2: ; IPR008614: Acidic fibroblast growth factor intracellular-binding protein	NA
comp13145_c0_seq1.p1	Ec-05_005960.1	Myosin light chain kinase-related	n/a;n/a;n/a	IPR020675: Myosin light chain kinase-related; IPR020683: Ankyrin repeat-containing domain; SSF140860:	NA
comp24864_c0_seq1.p1	Ec-05_005970.4	Mitochondrial transcription termination factor	GO:0003690;GO:0005739;GO:0006355	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR13068: ; IPR003690: Mitochondrial transcription termination factor; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31791_c0_seq10.p1	Ec-05_006030.2	Hypothetical protein	n/a;n/a;n/a	IPR001878: Zinc finger, CCHC-type	NA
comp31169_c0_seq14.p7	Ec-05_006040.1	Rab5-interacting protein family	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR029008: Rab5-interacting protein family; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24466_c0_seq1.p1	Ec-05_006050.1	HAD-like domain	n/a;n/a;n/a	IPR006353: HAD-superfamily hydrolase, subfamily IIA, CECR5; PTHR14269: ; PF13242: HAD-hyrolase-like; IPR006357: HAD-superfamily hydrolase, subfamily IIA; SignalP-TM: ; PTHR14269:SF4: ; IPR023214: HAD-like domain	NA
comp33010_c2_seq1.p1	Ec-05_006110.1	TATA element modulatory factor 1 TATA binding	n/a;n/a;n/a	Coil: ; IPR022091: TATA element modulatory factor 1 TATA binding	NA
comp27755_c0_seq4.p1	Ec-05_006130.1	Transmembrane protein 161A/B	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR019395: Transmembrane protein 161A/B; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp41061_c0_seq1.p1	Ec-05_006150.1	Dynein 18 kDa light chain, flagellar outer arm	GO:0005509	PF13833: EF-hand domain pair; PTHR10891: ; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; SSF47473:	NA
comp24520_c0_seq1.p1	Ec-05_006160.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24186_c0_seq1.p1	Ec-05_006180.1	Bulb-type lectin domain	GO:0005529	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001480: Bulb-type lectin domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31257_c0_seq2.p1	Ec-05_006190.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777	IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR001752: Kinesin motor domain	NA
comp24610_c0_seq3.p1	Ec-05_006200.1	Cytidine deaminase-like	GO:0002100;GO:0003824;GO:0008251	G3DSA:3.40.140.10: ; PTHR11079: ; IPR016193: Cytidine deaminase-like; IPR002125: Cytidine and deoxycytidylate deaminases, zinc-binding; IPR028883: tRNA-specific adenosine deaminase	NA
comp28848_c0_seq2.p1	Ec-05_006210.2	Cation/H+ exchanger, CPA1 family	GO:0006812;GO:0015299;GO:0016021	IPR018422: Cation/H+ exchanger, CPA1 family; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10110:SF86: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006153: Cation/H+ exchanger; IPR018490: Cyclic nucleotide-binding-like; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20594_c0_seq2.p1	Ec-05_006220.1	Methionine-R-sulfoxide reductase	GO:0033743;GO:0055114	IPR002579: Peptide methionine sulphoxide reductase MrsB; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR028427: Peptide methionine sulfoxide reductase; IPR011057: Mss4-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25367_c0_seq3.p1	Ec-05_006230.1	expressed unknown protein	n/a;n/a;n/a	SignalP-noTM: ; Coil:	NA
comp13576_c0_seq1.p1	Ec-05_006270.3	Axin interactor dorsalization-associated protein, C-terminal domain	n/a;n/a;n/a	PF13637: Ankyrin repeats (many copies); IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR13140: ; IPR001849: Pleckstrin homology domain; IPR000048: IQ motif, EF-hand binding site; IPR011993: PH domain-like; IPR020683: Ankyrin repeat-containing domain; IPR001609: Myosin head, motor domain; Coil: ; IPR002110: Ankyrin repeat; IPR025939: Axin interactor dorsalization-associated protein, C-terminal domain	NA
comp24249_c0_seq2.p2	Ec-05_006300.1	ferredoxin (cyanobacterial type ferredoxin family)	GO:0051536	PTHR25040: ; G3DSA:3.30.70.20: ; IPR017896: 4Fe-4S ferredoxin-type, iron-sulphur binding domain; PF13459: 4Fe-4S single cluster domain; Coil: ; SSF54862:	NA
comp28330_c0_seq2.p2	Ec-05_006340.1	Mitochondrial protein import TIM9.10 complex subunit, Tim9 homolog	GO:0042719;GO:0006626;GO:0045039	IPR004217: Tim10/DDP family zinc finger; PTHR10898:	KOG3479
comp28162_c0_seq1.p1	Ec-05_006350.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	GO:0005801;GO:0000139;GO:0016021;GO:0006888	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF12352: Snare region anchored in the vesicle membrane C-terminus; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023601: Golgi SNAP receptor complex, subunit 1; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3208
comp32522_c3_seq1.p2	Ec-05_006370.1	Histone deacetylase, CXXC zinc finger and AP2 domain protein	GO:0003677;GO:0003700;GO:0006355;GO:0008270;n/a	mobidb-lite: consensus disorder prediction; IPR001471: AP2/ERF domain; IPR023801: Histone deacetylase domain; Coil: ; PTHR10625:SF139: ; IPR002857: Zinc finger, CXXC-type; SSF52768: ; IPR000286: Histone deacetylase superfamily	NA
comp27587_c0_seq3.p1	Ec-05_006410.1	delta-1-pyrroline-5-carboxylate reductase	GO:0004735;GO:0006561;GO:0055114	IPR001841: Zinc finger, RING-type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14155: ; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011016: Zinc finger, RING-CH-type; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3124
comp34307_c0_seq1.p1	Ec-05_006415.1	delta-1-pyrroline-5-carboxylate reductase	GO:0004735;GO:0006561;GO:0055114	IPR028939: Pyrroline-5-carboxylate reductase, catalytic, N-terminal; SSF51735: ; IPR008927: 6-phosphogluconate dehydrogenase C-terminal domain-like; IPR016040: NAD(P)-binding domain; IPR000304: Pyrroline-5-carboxylate reductase; IPR029036: Pyrroline-5-carboxylate reductase, dimerisation domain	KOG3124
comp20868_c0_seq1.p2	Ec-05_006480.1	RNA-binding, CRM domain	GO:0003723	IPR001890: RNA-binding, CRM domain	NA
comp28003_c0_seq1.p1	Ec-05_006490.1	Acyl carrier protein-like	GO:0008152;GO:0003824	G3DSA:3.40.50.980: ; IPR000873: AMP-dependent synthetase/ligase; G3DSA:2.30.38.10: ; IPR020806: Polyketide synthase, phosphopantetheine-binding domain; PTHR22754: ; G3DSA:3.30.300.30: ; IPR009081: Acyl carrier protein-like; SSF56801:	NA
comp20868_c0_seq1.p1	Ec-05_006500.1	2-cys peroxiredoxin	GO:0045454	IPR000866: Alkyl hydroperoxide reductase subunit C/ Thiol specific antioxidant; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR019479: Peroxiredoxin, C-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10681: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0852
comp32683_c0_seq2.p1	Ec-05_006520.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29709_c0_seq1.p1	Ec-05_006570.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003677;GO:0006281;GO:0005524;GO:0004003	IPR014016: UvrD-like Helicase, ATP-binding domain; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR014017: DNA helicase, UvrD-like, C-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000212: DNA helicase, UvrD/REP type; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12145_c0_seq1.p1	Ec-05_006580.1	GroES (chaperonin 10)-like	GO:0005524;GO:0005737;GO:0006457	IPR020818: Chaperonin Cpn10; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011032: GroES (chaperonin 10)-like; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1641
comp32502_c0_seq1.p1	Ec-05_006670.2	Hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19804_c0_seq1.p1	Ec-05_006680.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26853_c0_seq1.p1	Ec-05_006690.1	Cytochrome b6-f complex iron-sulfur subunit	GO:0016020;GO:0051537;GO:0055114;GO:0042651;GO:0009496;GO:0045158;GO:0015979	IPR017941: Rieske [2Fe-2S] iron-sulphur domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR005805: Rieske iron-sulphur protein, C-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR014349: Rieske iron-sulphur protein; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR014909: Cytochrome b6-f complex Fe-S subunit; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023960: Cytochrome b6-f complex iron-sulfur subunit	KOG1671
comp11709_c0_seq2.p1	Ec-05_006700.3	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a	PTHR12121:SF31: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005135: Endonuclease/exonuclease/phosphatase; PTHR12121: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33786_c0_seq1.p1	Ec-05_006710.1	galactose-4-epimerase, UDP	GO:0003978;GO:0006012	PTHR10366:SF308: ; IPR001509: NAD-dependent epimerase/dehydratase, N-terminal domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR005886: UDP-glucose 4-epimerase GalE; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR10366:	NA
comp27079_c0_seq2.p1	Ec-05_006720.1	B-domain containing protein Kua	n/a;n/a;n/a	IPR019547: B-domain containing protein Kua; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33139_c0_seq30.p1	Ec-05_006730.1	WD40 repeat containing protein	GO:0005515	IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; PTHR19842: ; IPR020472: G-protein beta WD-40 repeat	KOG0315
comp31117_c1_seq9.p1	Ec-05_006740.1	Acyl-CoA binding protein	GO:0000062	IPR000582: Acyl-CoA-binding protein, ACBP; IPR014352: FERM/acyl-CoA-binding protein, 3-helical bundle; PTHR23310:	KOG0817
comp25546_c0_seq1.p1	Ec-05_006760.1	Cystathionine beta-lyase	GO:0004121;GO:0000097;GO:0003824;GO:0030170	IPR015424: Pyridoxal phosphate-dependent transferase; IPR006594: LIS1 homology motif; IPR000277: Cys/Met metabolism, pyridoxal phosphate-dependent enzyme; IPR006238: Cystathionine beta-lyase, eukaryotic; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	KOG0053
comp21793_c1_seq1.p1	Ec-05_006800.1	CRAL-TRIO domain	GO:0007165;GO:0005622	PTHR23176: ; IPR001251: CRAL-TRIO domain; IPR008936: Rho GTPase activation protein; IPR000198: Rho GTPase-activating protein domain	NA
comp19999_c0_seq1.p1	Ec-05_006830.1	Endoplasmic reticulum vesicle transporter, C-terminal	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10984: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF13850: Endoplasmic Reticulum-Golgi Intermediate Compartment (ERGIC); IPR012936: Endoplasmic reticulum vesicle transporter, C-terminal; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27754_c0_seq2.p1	Ec-05_006850.1	chitinase-domain containing protein	GO:0005975	IPR011583: Chitinase II; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR017853: Glycoside hydrolase superfamily; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11177: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013781: Glycoside hydrolase, catalytic domain	KOG2091
comp28731_c0_seq2.p1	Ec-05_006860.1	Misato Segment II tubulin-like domain	GO:0003924;GO:0051258;GO:0043234	IPR019605: Misato Segment II tubulin-like domain; IPR003008: Tubulin/FtsZ, GTPase domain; PTHR13391:	NA
comp32738_c0_seq15.p1	Ec-05_006880.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR011704: ATPase, dynein-related, AAA domain; IPR003593: AAA+ ATPase domain; PR00830: Endopeptidase La (Lon) serine protease (S16) signature; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR002035: von Willebrand factor, type A; PTHR22908:	NA
comp65043_c0_seq1.p1	Ec-05_006980.1	Protein-tyrosine phosphatase-like	n/a;GO:0008138;GO:0006470	IPR029021: Protein-tyrosine phosphatase-like; IPR016130: Protein-tyrosine phosphatase, active site; IPR000387: Protein-tyrosine/Dual specificity phosphatase; IPR003595: Protein-tyrosine phosphatase, catalytic; IPR000340: Dual specificity phosphatase, catalytic domain; IPR020422: Dual specificity phosphatase, subgroup, catalytic domain; PTHR23339:	NA
comp11846_c0_seq2.p1	Ec-05_006990.1	Jumonji and P-loop NTPase domain protein	NA	NA	NA
comp31851_c1_seq9.p1	Ec-05_007000.1	Ribosomal L11 methyltransferase, PrmA	GO:0008168;GO:0008276;GO:0006479;GO:0005737	PF06325: Ribosomal protein L11 methyltransferase (PrmA); IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; IPR025799: Protein arginine N-methyltransferase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:2.70.160.11: ; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29568_c0_seq1.p4	Ec-06_000050.1	Fibronectin type III	GO:0005515	IPR013783: Immunoglobulin-like fold; IPR003961: Fibronectin type III	NA
comp29891_c0_seq14.p1	Ec-06_000070.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32103_c0_seq17.p1	Ec-06_000080.1	NADP-dependent oxidoreductase domain	GO:0016491;GO:0055114	IPR001395: Aldo/keto reductase; IPR023210: NADP-dependent oxidoreductase domain	NA
comp11387_c0_seq1.p1	Ec-06_000090.1	Thioredoxin-like fold	GO:0045454;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005746: Thioredoxin; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PR00421: Thioredoxin family signature; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26325_c0_seq1.p2	Ec-06_000100.1	Siva	GO:0008270	IPR022773: Siva	NA
comp26325_c0_seq1.p1	Ec-06_000110.1	CMP/dCMP deaminase, zinc-binding	GO:0003824;GO:0016787;GO:0008270	PTHR11079: ; G3DSA:3.40.140.10: ; IPR016193: Cytidine deaminase-like; IPR002125: Cytidine and deoxycytidylate deaminases, zinc-binding	NA
comp27605_c0_seq1.p1	Ec-06_000120.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp27223_c0_seq1.p1	Ec-06_000130.1	SELO_like protein (not a selenoprotein)	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003846: Uncharacterised protein family UPF0061; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR32057: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30434_c1_seq2.p1	Ec-06_000140.1	SAP30-binding protein	GO:0006355	IPR012479: SAP30-binding protein	NA
comp32737_c1_seq13.p1	Ec-06_000150.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008168;GO:0003676;GO:0032259	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR002052: DNA methylase, N-6 adenine-specific, conserved site	NA
comp12931_c0_seq1.p1	Ec-06_000160.1	Acyl carrier protein	GO:0006633	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003231: Acyl carrier protein (ACP); IPR009081: Acyl carrier protein-like; PTHR20863: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1748
comp65776_c0_seq1.p1	Ec-06_000170.1	Endonuclease/exonuclease/phosphatase	n/a;GO:0005515	IPR013783: Immunoglobulin-like fold; IPR003961: Fibronectin type III; IPR005135: Endonuclease/exonuclease/phosphatase; PTHR12121:	NA
comp11965_c0_seq1.p1	Ec-06_000180.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp31544_c0_seq1.p1	Ec-06_000190.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp34575_c0_seq1.p1	Ec-06_000200.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp12902_c0_seq1.p2	Ec-06_000210.1	WD40 repeat	GO:0005515	PTHR22842: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; IPR020472: G-protein beta WD-40 repeat	NA
comp12902_c0_seq1.p1	Ec-06_000220.1	Mpv17/PMP22	GO:0016021	IPR007248: Mpv17/PMP22; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11266:SF16: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1944
comp17130_c0_seq1.p1	Ec-06_000230.1	Zinc finger, RING-type	GO:0005515;GO:0008270	IPR017907: Zinc finger, RING-type, conserved site; SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR23163: ; PF13923: Zinc finger, C3HC4 type (RING finger); Coil:	NA
comp20158_c0_seq2.p1	Ec-06_000240.1	Thylakoid lumenal 15 kDa protein, chloroplast precursor (p15)	NA	IPR001646: Pentapeptide repeat; SIGNAL_PEPTIDE: Signal peptide region; PTHR14136: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF141571: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25277_c0_seq1.p2	Ec-06_000250.1	Neurotransmitter-gated ion-channel transmembrane domain	GO:0016020;GO:0006811	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006029: Neurotransmitter-gated ion-channel transmembrane domain; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28298_c0_seq5.p1	Ec-06_000260.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp28298_c0_seq5.p3	Ec-06_000280.1	RNA polymerase II, Rpb4	GO:0000166;GO:0003824;GO:0003899;GO:0006351;GO:0044237	PTHR15561:SF0: ; IPR010997: HRDC-like; PTHR15561: ; IPR005574: RNA polymerase II, Rpb4; IPR006590: RNA polymerase II, Rpb4, core	NA
comp29596_c0_seq1.p1	Ec-06_000290.1	Homeodomain-like	GO:0003677	PTHR10641: ; PF13921: Myb-like DNA-binding domain; IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; IPR017877: Myb-like domain; IPR017930: Myb domain	NA
comp30970_c0_seq2.p1	Ec-06_000320.1	Sjoegren syndrome/scleroderma autoantigen 1	n/a;n/a;n/a	IPR009563: Sjoegren syndrome/scleroderma autoantigen 1	NA
comp25569_c0_seq1.p1	Ec-06_000330.1	CRAL-TRIO domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001251: CRAL-TRIO domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR23324: ; IPR011074: CRAL/TRIO, N-terminal domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32728_c0_seq55.p1	Ec-06_000350.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp11779_c0_seq1.p2	Ec-06_000360.1	Cyclin-dependent kinase, regulatory subunit	GO:0016538;GO:0007049	IPR000789: Cyclin-dependent kinase, regulatory subunit; PTHR23415:	NA
comp29444_c0_seq4.p1	Ec-06_000370.2	Pre-mRNA-processing protein PRP40	GO:0005515	IPR002713: FF domain; IPR001202: WW domain; PTHR11864: ; PTHR11864:SF0: ; Coil: ; G3DSA:2.20.70.10:	NA
comp12965_c0_seq1.p1	Ec-06_000380.1	SGNH hydrolase-type esterase domain	n/a;n/a;n/a	PF13472: GDSL-like Lipase/Acylhydrolase family; IPR013830: SGNH hydrolase-type esterase domain	NA
comp12934_c0_seq1.p1	Ec-06_000390.1	expressed unknown protein	GO:0005215;GO:0005488;GO:0006810	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32596_c0_seq4.p2	Ec-06_000550.1	Light harvesting complex protein	GO:0009765;GO:0016020	SIGNAL_PEPTIDE: Signal peptide region; IPR022796: Chlorophyll A-B binding protein; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023329: Chlorophyll a/b binding protein domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001344: Chlorophyll A-B binding protein, plant; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32596_c0_seq4.p1	Ec-06_000610.1	Cation efflux protein	GO:0055085;GO:0006812;GO:0016021;GO:0008324	PTHR13414: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF161111: ; IPR027469: Cation efflux protein transmembrane domain; Coil: ; IPR002524: Cation efflux protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30206_c0_seq2.p1	Ec-06_000620.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0005515;GO:0008270	IPR001594: Zinc finger, DHHC-type, palmitoyltransferase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24161: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020683: Ankyrin repeat-containing domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002110: Ankyrin repeat	NA
comp24919_c0_seq1.p1	Ec-06_000630.1	Lsg1, cytoplasmic GTPase involved in the ribosome assembly	GO:0005525;GO:0005622	PTHR11089: ; IPR006073: GTP binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp32938_c1_seq13.p1	Ec-06_000640.1	Galactose oxidase, beta-propeller	n/a;GO:0005515	PTHR24412: ; IPR006652: Kelch repeat type 1; IPR011043: Galactose oxidase/kelch, beta-propeller; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF13418: Galactose oxidase, central domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015916: Galactose oxidase, beta-propeller; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31067_c0_seq2.p1	Ec-06_000650.1	conserved unknown protein	n/a;GO:0005515	Coil: ; IPR000048: IQ motif, EF-hand binding site	NA
comp26483_c1_seq2.p1	Ec-06_000660.2	Forkhead-associated (FHA) domain	GO:0005515	SSF57850: ; IPR001841: Zinc finger, RING-type; IPR018957: Zinc finger, C3HC4 RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; Coil:	NA
comp24777_c0_seq2.p1	Ec-06_000670.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR002885: Pentatricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; PTHR24015:	NA
comp13048_c0_seq1.p1	Ec-06_000690.1	2Fe-2S ferredoxin-type domain	GO:0009055;GO:0051536	PTHR19370: ; IPR001041: 2Fe-2S ferredoxin-type domain; IPR012675: Beta-grasp domain	NA
comp19750_c0_seq1.p1	Ec-06_000700.1	cysteine desulfuration protein	NA	SSF82649: ; IPR003808: Fe-S metabolism associated domain, SufE-like; SIGNAL_PEPTIDE: Signal peptide region; PTHR12735: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002634: BolA protein; G3DSA:3.90.1010.10:	NA
comp23402_c0_seq2.p1	Ec-06_000740.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp29425_c0_seq2.p1	Ec-06_000760.1	C2 domain	GO:0005515	IPR000008: C2 domain; IPR010734: Copine; PTHR10857: ; IPR002035: von Willebrand factor, type A	NA
comp27156_c0_seq3.p1	Ec-06_000770.1	Aldolase-type TIM barrel	GO:0050660;GO:0003824;GO:0055114;GO:0008033;GO:0017150	IPR013785: Aldolase-type TIM barrel; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001269: tRNA-dihydrouridine synthase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF51395: ; IPR018517: tRNA-dihydrouridine synthase, conserved site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31109_c0_seq1.p2	Ec-06_000780.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR000629: ATP-dependent RNA helicase DEAD-box, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001870: B30.2/SPRY domain; PTHR24031: ; IPR013320: Concanavalin A-like lectin/glucanase domain; IPR003877: SPRY domain; IPR014014: RNA helicase, DEAD-box type, Q motif; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal	KOG0349
comp20648_c0_seq1.p1	Ec-06_000790.1	imm downregulated 23	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp27803_c0_seq2.p1	Ec-06_000800.1	tRNA methyltransferase TRMD/TRM10-type domain	n/a;n/a;n/a	IPR028564: tRNA methyltransferase TRM10-type domain; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR016009: tRNA methyltransferase TRMD/TRM10-type domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007356: tRNA (guanine-N1-)-methyltransferase, eukaryotic; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33032_c2_seq24.p2	Ec-06_000810.1	TRAM domain	n/a;GO:0030697;GO:0008033	IPR012340: Nucleic acid-binding, OB-fold; IPR030391: RNA methyltransferase TrmA, conserved site; SIGNAL_PEPTIDE: Signal peptide region; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR11061: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR030390: RNA methyltransferase TrmA, active site; IPR002792: TRAM domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR010280: (Uracil-5)-methyltransferase family; IPR025795: tRNA (uracil-5-)-methyltransferase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31109_c0_seq1.p1	Ec-06_000960.1	SNF2-related	GO:0046872;GO:0003677;GO:0005524;GO:0005515;GO:0008270	NA	NA
comp19554_c0_seq1.p1	Ec-06_000970.1	Methionine synthase	GO:0046872;GO:0031419;GO:0008705;GO:0019284;GO:0042558	IPR004223: Vitamin B12-dependent methionine synthase, activation domain; IPR011822: Cobalamin-dependent methionine synthase; IPR003726: Homocysteine-binding domain; PTHR21091:SF112: ; IPR011005: Dihydropteroate synthase-like; PTHR21091: ; IPR003759: Cobalamin (vitamin B12)-binding module, cap domain; Coil: ; IPR000489: Pterin-binding domain; IPR006158: Cobalamin (vitamin B12)-binding domain	NA
comp30280_c0_seq1.p3	Ec-06_000990.1	Snf7 vacuolar protein sorting protein	GO:0007034;GO:0015031	IPR005024: Snf7 family; PTHR10476:	NA
comp30280_c0_seq1.p2	Ec-06_001000.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp30280_c0_seq1.p1	Ec-06_001010.1	class-V aminotransferase	n/a;GO:0003824;GO:0030170	IPR015424: Pyridoxal phosphate-dependent transferase; PTHR11601: ; IPR000192: Aminotransferase class V domain; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2	KOG1549
comp29481_c0_seq2.p1	Ec-06_001040.1	Vacuolar membrane-associated protein Iml1	n/a;n/a;n/a	IPR027244: Vacuolar membrane-associated protein Iml1; Coil:	NA
comp30494_c2_seq3.p1	Ec-06_001070.1	hypothetical protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25154_c0_seq1.p1	Ec-06_001080.1	Heat Shock transcription factor	GO:0005634;GO:0006355;GO:0043565;GO:0003700	NA	NA
comp30016_c0_seq3.p1	Ec-06_001090.1	Myo-inositol-1-phosphate synthase	GO:0003824;GO:0005488;GO:0008152	IPR011611: Carbohydrate kinase PfkB; SSF51735: ; IPR013021: Myo-inositol-1-phosphate synthase, GAPDH-like; SSF55347: ; SignalP-TM: ; IPR002587: Myo-inositol-1-phosphate synthase; G3DSA:3.30.360.10: ; IPR016040: NAD(P)-binding domain; IPR029056: Ribokinase-like	KOG0693
comp32557_c1_seq3.p1	Ec-06_001100.1	Cyclic nucleotide-binding domain	GO:0016020;n/a	IPR000595: Cyclic nucleotide-binding domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; mobidb-lite: consensus disorder prediction; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018490: Cyclic nucleotide-binding-like; cd00038: CAP_ED; IPR014710: RmlC-like jelly roll fold; IPR006916: Popeye protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26808_c0_seq1.p1	Ec-06_001110.1	Nucleic acid-binding, OB-fold	n/a;GO:0005634;GO:0003677;GO:0006260	IPR004591: Replication factor A protein 1; PTHR23273: ; IPR012340: Nucleic acid-binding, OB-fold; IPR004365: OB-fold nucleic acid binding domain, AA-tRNA synthetase-type; IPR013955: Replication factor A, C-terminal; IPR007199: Replication factor-A protein 1, N-terminal	NA
comp11905_c0_seq1.p1	Ec-06_001120.1	Bromodomain	GO:0005515	PTHR22880: ; Coil: ; IPR001487: Bromodomain	NA
comp24901_c0_seq3.p1	Ec-06_001130.1	AMMECR1 domain	n/a;n/a;n/a	IPR027485: AMMECR1, N-terminal; IPR023473: AMMECR1; IPR002733: AMMECR1 domain	NA
comp28675_c0_seq1.p1	Ec-06_001140.2	Domain of unknown function DUF3449	GO:0003676;GO:0005634;GO:0008270	PF13297: Telomere stability C-terminal; PTHR12786: ; IPR031776: Splicing factor 3A subunit 3; IPR000690: Zinc finger, C2H2-type matrin; IPR031774: SF3A3 domain; Coil: ; IPR024598: Domain of unknown function DUF3449	NA
comp33008_c0_seq8.p1	Ec-06_001150.1	small heat shock protein; heat shock protein 20	NA	IPR031107: Small heat shock protein HSP20; IPR002068: Alpha crystallin/Hsp20 domain; IPR008978: HSP20-like chaperone	NA
comp26395_c0_seq1.p1	Ec-06_001160.1	ENTH domain protein	n/a;n/a;n/a	PTHR12276: ; IPR013809: ENTH domain; PTHR12276:SF45: ; IPR008942: ENTH/VHS	NA
comp26395_c0_seq1.p3	Ec-06_001170.1	Proteasome component (PCI) domain	GO:0005515	IPR000717: Proteasome component (PCI) domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR15350:	NA
comp26395_c0_seq1.p2	Ec-06_001180.1	Glycosyltransferase, family GT64	GO:0016758;GO:0006024;GO:0031227;GO:0016021;GO:0015012	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR029044: Nucleotide-diphospho-sugar transferases; IPR015338: Exostosin , C-terminal; PTHR11062: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32622_c0_seq18.p1	Ec-06_001210.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR12176: ; IPR013216: Methyltransferase type 11	NA
comp29463_c0_seq1.p1	Ec-06_001230.1	P-loop containing nucleoside triphosphate hydrolase	GO:0000166	PTHR19306: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027131: Structural maintenance of chromosomes protein 5; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29247_c0_seq3.p2	Ec-06_001250.1	Vacuolar protein sorting-associated, VPS28	n/a;n/a;n/a	IPR017899: Vacuolar protein sorting-associated, VPS28, C-terminal; IPR017898: Vacuolar protein sorting-associated, VPS28, N-terminal; SSF140111: ; Coil: ; IPR007143: Vacuolar protein sorting-associated, VPS28; SSF140427:	NA
comp29247_c0_seq3.p1	Ec-06_001260.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp19466_c0_seq1.p1	Ec-06_001270.1	C2H2 zinc finger protein	GO:0005622;GO:0003676;GO:0046872;GO:0008270	IPR015880: Zinc finger, C2H2-like; PF12874: Zinc-finger of C2H2 type; PF12756: C2H2 type zinc-finger (2 copies); IPR007087: Zinc finger, C2H2; Coil: ; SSF57667:	NA
comp21646_c0_seq2.p1	Ec-06_001280.1	Class I glutamine amidotransferase-like	n/a;GO:0042819;GO:0042823;GO:0004359	PTHR31559: ; IPR021196: PdxT/SNO family, conserved site; IPR029062: Class I glutamine amidotransferase-like; IPR002161: Pyridoxal 5'-phosphate synthase subunit PdxT/SNO	NA
comp29854_c0_seq1.p1	Ec-06_001290.1	ADC synthase	GO:0009058	PR00099: Carbamoyl-phosphate synthase protein GATase domain signature; IPR006221: Anthranilate synthase/para-aminobenzoate synthase like domain; PTHR11236: ; PR00096: Glutamine amidotransferase superfamily signature; IPR029062: Class I glutamine amidotransferase-like; PR00097: Anthranilate synthase component II signature; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015890: Chorismate-utilising enzyme, C-terminal; IPR005801: ADC synthase; IPR017926: Glutamine amidotransferase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1224
comp30630_c0_seq1.p2	Ec-06_001300.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30630_c0_seq6.p1	Ec-06_001310.1	bHLH domain protein	GO:0046983	NA	NA
comp11667_c0_seq1.p1	Ec-06_001330.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003677;GO:0004003;GO:0005524;GO:0006281	IPR014017: DNA helicase, UvrD-like, C-terminal; IPR014016: UvrD-like Helicase, ATP-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:1.10.486.10: ; PF12705: PD-(D/E)XK nuclease superfamily	NA
comp30303_c0_seq7.p1	Ec-06_001340.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp26927_c1_seq1.p1	Ec-06_001350.1	haloacid dehalogenase-like hydrolase family protein	NA	SIGNAL_PEPTIDE: Signal peptide region; PTHR18901: ; IPR006439: HAD hydrolase, subfamily IA; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023214: HAD-like domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30149_c0_seq2.p1	Ec-06_001370.1	SWAP/Surp	GO:0003723;GO:0006396	IPR000061: SWAP/Surp; PTHR15316: ; IPR022030: Pre-mRNA splicing factor PRP21-like protein; Coil:	NA
comp24831_c0_seq1.p1	Ec-06_001380.1	beta-hydroxyacyl-ACP dehydratase	GO:0005737;GO:0006633;GO:0016836;n/a	SIGNAL_PEPTIDE: Signal peptide region; PTHR30272: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR013114: Beta-hydroxydecanoyl thiol ester dehydrase, FabA/FabZ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR029069: HotDog domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28769_c1_seq1.p1	Ec-06_001390.1	Histidine triad (HIT) protein	GO:0003824;n/a	IPR011146: HIT-like domain; IPR001310: Histidine triad (HIT) protein; PF11969: Scavenger mRNA decapping enzyme C-term binding	NA
comp31157_c0_seq1.p1	Ec-06_001400.1	Phospholipid/glycerol acyltransferase	GO:0016746;GO:0008152	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10434: ; IPR002123: Phospholipid/glycerol acyltransferase; G3DSA:3.40.1130.10: ; SSF69593: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27168_c0_seq1.p1	Ec-06_001410.1	Beta-galactosidase, family GH2	GO:0003824;GO:0043169;GO:0005975	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004199: Beta galactosidase small chain/ domain 5; IPR017853: Glycoside hydrolase superfamily; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR008979: Galactose-binding domain-like; IPR013812: Glycoside hydrolase, family 2/20, immunoglobulin-like beta-sandwich domain; IPR013781: Glycoside hydrolase, catalytic domain; IPR006102: Glycoside hydrolase, family 2, immunoglobulin-like beta-sandwich; IPR006103: Glycoside hydrolase, family 2, TIM barrel; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR023232: Glycoside hydrolase, family 2, active site; IPR011013: Galactose mutarotase-like domain; PTHR10066: ; IPR006104: Glycosyl hydrolases family 2, sugar binding domain; IPR014718: Glycoside hydrolase-type carbohydrate-binding, subgroup; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2024
comp21509_c0_seq1.p1	Ec-06_001420.1	Ribosomal protein L44e	GO:0005840;GO:0006412;GO:0005622;GO:0003735	NA	NA
comp30799_c0_seq2.p1	Ec-06_001430.1	Immunoglobulin E-set	n/a;n/a;n/a	IPR011021: Arrestin-like, N-terminal; IPR014756: Immunoglobulin E-set; PTHR11188:	NA
comp32125_c0_seq3.p1	Ec-06_001460.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26926_c0_seq2.p1	Ec-06_001490.1	XPG-I domain	GO:0004518	IPR006084: XPG/Rad2 endonuclease; IPR032641: Exonuclease 1; IPR020045: 5'-3' exonuclease, C-terminal domain; IPR006086: XPG-I domain; IPR006085: XPG N-terminal; G3DSA:1.10.150.20: ; Coil: ; IPR029060: PIN domain-like	NA
comp25114_c0_seq1.p1	Ec-06_001500.1	Alpha/Beta hydrolase fold	GO:0016787	IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002925: Dienelactone hydrolase; SSF68906: ; IPR003034: SAP domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR17630: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30961_c1_seq2.p1	Ec-06_001510.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp30961_c1_seq2.p3	Ec-06_001520.1	Csl4 is a component of the exosome 3'->5' exoribonuclease complex, a complex that degrades mRNAs.	GO:0003723;GO:0000178	IPR012340: Nucleic acid-binding, OB-fold; IPR025721: Exosome complex component, N-terminal domain; IPR003029: Ribosomal protein S1, RNA-binding domain; IPR022967: RNA-binding domain, S1; IPR019495: Exosome complex component CSL4; SSF110324: ; PTHR12686:	NA
comp26801_c0_seq4.p1	Ec-06_001530.1	divalent metal transporter	GO:0016020;GO:0006810;GO:0005215	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001046: NRAMP family; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30757_c0_seq3.p1	Ec-06_001550.1	putative Translation Initiation Inhibitor	n/a;n/a;n/a	IPR006175: YjgF/YER057c/UK114 family; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF14588: YjgF/chorismate_mutase-like, putative endoribonuclease; SignalP-noTM: ; IPR013813: Endoribonuclease L-PSP/chorismate mutase-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2317
comp30495_c0_seq3.p1	Ec-06_001570.1	Cyclic nucleotide-binding domain	n/a;n/a;n/a	SSF81324: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR005821: Ion transport domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33024_c1_seq27.p1	Ec-06_001580.1	Signal recognition particle subunit SRP68	GO:0005786;GO:0005047;GO:0006614;GO:0030942;GO:0008312	PTHR12860: ; IPR026258: Signal recognition particle subunit SRP68; Coil:	NA
comp25090_c0_seq2.p2	Ec-06_001590.1	GOLD	GO:0006810;GO:0016021	Coil: ; IPR009038: GOLD; PTHR23324:	NA
comp25090_c0_seq2.p1	Ec-06_001600.1	RPA-interacting protein	n/a;n/a;n/a	IPR028159: RPA-interacting protein, C-terminal domain; IPR028156: RPA-interacting protein; PD472859: RPA-INTERACTING METAL-BINDING ZINC-FINGER NUCLEAR ZINC UBL CONJUGATION SPLICING ALTERNATIVE A	NA
comp25252_c0_seq2.p1	Ec-06_001610.2	Threonine aldolase	GO:0003824;GO:0004793;GO:0006520;GO:0030170	PTHR10289: ; IPR001597: Aromatic amino acid beta-eliminating lyase/threonine aldolase; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR015424: Pyridoxal phosphate-dependent transferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2	KOG1368
comp25252_c0_seq2.p3	Ec-06_001620.1	Hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp21310_c0_seq1.p1	Ec-06_001720.2	eukaryotic translation initiation factor 3 k subunit	n/a;n/a;n/a	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR016020: Translation initiation factor 3, subunit 12, N-terminal, eukaryotic; PF10075: CSN8/PSMD8/EIF3K family; IPR009374: Eukaryotic translation initiation factor 3 subunit K; IPR016024: Armadillo-type fold	NA
comp32293_c0_seq2.p1	Ec-06_001730.1	expressed unknown protein	n/a;n/a;n/a	SignalP-noTM: ; SignalP-TM:	NA
comp24913_c0_seq1.p1	Ec-06_001740.1	Predicted HD phosphohydrolase	n/a;n/a;n/a	SSF109604: ; IPR009218: Predicted HD phosphohydrolase	NA
comp20081_c0_seq2.p1	Ec-06_001750.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp33496_c0_seq1.p2	Ec-06_001760.1	Phosphoglycerate mutase	GO:0015986;GO:0016020;GO:0016820;GO:0045263;GO:0015078;GO:0016469;GO:0015992	IPR013078: Histidine phosphatase superfamily, clade-1; IPR029033: Histidine phosphatase superfamily; PTHR23029:	NA
comp11665_c0_seq1.p1	Ec-06_001770.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp11665_c0_seq1.p2	Ec-06_001780.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp25114_c0_seq1.p3	Ec-06_001790.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR000719: Protein kinase domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR020636: Calcium/calmodulin-dependent/calcium-dependent protein kinase; IPR011009: Protein kinase-like domain	NA
comp26878_c0_seq1.p1	Ec-06_001810.1	CAS/CSE, C-terminal	GO:0006886;GO:0005515	PTHR10997: ; IPR001494: Importin-beta, N-terminal domain; IPR005043: CAS/CSE, C-terminal; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold; IPR013713: Exportin/Importin, Cse1-like	NA
comp32875_c1_seq2.p1	Ec-06_001860.2	Signal recognition particle, SRP9/SRP14 subunit	GO:0006614;GO:0008312;GO:0048500	IPR003210: Signal recognition particle, SRP14 subunit; IPR009018: Signal recognition particle, SRP9/SRP14 subunit	NA
comp11679_c0_seq1.p1	Ec-06_001870.1	serine/threonine-protein kinase	GO:0016772	IPR000719: Protein kinase domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR020636: Calcium/calmodulin-dependent/calcium-dependent protein kinase; IPR011009: Protein kinase-like domain	NA
comp13601_c0_seq1.p1	Ec-06_001880.1	conserved unknown protein	GO:0005506;GO:0006118;GO:0009055;GO:0009060;GO:0016021;GO:0020037	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp34074_c0_seq1.p1	Ec-06_001890.1	Ribosomal protein L31e	GO:0003735;GO:0005622;GO:0005840;GO:0006412	IPR000054: Ribosomal protein L31e; IPR023621: Ribosomal protein L31e domain	NA
comp26674_c0_seq1.p1	Ec-06_001900.1	MIF4G-like, type 3	GO:0003723;GO:0005515	IPR003891: Initiation factor eIF-4 gamma, MA3; IPR016024: Armadillo-type fold; IPR003890: MIF4G-like, type 3; Coil: ; PTHR18034: ; IPR016021: MIF4-like, type 1/2/3	NA
comp28700_c0_seq2.p1	Ec-06_001910.1	Amidohydrolase 3	GO:0016810;n/a	IPR013108: Amidohydrolase 3; IPR032466: Metal-dependent hydrolase; PTHR22642: ; PTHR22642:SF2: ; G3DSA:3.20.20.140: ; IPR011059: Metal-dependent hydrolase, composite domain	NA
comp88035_c0_seq1.p1	Ec-06_001920.1	EPS15 homology (EH)	GO:0005515	IPR018247: EF-Hand 1, calcium-binding site; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; SSF47473: ; IPR001293: Zinc finger, TRAF-type; IPR000261: EPS15 homology (EH); PTHR11216: ; Coil: ; PF12763: Cytoskeletal-regulatory complex EF hand	NA
comp30975_c1_seq9.p1	Ec-06_001930.1	tRNA methyltransferase, Trm1	GO:0003723;GO:0004809;GO:0008033	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002905: tRNA methyltransferase, Trm1; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30975_c0_seq4.p1	Ec-06_001950.1	carbohydrate kinase	GO:0016773;GO:0005975	PTHR10196: ; SIGNAL_PEPTIDE: Signal peptide region; IPR018485: Carbohydrate kinase, FGGY, C-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF53067: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.30.420.40: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29476_c0_seq1.p1	Ec-06_001980.1	Glutamate dehydrogenase (NAD-dependent)	GO:0008152;GO:0003824;GO:0019551;GO:0005488;GO:0006536;GO:0004352	PTHR11606: ; SSF51735: ; IPR006096: Glutamate/phenylalanine/leucine/valine dehydrogenase, C-terminal; SSF53223: ; IPR016040: NAD(P)-binding domain; IPR028971: NAD-glutamate dehydrogenase; G3DSA:3.40.192.10: ; SignalP-TM:	KOG2250
comp24423_c0_seq1.p1	Ec-06_001990.1	Major facilitator superfamily domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020846: Major facilitator superfamily domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:1.20.1250.20: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33833_c0_seq1.p1	Ec-06_002010.1	Major facilitator superfamily	GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; PTHR23121: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12705_c0_seq1.p1	Ec-06_002040.1	Zinc finger, RanBP2-type	GO:0008270	SSF90209: ; PTHR12999: ; IPR001876: Zinc finger, RanBP2-type	NA
comp32232_c0_seq7.p3	Ec-06_002060.1	Uncharacterised protein family Ycf36	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR009631: Uncharacterised protein family Ycf36; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32481_c0_seq2.p1	Ec-06_002100.1	CRC domain	n/a;n/a;n/a	IPR005172: CRC domain; IPR028307: Lin-54 family	NA
comp31001_c0_seq1.p1	Ec-06_002110.3	Homeodomain-like	GO:0003677	PTHR10641: ; PF13921: Myb-like DNA-binding domain; IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; IPR028311: Myb-related protein B; IPR017930: Myb domain; IPR017877: Myb-like domain	NA
comp31338_c0_seq29.p3	Ec-06_002120.1	diacylglycerol kinase	GO:0007205;GO:0004143	IPR001206: Diacylglycerol kinase, catalytic domain; PTHR11255: ; IPR000756: Diacylglycerol kinase, accessory domain; IPR016064: NAD kinase/diacylglycerol kinase-like domain	KOG1169
comp31478_c1_seq2.p1	Ec-06_002190.1	NBS type disease resistance protein	n/a;n/a;n/a	IPR029016: GAF domain-like; Coil:	NA
comp21239_c0_seq2.p1	Ec-06_002200.1	Protein of unknown function DUF393	n/a;n/a;n/a	PTHR33639: ; IPR007263: Protein of unknown function DUF393	NA
comp31025_c0_seq1.p2	Ec-06_002220.1	Exon junction complex, Pym	GO:0005515	IPR015362: WIBG family	NA
comp31025_c0_seq4.p1	Ec-06_002230.1	conserved unknown protein	n/a;n/a;n/a	IPR010736: Sperm-tail PG-rich repeat	NA
comp32457_c0_seq10.p1	Ec-06_002250.1	Taurine catabolism dioxygenase TauD/TfdA	GO:0016491;GO:0055114	IPR010376: Domain of unknown function DUF971; SSF51197: ; PTHR10696:SF25: ; SignalP-noTM: ; PTHR10696: ; G3DSA:3.60.130.10: ; IPR003819: TauD/TfdA-like domain; SignalP-TM:	NA
comp31751_c0_seq4.p1	Ec-06_002260.1	Winged helix-turn-helix DNA-binding domain	GO:0035556;GO:0007242	PTHR10774: ; IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; IPR000008: C2 domain; IPR000591: DEP domain	NA
comp20258_c0_seq1.p1	Ec-06_002270.1	Calmodulin	NA	IPR018247: EF-Hand 1, calcium-binding site; PTHR23050: ; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; PR00450: Recoverin family signature; SSF47473:	KOG0027
comp28804_c0_seq1.p1	Ec-06_002280.1	DNA primase	GO:0003677;GO:0003896;GO:0006260;GO:0008270	SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR006311: Twin-arginine translocation pathway, signal sequence; SignalP-TM: ; SSF56731: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR30313: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013264: DNA primase, catalytic core, N-terminal; SIGNAL_PEPTIDE: Signal peptide region; IPR002694: Zinc finger, CHC2-type; SSF57783: ; IPR030846: DNA primase DnaG, bacteria; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-noTM: ; IPR006171: Toprim domain; G3DSA:3.40.1360.10: ; Coil:	NA
comp12300_c0_seq1.p1	Ec-06_002300.1	Sorting and Assembly Machinery 50kDa protein (N-terminal)	GO:0019867	G3DSA:2.40.160.50: ; IPR000184: Bacterial surface antigen (D15); PTHR12815:	NA

comp58236_c0_seq1.p1	Ec-06_002340.1	Six-bladed beta-propeller, TolB-like	n/a;n/a;n/a	IPR000033: LDLR class B repeat; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011042: Six-bladed beta-propeller, TolB-like; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF63825: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013783: Immunoglobulin-like fold; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12770_c0_seq1.p1	Ec-06_002390.1	Rab7, RAB family GTPase	GO:0005622;GO:0007264;GO:0005525;GO:0015031	IPR002041: Ran GTPase; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR003578: Small GTPase superfamily, Rho type; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005225: Small GTP-binding protein domain; IPR001806: Small GTPase superfamily; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020849: Small GTPase superfamily, Ras type; IPR003579: Small GTPase superfamily, Rab type; PS51419: small GTPase Rab1 family profile.; PTHR24073: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp78713_c0_seq1.p1	Ec-06_002400.1	Ankyrin repeat Transient receptor potential channel	GO:0005216;GO:0006811;GO:0016020;GO:0055085	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10582: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005821: Ion transport domain; IPR020683: Ankyrin repeat-containing domain; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3676
comp31808_c0_seq2.p1	Ec-06_002430.1	Nucleic acid-binding, OB-fold	GO:0006351;GO:0006350	IPR012340: Nucleic acid-binding, OB-fold; IPR005570: RNA polymerase, Rpb8	NA
comp9653_c0_seq2.p2	Ec-06_002440.1	Peptidase C15, pyroglutamyl peptidase I-like	n/a;n/a;n/a	SSF53182: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR016125: Peptidase C15, pyroglutamyl peptidase I-like	NA
comp20025_c0_seq1.p1	Ec-06_002450.1	TRAF-like	GO:0016567;GO:0004842;GO:0005515;GO:0008270	IPR001293: Zinc finger, TRAF-type; IPR008974: TRAF-like; G3DSA:3.80.10.10: ; IPR013323: SIAH-type domain	NA
comp11817_c0_seq1.p1	Ec-06_002460.1	Gamma-glutamylcyclotransferase	GO:0003839;GO:0006750	IPR013024: Butirosin biosynthesis, BtrG-like; IPR017939: Gamma-glutamylcyclotransferase; IPR009288: AIG2-like	NA
comp20073_c0_seq1.p1	Ec-06_002470.1	Uricase	GO:0004846;GO:0006144;GO:0016491;GO:0055114	PD003367: URICASE OXIDOREDUCTASE URATE OXIDASE METABOLISM PURINE PEROXISOME ACETYLATION II DIRECT; G3DSA:3.10.270.10: ; SSF55620: ; IPR002042: Uricase; PTHR10395:	NA
comp25511_c0_seq1.p1	Ec-06_002480.1	Xanthine/uracil/vitamin C permease	GO:0016020;GO:0006810;GO:0055085;GO:0005215	IPR029938: Xanthine permease XanQ/UapA; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006043: Xanthine/uracil/vitamin C permease; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25511_c0_seq3.p1	Ec-06_002490.1	Xanthine/uracil/vitamin C permease	GO:0005215;GO:0006810;GO:0016020;GO:0055085	PTHR11119:SF36: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006043: Xanthine/uracil/vitamin C permease; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28514_c0_seq3.p1	Ec-06_002510.1	CMP/dCMP deaminase, zinc-binding	GO:0003824;GO:0016787;GO:0008270	G3DSA:3.40.140.10: ; PTHR11079: ; IPR016193: Cytidine deaminase-like; IPR002125: Cytidine and deoxycytidylate deaminases, zinc-binding	NA
comp20829_c0_seq1.p1	Ec-06_002530.1	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	n/a;n/a;n/a	IPR029068: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	NA
comp47183_c0_seq1.p1	Ec-06_002540.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33167_c1_seq4.p1	Ec-06_002550.1	Nucleotide-diphospho-sugar transferases	n/a;n/a;n/a	IPR029044: Nucleotide-diphospho-sugar transferases	NA
comp34555_c0_seq1.p1	Ec-06_002560.1	Actin-related protein 2/3 complex subunit ARPC1B or p41-Arc (Arp2/3 complex 41 kDa subunit)	GO:0005515	IPR017383: Actin-related protein 2/3 complex subunit 1; IPR017986: WD40-repeat-containing domain; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	KOG1523
comp11902_c0_seq1.p1	Ec-06_002570.1	oxidoreductase domain protein	GO:0008152;GO:0016491;GO:0055114	IPR000683: Oxidoreductase, N-terminal; SSF51735: ; IPR004104: Oxidoreductase, C-terminal; G3DSA:3.30.360.10: ; IPR016040: NAD(P)-binding domain; PTHR22604: ; SSF55347:	NA
comp11902_c0_seq1.p2	Ec-06_002580.1	Thiamin pyrophosphokinase, catalytic domain	GO:0005524;GO:0004788;GO:0009229	IPR007373: Thiamin pyrophosphokinase, vitamin B1-binding domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR13622: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR006282: Thiamin pyrophosphokinase; IPR007371: Thiamin pyrophosphokinase, catalytic domain	NA
comp31808_c0_seq9.p2	Ec-06_002590.1	Related to G-protein coupled receptors	GO:0004930;GO:0007186;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:1.20.1070.10: ; PTHR23112: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF81321: ; IPR000276: G protein-coupled receptor, rhodopsin-like; IPR022343: GCR1-cAMP receptor; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26632_c0_seq2.p1	Ec-06_002600.1	eukaryotic translation initiation factor 2B gamma subunit	GO:0016779;GO:0009058	IPR011004: Trimeric LpxA-like; IPR001451: Bacterial transferase hexapeptide repeat; IPR005835: Nucleotidyl transferase; IPR029044: Nucleotide-diphospho-sugar transferases; PTHR22572:	NA
comp31808_c0_seq9.p1	Ec-06_002620.1	Protein arginine N-methyltransferase	GO:0008168;GO:0006479	NA	NA
comp32966_c1_seq4.p1	Ec-06_002640.1	P-loop containing nucleoside triphosphate hydrolase	GO:0004176;GO:0004252;GO:0006508	IPR015947: PUA-like domain; IPR003959: ATPase, AAA-type, core; IPR008268: Peptidase S16, active site; IPR004815: Lon protease, bacterial/eukaryotic-type; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR008269: Peptidase S16, Lon C-terminal; IPR003111: Peptidase S16, lon N-terminal; IPR003593: AAA+ ATPase domain; PR00830: Endopeptidase La (Lon) serine protease (S16) signature; G3DSA:1.10.8.60: ; IPR020568: Ribosomal protein S5 domain 2-type fold; IPR027065: Lon protease; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup	NA
comp34535_c0_seq1.p1	Ec-06_002680.1	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplast precursor	GO:0019288;GO:0050992;GO:0046872;GO:0051745	IPR003451: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR31619: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28224_c0_seq1.p1	Ec-06_002690.1	hypothetical protein	n/a;n/a;n/a	Coil: ; SignalP-TM:	NA
comp30244_c3_seq4.p1	Ec-06_002700.1	Armadillo-type fold	GO:0005488	IPR001313: Pumilio RNA-binding repeat; IPR011989: Armadillo-like helical; PTHR12537: ; IPR016024: Armadillo-type fold	NA
comp30696_c0_seq9.p1	Ec-06_002710.1	Hypothetical leucine rich repeat and MORN motif protein	NA	G3DSA:3.80.10.10: ; G3DSA:2.20.110.10: ; PTHR24106: ; SSF52047: ; PF13516: Leucine Rich repeat; IPR003409: MORN motif; SSF82185: ; IPR003590: Leucine-rich repeat, ribonuclease inhibitor subtype	NA
comp12587_c0_seq1.p1	Ec-06_002720.1	peroxisomal membrane protein-related	GO:0016021	IPR007248: Mpv17/PMP22	NA
comp19560_c0_seq1.p1	Ec-06_002740.2	Cytochrome b5-like heme/steroid binding domain	GO:0020037	IPR001199: Cytochrome b5-like heme/steroid binding domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR10366:SF242: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002225: 3-beta hydroxysteroid dehydrogenase/isomerase; IPR016040: NAD(P)-binding domain; G3DSA:3.90.25.10: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10366:	NA
comp12138_c0_seq1.p1	Ec-06_002750.1	ATPase, F1 complex alpha/beta subunit, N-terminal domain	GO:0046034;GO:0015992	IPR000793: ATPase, F1/V1/A1 complex, alpha/beta subunit, C-terminal; IPR004100: ATPase, F1 complex alpha/beta subunit, N-terminal domain; PTHR15184: ; IPR000194: ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain; IPR005725: ATPase, V1 complex, subunit A; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR024034: ATPase, F1 complex beta subunit/V1 complex, C-terminal; IPR022878: V-type ATP synthase catalytic alpha chain	NA
comp21305_c0_seq1.p2	Ec-06_002760.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27342_c0_seq1.p2	Ec-06_002890.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31706_c1_seq1.p1	Ec-06_002900.1	Insulin-like growth factor binding protein, N-terminal	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR009030: Insulin-like growth factor binding protein, N-terminal; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:2.10.50.10: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR22727:	NA
comp20253_c0_seq1.p1	Ec-06_002910.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11439_c0_seq1.p1	Ec-06_002920.1	expressed unknown protein	n/a;n/a;n/a	IPR005162: Retrotransposon gag domain; Coil:	NA
comp31751_c0_seq7.p1	Ec-06_002930.1	CYTH-like domain	GO:0004016;GO:0006171	IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; IPR000073: Alpha/beta hydrolase fold-1; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14586: ; PD009560: CYCLASE ADENYLATE CYCLASE ADENYLYL CYAB LYASE CLASS CYAB-TYPE THERMOPHILIC MJ0240; IPR023577: CYTH-like domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25015_c0_seq1.p1	Ec-06_002940.1	Prolyl 4-hydroxylase, alpha subunit	GO:0005506;GO:0031418;GO:0055114;GO:0016705;GO:0016706;GO:0016491	IPR006620: Prolyl 4-hydroxylase, alpha subunit; SSF51197: ; IPR005123: Oxoglutarate/iron-dependent dioxygenase; G3DSA:2.60.120.620: ; PTHR12907:	NA
comp28080_c0_seq3.p1	Ec-06_002960.1	SET domain protein	GO:0005515	NA	NA
comp34439_c0_seq1.p1	Ec-06_002970.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	PTHR11440:SF48: ; IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000073: Alpha/beta hydrolase fold-1; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR11440: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20764_c0_seq1.p1	Ec-06_002990.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34114_c0_seq1.p1	Ec-06_003000.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33881_c0_seq1.p1	Ec-06_003010.1	Complex 1 LYR protein	n/a;n/a;n/a	IPR008011: Complex 1 LYR protein	NA
comp28079_c0_seq1.p1	Ec-06_003020.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp31966_c2_seq6.p1	Ec-06_003030.1	Monooxygenase	GO:0004497;GO:0006118;GO:0006725;GO:0055114	IPR002938: Monooxygenase, FAD-binding; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.50.50.60: ; PTHR13789: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PR00420: Aromatic-ring hydroxylase (flavoprotein monooxygenase) signature; SSF51905:	KOG2614
comp32529_c0_seq4.p3	Ec-06_003040.1	Cyclin, C-terminal domain	GO:0005634	IPR004367: Cyclin, C-terminal domain; IPR013763: Cyclin-like; PTHR10177:	NA
comp28664_c0_seq2.p1	Ec-06_003050.1	EF-hand domain pair	GO:0005509	IPR011992: EF-hand domain pair; IPR002048: EF-hand domain	NA
comp30439_c0_seq3.p1	Ec-06_003060.2	hypothetical protein	n/a;n/a;n/a	IPR019358: NEMP family; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24632_c0_seq1.p1	Ec-06_003070.1	Histidine phosphatase superfamily, clade-1	n/a;n/a;n/a	PTHR23029: ; IPR029033: Histidine phosphatase superfamily; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR013078: Histidine phosphatase superfamily, clade-1; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp34268_c0_seq1.p1	Ec-06_003080.1	flagellar adenylate kinase	GO:0005524;GO:0006139;GO:0019205;GO:0009041;GO:0006221;GO:0006207;GO:0004127	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR006266: UMP-CMP kinase; IPR000850: Adenylate kinase/UMP-CMP kinase; PF00406: Adenylate kinase	KOG3079
comp31587_c3_seq3.p1	Ec-06_003090.1	MIF4-like, type 1/2/3	GO:0005488	IPR016189: Translation initiation factor IF2/IF5, N-terminal; IPR003307: W2 domain; IPR016190: Translation initiation factor IF2/IF5, zinc-binding; IPR002735: Translation initiation factor IF2/IF5; IPR016024: Armadillo-type fold; Coil: ; PTHR23001: ; IPR016021: MIF4-like, type 1/2/3	NA
comp31722_c2_seq2.p1	Ec-06_003100.1	Regulator of chromosome condensation	GO:0005515	NA	KOG1426
comp31722_c0_seq1.p2	Ec-06_003110.1	expressed unknown protein	n/a;n/a;n/a	IPR001486: Truncated hemoglobin; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009050: Globin-like; SIGNAL_PEPTIDE: Signal peptide region; PTHR10681: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR012292: Globin/Protoglobin	NA
comp76958_c0_seq1.p1	Ec-06_003130.1	EF-hand domain pair	GO:0005509;GO:0005515	IPR018247: EF-Hand 1, calcium-binding site; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; mobidb-lite: consensus disorder prediction; G3DSA:1.10.238.10: ; G3DSA:4.10.270.10: ; IPR000048: IQ motif, EF-hand binding site; Coil: ; G3DSA:1.20.5.190:	NA
comp30738_c0_seq2.p1	Ec-06_003140.1	Trehalose 6-phosphate synthase, family GT20 / Trehalose 6-phosphate phosphatase	GO:0003824;GO:0005992	SSF53756: ; IPR006379: HAD-superfamily hydrolase, subfamily IIB; IPR001830: Glycosyl transferase, family 20; mobidb-lite: consensus disorder prediction; PTHR10788: ; IPR023214: HAD-like domain; IPR003337: Trehalose-phosphatase; G3DSA:3.40.50.2000:	KOG1050
comp44008_c0_seq1.p1	Ec-06_003150.1	cell surface protein	n/a;n/a;n/a	Coil:	NA
comp26848_c0_seq1.p1	Ec-06_003170.1	Actin-depolymerising factor homology domain	GO:0005622;GO:0003779;GO:0015629;GO:0030042	SSF55753: ; IPR029006: ADF-H/Gelsolin-like domain; IPR002108: Actin-depolymerising factor homology domain; IPR017904: ADF/Cofilin/Destrin	NA
comp33006_c1_seq3.p1	Ec-06_003200.1	NB-ARC and TPR repeat-containig protein	GO:0005515	SSF48452: ; PF13424: Tetratricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; IPR002182: NB-ARC; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PF13374: Tetratricopeptide repeat; IPR002151: Kinesin light chain; PTHR19959: ; Coil: ; IPR019734: Tetratricopeptide repeat	NA
comp29575_c0_seq2.p1	Ec-06_003210.1	RNA-binding domain, S1	GO:0003676;GO:0008270	IPR012340: Nucleic acid-binding, OB-fold; IPR003029: Ribosomal protein S1, RNA-binding domain; IPR022967: RNA-binding domain, S1; IPR001878: Zinc finger, CCHC-type; PTHR15838:	NA
comp30353_c0_seq2.p1	Ec-06_003220.1	Pseudouridine synthase, catalytic domain	GO:0003723;GO:0001522;GO:0009451;GO:0009982	IPR020103: Pseudouridine synthase, catalytic domain; PTHR21568:	NA
comp33879_c0_seq1.p1	Ec-06_003230.1	Domain of unknown function DUF2061, membrane	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR018638: Domain of unknown function DUF2061, membrane; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20352_c0_seq1.p1	Ec-06_003240.3	TatD family	GO:0016888	PTHR10060:SF24: ; IPR032466: Metal-dependent hydrolase; IPR001130: TatD family; G3DSA:3.20.20.140:	NA
comp32698_c0_seq14.p1	Ec-06_003250.1	Sec7 domain protein	GO:0032012;GO:0005086	NA	NA
comp29238_c0_seq1.p1	Ec-06_003270.1	PPPDE putative peptidase domain	n/a;n/a;n/a	PTHR12378: ; IPR008580: PPPDE putative peptidase domain	NA
comp26602_c0_seq2.p1	Ec-06_003290.1	Rossmann-like alpha/beta/alpha sandwich fold	n/a;n/a;n/a	IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; PTHR11807: ; SSF52402: ; IPR011063: tRNA(Ile)-lysidine/2-thiocytidine synthase	NA
comp29887_c1_seq1.p1	Ec-06_003320.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp33072_c0_seq42.p1	Ec-06_003330.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30345_c1_seq2.p1	Ec-06_003340.1	Ubiquitin-related domain	n/a;n/a;n/a	IPR029071: Ubiquitin-related domain	NA
comp30639_c1_seq1.p1	Ec-06_003360.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PTHR17204: ; IPR011990: Tetratricopeptide-like helical domain; IPR003107: HAT (Half-A-TPR) repeat; Coil:	NA
comp26802_c0_seq2.p1	Ec-06_003370.1	Armadillo-like helical	n/a;GO:0005488	PTHR12363: ; IPR001494: Importin-beta, N-terminal domain; IPR013598: Exportin-1/Importin-beta-like; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold	NA
comp26928_c0_seq2.p1	Ec-06_003440.1	Methylmalonate Semialdehyde Dehydrogenase	GO:0016620;GO:0008152;GO:0055114;GO:0004491;GO:0006573;GO:0016491	IPR016161: Aldehyde/histidinol dehydrogenase; IPR015590: Aldehyde dehydrogenase domain; IPR016162: Aldehyde dehydrogenase N-terminal domain; IPR016160: Aldehyde dehydrogenase, cysteine active site; IPR010061: Methylmalonate-semialdehyde dehydrogenase; PTHR11699: ; IPR016163: Aldehyde dehydrogenase, C-terminal	KOG2449
comp20854_c0_seq2.p1	Ec-06_003460.1	BTB/POZ fold	GO:0005515	PTHR24412: ; IPR011333: BTB/POZ fold; IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR020472: G-protein beta WD-40 repeat; IPR013069: BTB/POZ; IPR017986: WD40-repeat-containing domain; IPR011705: BTB/Kelch-associated; IPR015943: WD40/YVTN repeat-like-containing domain; IPR000210: BTB/POZ-like; G3DSA:3.30.710.10:	NA
comp33998_c0_seq1.p1	Ec-06_003470.1	expressed unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25740_c0_seq1.p1	Ec-06_003480.1	Tetratricopeptide repeat-containing domain protein	n/a;GO:0005515	SSF48452: ; IPR013105: Tetratricopeptide TPR2; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain	NA
comp32991_c0_seq2.p1	Ec-06_003490.1	Dolichyl-phosphate beta-glucosyltransferase, family GT2	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029044: Nucleotide-diphospho-sugar transferases; PTHR10859: ; IPR001173: Glycosyltransferase 2-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2977
comp14913_c0_seq1.p1	Ec-06_003500.1	preprotein translocase subunit SecA	GO:0016020;GO:0006605;GO:0005524;GO:0017038;GO:0006886	SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR014018: SecA motor DEAD; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR011116: SecA Wing/Scaffold; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR30612: ; IPR011130: SecA preprotein, cross-linking domain; SignalP-noTM: ; IPR020937: SecA conserved site; IPR011115: SecA DEAD-like, N-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR000185: Protein translocase subunit SecA	NA
comp27010_c0_seq1.p1	Ec-06_003520.2	WD40 repeat	GO:0005515	PTHR19919: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp30312_c0_seq3.p1	Ec-06_003520.3	WD40 repeat	GO:0005515	PTHR35213:	NA
comp24862_c0_seq1.p1	Ec-06_003550.1	Haem peroxidase, plant/fungal/bacterial	GO:0020037;GO:0055114;GO:0006979;GO:0004601	G3DSA:1.10.520.10: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR010255: Haem peroxidase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002207: Plant ascorbate peroxidase; SignalP-noTM: ; G3DSA:1.10.420.10: ; PTHR31356: ; IPR002016: Haem peroxidase, plant/fungal/bacterial; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33093_c0_seq9.p1	Ec-06_003570.1	conserved unknown protein	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19971_c0_seq1.p1	Ec-06_003580.1	CDC50/LEM3 family	GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005045: CDC50/LEM3 family; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26637_c1_seq1.p1	Ec-06_003590.1	Armadillo-type fold	GO:0005488	IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold	NA
comp31282_c0_seq6.p1	Ec-06_003600.1	SAP domain	GO:0003715;GO:0006353	IPR003034: SAP domain; IPR018306: Bacteriophage T5, Orf172 DNA-binding	NA
comp30807_c0_seq4.p1	Ec-06_003610.1	Hid-1	n/a;n/a;n/a	PF12722: High-temperature-induced dauer-formation protein; Coil: ; IPR026705: Hid-1	NA
comp20041_c0_seq1.p1	Ec-06_003630.1	Sucraseferredoxin-like	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR31902: ; SignalP-noTM: ; IPR009737: Sucraseferredoxin-like; IPR030108: Actin patches distal protein 1; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29857_c0_seq1.p1	Ec-06_003640.2	expressed unknown protein	n/a;n/a;n/a	SignalP-noTM:	NA
comp30807_c0_seq4.p2	Ec-06_003660.1	Tyrosine/serine-protein phosphatase IphP-type	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; IPR025163: Tyrosine-protein phosphatase family, C-terminal domain; IPR026893: Tyrosine/serine-protein phosphatase IphP-type; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR029021: Protein-tyrosine phosphatase-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR31126:	NA
comp30639_c0_seq1.p1	Ec-06_003690.1	putative glutamate/ornithine acetyltransferase (ISS)	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR12770:SF20: ; IPR006968: Root UVB sensitive family; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19454_c0_seq1.p1	Ec-06_003700.1	Conserved oligomeric Golgi complex, subunit 4	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013167: Conserved oligomeric Golgi complex, subunit 4; PTHR24016: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28951_c0_seq5.p2	Ec-06_003720.1	conserved unknown protein	n/a;n/a;n/a	G3DSA:2.170.270.10:	NA
comp28951_c0_seq5.p1	Ec-06_003730.1	Rab-GTPase-TBC domain	GO:0005097;GO:0032313	PTHR16110: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000195: Rab-GTPase-TBC domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34966_c0_seq1.p1	Ec-06_003750.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp34240_c0_seq1.p1	Ec-06_003760.1	conserved unknown protein	GO:0016746;GO:0008152;GO:0008415	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002123: Phospholipid/glycerol acyltransferase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF69593: ; PTHR23063: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG4666
comp32933_c0_seq3.p3	Ec-06_003770.1	RNA polymerase II, Rpb4	GO:0003899;GO:0006351	IPR010997: HRDC-like; IPR005574: RNA polymerase II, Rpb4; PTHR21297: ; IPR006590: RNA polymerase II, Rpb4, core	NA
comp32933_c0_seq1.p1	Ec-06_003780.1	Nucleic acid-binding, OB-fold	GO:0005634;GO:0003677;GO:0005524;GO:0006270;GO:0042555;GO:0003678	IPR012340: Nucleic acid-binding, OB-fold; IPR004039: Rubredoxin-type fold; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001208: Mini-chromosome maintenance, DNA-dependent ATPase; IPR018525: Mini-chromosome maintenance, conserved site; PTHR11630: ; G3DSA:3.30.1640.10: ; Coil: ; IPR027925: MCM N-terminal domain; IPR008049: DNA replication licensing factor Mcm6	NA
comp34004_c0_seq1.p1	Ec-06_003790.1	Mitochondrial import receptor, Tom22 homolog	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21292_c0_seq1.p5	Ec-06_003800.1	Cytochrome c	GO:0009055;GO:0020037;GO:0005506;GO:0006118	IPR002327: Cytochrome c, class IA/ IB; IPR009056: Cytochrome c-like domain	NA
comp34312_c0_seq1.p1	Ec-06_003810.1	Aspartyl-tRNA Synthetase	GO:0000166;GO:0004815;GO:0005524;GO:0005737;GO:0006422	IPR004523: Aspartyl-tRNA synthetase, archaeal-type; IPR012340: Nucleic acid-binding, OB-fold; IPR004365: OB-fold nucleic acid binding domain, AA-tRNA synthetase-type; IPR000738: WHEP-TRS; IPR002312: Aspartyl/Asparaginyl-tRNA synthetase, class IIb; IPR006195: Aminoacyl-tRNA synthetase, class II; SSF55681: ; IPR004364: Aminoacyl-tRNA synthetase, class II (D/K/N); IPR018150: Aminoacyl-tRNA synthetase, class II (D/K/N)-like; IPR009068: S15/NS1, RNA-binding; G3DSA:3.30.930.10: ; Coil:	KOG0556
comp31783_c0_seq6.p1	Ec-06_003830.1	Armadillo-type fold	GO:0005488	PF13513: HEAT-like repeat; PTHR23315: ; IPR011989: Armadillo-like helical; IPR000225: Armadillo; IPR016024: Armadillo-type fold; Coil: ; IPR004155: PBS lyase HEAT-like repeat	NA
comp29977_c0_seq1.p2	Ec-06_003840.1	Ubiquitin fusion degradation protein UFD1	GO:0006511	G3DSA:3.10.20.90: ; IPR001012: UBX domain; IPR029071: Ubiquitin-related domain; Coil: ; IPR004854: Ubiquitin fusion degradation protein UFD1	NA
comp31783_c0_seq7.p2	Ec-06_003850.1	AAA+ ATPase domain	GO:0005524	IPR003593: AAA+ ATPase domain; IPR003959: ATPase, AAA-type, core; IPR003960: ATPase, AAA-type, conserved site; G3DSA:1.10.8.60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR23077:	NA
comp29977_c0_seq1.p1	Ec-06_003860.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28217_c0_seq2.p1	Ec-06_003880.1	conserved unknown protein	n/a;n/a;n/a	PTHR13162:	NA
comp20927_c0_seq1.p1	Ec-06_003890.1	CCR4-Not complex component, Not1, C-terminal	GO:0005488	IPR007196: CCR4-Not complex component, Not1, C-terminal; PTHR13162: ; Coil: ; IPR024557: CCR4-Not complex, Not1 subunit, domain of unknown function DUF3819	NA
comp27819_c0_seq1.p1	Ec-06_003920.1	Protein kinase domain	GO:0005524;GO:0006468;GO:0004672	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; PTHR24361: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain	NA
comp32682_c1_seq2.p1	Ec-06_003930.1	Hypoxia induced protein, domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007667: Hypoxia induced protein, domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33102_c3_seq1.p1	Ec-06_003950.1	N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein PigA, family GT4	GO:0009058	IPR013234: PIGA, GPI anchor biosynthesis; SSF53756: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001296: Glycosyl transferase, family 1; PTHR12526: ; G3DSA:3.40.50.2000: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25748_c0_seq2.p1	Ec-06_003970.1	Cyclin-dependent kinase, regulatory subunit	GO:0016538;GO:0007049	IPR000789: Cyclin-dependent kinase, regulatory subunit; PTHR23415:	NA
comp30859_c0_seq1.p1	Ec-06_004000.1	PAS domain	GO:0004871;GO:0007165	IPR013767: PAS fold; SSF57959: ; IPR000014: PAS domain; G3DSA:1.20.5.170: ; Coil: ; G3DSA:3.30.450.20:	NA
comp32848_c1_seq3.p1	Ec-06_004010.2	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp24416_c0_seq3.p2	Ec-06_004060.2	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp32203_c1_seq3.p1	Ec-06_004070.1	Domain of unknown function DUF1995	GO:0016491;GO:0020037;GO:0051536;GO:0006118	IPR018962: Domain of unknown function DUF1995	NA
comp27210_c0_seq1.p1	Ec-06_004080.1	SET domain and Rubisco LSMT substrate-binding domain protein	n/a;n/a;n/a	NA	NA
comp25953_c0_seq1.p1	Ec-06_004090.1	F-box domain	GO:0005515	IPR001810: F-box domain; G3DSA:1.20.1280.50:	NA
comp31534_c0_seq2.p1	Ec-06_004120.1	carbonic anhydrase	GO:0008270;GO:0004089	IPR015892: Carbonic anhydrase, prokaryotic-like, conserved site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001765: Carbonic anhydrase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1578
comp24836_c0_seq2.p1	Ec-06_004130.1	Ubiquitin-like	GO:0005515	IPR000449: Ubiquitin-associated domain/translation elongation factor EF-Ts, N-terminal; G3DSA:3.10.20.90: ; IPR015940: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote; G3DSA:1.10.8.10: ; IPR029071: Ubiquitin-related domain; PTHR12948: ; IPR000626: Ubiquitin-like; Coil: ; IPR009060: UBA-like	NA
comp25114_c0_seq1.p2	Ec-06_004140.1	Interferon-related developmental regulator, N-terminal	GO:0005488	PTHR12354: ; IPR007701: Interferon-related developmental regulator, N-terminal; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold	NA
comp32971_c0_seq1.p1	Ec-06_004160.1	hypothetical protein	n/a;n/a;n/a	SignalP-TM:	NA
comp21044_c0_seq1.p1	Ec-06_004170.1	uroporphyrinogen-III C-methyltransferase, putative chloroplast precursor	GO:0008152;GO:0008168;GO:0055114;GO:0006779	IPR014777: Tetrapyrrole methylase, subdomain 1; SIGNAL_PEPTIDE: Signal peptide region; IPR014776: Tetrapyrrole methylase, subdomain 2; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR012066: Uroporphyrin-III C-methyltransferase, yeast; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000878: Tetrapyrrole methylase; PTHR21091: ; SignalP-noTM: ; IPR006366: Uroporphyrin-III C-methyltransferase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33705_c0_seq1.p1	Ec-06_004180.1	Winged helix-turn-helix DNA-binding domain	n/a;GO:0005524;GO:0006468;GO:0004674	IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; IPR018934: RIO domain; G3DSA:3.30.200.20: ; IPR000687: RIO kinase; IPR011009: Protein kinase-like domain; IPR030484: Serine/threonine-protein kinase Rio2; PTHR10593: ; G3DSA:1.10.510.10: ; IPR015285: RIO2 kinase winged helix domain, N-terminal	NA
comp49645_c0_seq1.p2	Ec-06_004190.1	Histidine kinase-like ATPase, C-terminal domain	GO:0005524	IPR011006: CheY-like superfamily; PTHR24423: ; IPR000014: PAS domain; IPR001789: Signal transduction response regulator, receiver domain; IPR003594: Histidine kinase-like ATPase, C-terminal domain; G3DSA:3.40.50.2300: ; G3DSA:3.30.450.20:	NA
comp26674_c0_seq2.p1	Ec-06_004200.1	fructose-1,6 bisphosphatase	GO:0005975;GO:0042132;GO:0042578	G3DSA:3.30.540.10: ; SSF56655: ; IPR000146: Fructose-1,6-bisphosphatase class 1/Sedoheputulose-1,7-bisphosphatase; G3DSA:3.40.190.80: ; Coil: ; IPR028343: Fructose-1,6-bisphosphatase	NA
comp33614_c0_seq1.p1	Ec-06_004230.1	Protease-associated domain, PA	GO:0004571;GO:0005509;GO:0016020	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SSF52025: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; G3DSA:3.50.30.30: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003137: Protease-associated domain, PA; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22765: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20882_c0_seq2.p1	Ec-06_004240.1	Lipase domain protein, partial	GO:0003824;GO:0004806;GO:0006629	IPR002921: Fungal lipase-like domain; IPR029058: Alpha/Beta hydrolase fold; PTHR21493:	no relat
comp32544_c0_seq24.p1	Ec-06_004260.1	Pre-mRNA cleavage complex II Clp1	n/a;n/a;n/a	IPR010655: Pre-mRNA cleavage complex II Clp1; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR12755: ; IPR028606: Polyribonucleotide 5-hydroxyl-kinase Clp1; IPR029007: MobB-type P-loop domain	NA
comp29964_c0_seq1.p1	Ec-06_004280.1	Pleckstrin homology domain	n/a;n/a;n/a	SSF50729: ; IPR001841: Zinc finger, RING-type; SSF82185: ; IPR001849: Pleckstrin homology domain; G3DSA:2.20.110.10: ; IPR011993: Pleckstrin homology-like domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR23084: ; PF13920: Zinc finger, C3HC4 type (RING finger); Coil: ; IPR003409: MORN motif	NA
comp32709_c0_seq1.p1	Ec-06_004290.1	Phox homologous domain	GO:0035091	Coil: ; IPR001683: Phox homologous domain	NA
comp31684_c0_seq27.p2	Ec-06_004310.1	ATPase, V1/A1 complex, subunit E	GO:0033178;GO:0015991;GO:0046961	PTHR11583: ; SSF160527: ; IPR002842: ATPase, V1/A1 complex, subunit E	NA
comp26996_c0_seq2.p1	Ec-06_004320.1	Histone deacetylase domain and ankyrin repeat protein	n/a;n/a;n/a	NA	NA
comp29835_c0_seq3.p1	Ec-06_004330.2	conserved unknown protein	n/a;n/a;n/a	PTHR15000:SF1: ; PTHR15000: ; Coil:	NA
comp31292_c0_seq2.p1	Ec-06_004360.4	EF-hand domain pair	GO:0004221;GO:0006511	IPR018247: EF-Hand 1, calcium-binding site; SSF54001: ; IPR006615: Peptidase C19, ubiquitin-specific peptidase, DUSP domain; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase; PTHR24006: ; IPR018200: Ubiquitin specific protease, conserved site; IPR028135: Ubiquitin-like domain, USP-type; IPR028889: Ubiquitin specific protease domain; Coil:	NA
comp61161_c0_seq1.p1	Ec-06_004370.1	flagellar associated protein	n/a;GO:0005515	IPR003959: ATPase, AAA-type, core; IPR003593: AAA+ ATPase domain; PTHR14690: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR000048: IQ motif, EF-hand binding site	NA
comp16081_c0_seq2.p1	Ec-06_004400.1	Integrin alpha	NA	IPR000413: Integrin alpha chain; PTHR23221: ; IPR013519: Integrin alpha beta-propellor; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SSF69318: ; G3DSA:2.130.10.130: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013517: FG-GAP repeat; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31229_c0_seq1.p1	Ec-06_004410.1	transducin family protein	NA	PTHR22874: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp29149_c0_seq2.p1	Ec-06_004430.1	expressed unknown protein	GO:0006118;GO:0009055;GO:0051536	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp27124_c0_seq2.p2	Ec-06_004440.1	50S ribosomal protein L3	NA	IPR000597: Ribosomal protein L3; G3DSA:4.10.960.10: ; IPR019927: Ribosomal protein L3, bacterial/organelle-type; IPR019926: Ribosomal protein L3, conserved site; G3DSA:2.40.30.10: ; IPR009000: Translation protein, beta-barrel domain; SignalP-TM:	NA
comp27124_c0_seq2.p1	Ec-06_004470.1	SMAD/FHA domain	GO:0005515	IPR008984: SMAD/FHA domain; Coil: ; IPR000253: Forkhead-associated (FHA) domain	NA
comp32983_c1_seq56.p2	Ec-06_004480.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp32983_c1_seq56.p1	Ec-06_004490.1	Pseudouridine synthase, RsuA/RluB/C/D/E/F	GO:0003723;GO:0001522;GO:0009451;GO:0009982	IPR020103: Pseudouridine synthase, catalytic domain; IPR006145: Pseudouridine synthase, RsuA/RluB/C/D/E/F; IPR006224: Pseudouridine synthase, RluC/RluD, conserved site; PTHR10436:	NA
comp12383_c0_seq1.p1	Ec-06_004510.1	GDP-mannose 3,5-epimerase	GO:0008152;GO:0016853;GO:0047918;GO:0003824;GO:0005488	IPR001509: NAD-dependent epimerase/dehydratase, N-terminal domain; SSF51735: ; IPR016040: NAD(P)-binding domain; G3DSA:3.90.25.10: ; PTHR10366:	NA
comp32168_c0_seq6.p1	Ec-06_004520.1	protein disulfide isomerase	GO:0005783;GO:0045454	IPR005788: Disulphide isomerase; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011679: Endoplasmic reticulum, protein ERp29, C-terminal; IPR013766: Thioredoxin domain; IPR017937: Thioredoxin, conserved site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PR00421: Thioredoxin family signature; PTHR18929: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25189_c0_seq3.p1	Ec-06_004530.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp18454_c0_seq1.p1	Ec-06_004540.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; Coil: ; IPR002110: Ankyrin repeat; PTHR24193:	NA
comp70297_c0_seq1.p1	Ec-06_004570.1	Ankyrin repeat	GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; IPR002110: Ankyrin repeat	NA
comp33143_c2_seq1.p1	Ec-06_004580.1	PLC-like phosphodiesterase, TIM beta/alpha-barrel domain	GO:0008081;GO:0006629	IPR000909: Phospholipase C, phosphatidylinositol-specific , X domain; PTHR13593: ; IPR017946: PLC-like phosphodiesterase, TIM beta/alpha-barrel domain	NA
comp34874_c0_seq1.p1	Ec-06_004590.1	tRNA (guanine-N1-)-methyltransferase, N-terminal	GO:0006364;GO:0008168;n/a	PTHR30027: ; IPR029028: Alpha/beta knot methyltransferases; IPR006700: Ribosomal RNA small subunit methyltransferase E; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029026: tRNA (guanine-N1-)-methyltransferase, N-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp86314_c0_seq1.p1	Ec-06_004610.2	Insulin-like growth factor binding protein, N-terminal	GO:0005576;GO:0006030;GO:0008061	IPR001368: TNFR/NGFR cysteine-rich region; PTHR22727:SF23: ; IPR009030: Growth factor receptor cysteine-rich domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:2.10.50.10: ; IPR002557: Chitin binding domain; Coil: ; PTHR22727: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30907_c0_seq8.p2	Ec-06_004620.1	4'-phosphopantetheinyl transferase superfamily	GO:0000287;GO:0009059;GO:0008897	SIGNAL_PEPTIDE: Signal peptide region; IPR008278: 4'-phosphopantetheinyl transferase superfamily; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; PTHR12215: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30733_c0_seq3.p1	Ec-06_004630.1	Prolyl 4-hydroxylase, alpha subunit	GO:0005506;GO:0016705;GO:0031418;GO:0055114	IPR006620: Prolyl 4-hydroxylase, alpha subunit; G3DSA:2.170.270.10: ; PTHR10730: ; IPR011990: Tetratricopeptide-like helical domain; IPR005123: Oxoglutarate/iron-dependent dioxygenase; PTHR10730:SF31: ; SSF82199:	NA
comp20889_c0_seq2.p1	Ec-06_004650.1	Serine/threonine-protein kinase CTR1	GO:0016772	PTHR23257: ; IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR011009: Protein kinase-like domain	NA
comp13852_c0_seq1.p1	Ec-06_004660.1	60S ribosomal protein L5	GO:0005840;GO:0005622;GO:0006412;GO:0003735	G3DSA:3.30.420.100: ; IPR005485: Ribosomal protein L5 eukaryotic/L18 archaeal; IPR005484: Ribosomal protein L18/L5; SSF53137: ; IPR025607: Ribosomal protein L5 eukaryotic/L18 archaeal, C-terminal	NA
comp30907_c0_seq8.p1	Ec-06_004670.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp27830_c0_seq1.p1	Ec-06_004700.3	hypothetical protein	n/a;n/a;n/a	Coil: ; IPR003169: GYF domain	NA
comp27515_c0_seq2.p2	Ec-06_004720.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	GO:0016020;GO:0016192;GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000727: Target SNARE coiled-coil domain; G3DSA:1.20.58.70: ; IPR010989: t-SNARE; PTHR19957: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF58038: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0812
comp27515_c0_seq2.p1	Ec-06_004750.1	UbiB domain	n/a;n/a;n/a	IPR004147: UbiB domain; PTHR10566:	NA
comp30751_c0_seq2.p1	Ec-06_004760.1	BRCT domain-containing protein	GO:0005622	IPR031099: BRCA1-associated; PTHR13763: ; IPR001357: BRCT domain	NA
comp30751_c0_seq3.p9	Ec-06_004800.1	Protein of unknown function DUF1395	n/a;n/a;n/a	IPR009829: Protein of unknown function DUF1395	NA
comp30751_c0_seq4.p4	Ec-06_004810.1	Nucleic acid-binding, OB-fold	GO:0003676	IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; IPR012340: Nucleic acid-binding, OB-fold; IPR004365: OB-fold nucleic acid binding domain, AA-tRNA synthetase-type; IPR014892: Replication protein A, C-terminal; PTHR13989:	NA
comp25883_c0_seq1.p1	Ec-06_004820.1	Aldolase-type TIM barrel	GO:0050660;GO:0003824;GO:0055114;GO:0008033;GO:0017150	IPR013785: Aldolase-type TIM barrel; IPR001269: tRNA-dihydrouridine synthase; SSF51395: ; IPR018517: tRNA-dihydrouridine synthase, conserved site	NA
comp24133_c0_seq2.p1	Ec-06_004840.1	conserved unknown protein	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31684_c0_seq24.p1	Ec-06_004850.1	NAD(P)-binding domain	n/a;GO:0008152;GO:0016491	SSF51735: ; IPR016040: NAD(P)-binding domain; PTHR24320: ; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR	NA
comp11829_c0_seq2.p1	Ec-06_004860.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR23083:	NA
comp32740_c0_seq6.p1	Ec-06_004960.2	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30362_c0_seq2.p1	Ec-06_005140.1	Histidine kinase-like protein	GO:0016310;GO:0016772	IPR001610: PAC motif; IPR009082: Signal transduction histidine kinase, homodimeric domain; PTHR24423: ; IPR005467: Signal transduction histidine kinase, core; IPR000014: PAS domain; G3DSA:3.30.450.20: ; IPR003594: Histidine kinase-like ATPase, C-terminal domain; IPR011006: CheY-like superfamily; IPR013655: PAS fold-3; IPR001789: Signal transduction response regulator, receiver domain; IPR003661: Signal transduction histidine kinase EnvZ-like, dimerisation/phosphoacceptor domain; G3DSA:3.40.50.2300: ; IPR004358: Signal transduction histidine kinase-related protein, C-terminal	NA
comp19508_c0_seq2.p1	Ec-06_006660.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp26249_c0_seq1.p1	Ec-06_006800.1	Glycosyltransferase, family GT49	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13896: Glycosyl-transferase for dystroglycan; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR029044: Nucleotide-diphospho-sugar transferases; PTHR12270: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27989_c0_seq1.p1	Ec-06_006820.1	TSO1; transcription factor	n/a;n/a;n/a	IPR005172: CRC domain; Coil: ; IPR028307: Lin-54 family; SignalP-TM:	NA
comp31814_c0_seq4.p2	Ec-06_006830.1	glutathione s-transferase	GO:0003824	IPR001310: Histidine triad (HIT) protein; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR004045: Glutathione S-transferase, N-terminal; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; PF13410: Glutathione S-transferase, C-terminal domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011146: HIT-like domain; IPR010987: Glutathione S-transferase, C-terminal-like; IPR019808: Histidine triad, conserved site; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26975_c0_seq4.p1	Ec-06_006840.1	TatD family	GO:0016888	IPR018228: Deoxyribonuclease, TatD-related, conserved site; IPR001130: TatD family; SSF51556: ; G3DSA:3.20.20.140:	NA
comp29900_c1_seq2.p1	Ec-06_006850.1	Ribosomal protein L10/acidic P0	GO:0005622;GO:0042254	IPR030670: 60S acidic ribosomal protein P0; SSF160369: ; PF00428: 60s Acidic ribosomal protein; PTHR21141:SF3: ; IPR001790: Ribosomal protein L10P; PTHR21141:	NA
comp32144_c0_seq5.p1	Ec-06_006860.1	Pyruvate kinase	GO:0000287;GO:0004743;GO:0006096;GO:0030955	IPR015806: Pyruvate kinase, beta-barrel insert domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR015795: Pyruvate kinase, C-terminal; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR018209: Pyruvate kinase, active site; IPR015794: Pyruvate kinase, alpha/beta; IPR015813: Pyruvate/Phosphoenolpyruvate kinase-like domain; IPR011037: Pyruvate kinase-like, insert domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001697: Pyruvate kinase; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR015793: Pyruvate kinase, barrel	KOG2323
comp28634_c0_seq3.p1	Ec-06_006870.1	Thiamine monophosphate synthase	GO:0003824	IPR022998: Thiamin phosphate synthase superfamily; IPR004399: Hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase; IPR003733: Thiamine phosphate synthase; IPR013785: Aldolase-type TIM barrel; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR20858: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR029056: Ribokinase-like; IPR013749: Pyridoxamine kinase/Phosphomethylpyrimidine kinase	NA
comp19809_c0_seq1.p1	Ec-06_006890.1	Iron sulphur-containing domain, CDGSH-type, subfamily	GO:0043231;GO:0051537	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR13680: ; IPR018967: Iron sulphur-containing domain, CDGSH-type; IPR006622: Iron sulphur-containing domain, CDGSH-type, subfamily	NA
comp16712_c0_seq2.p1	Ec-06_006900.1	Methyl transferase	n/a;n/a;n/a	PF12847: Methyltransferase domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase	NA
comp32610_c0_seq9.p1	Ec-06_006920.2	vacuolar protein sorting-associated protein, putative	GO:0004252;GO:0005506;GO:0006118;GO:0006508;GO:0009055;GO:0020037	IPR026847: Vacuolar protein sorting-associated protein 13; IPR031642: VPS13, repeated coiled region; IPR031646: Vacuolar protein sorting-associated protein 13, second N-terminal domain; Coil: ; IPR026854: Vacuolar protein sorting-associated protein 13, N-terminal domain	NA
comp30027_c0_seq1.p1	Ec-06_006940.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp31221_c0_seq2.p1	Ec-06_006950.4	Major facilitator superfamily domain	n/a;n/a;n/a	PTHR23504:SF15: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR23504: ; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28261_c0_seq3.p1	Ec-06_006960.1	Equilibrative nucleoside transporter	GO:0006810;GO:0005337;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002259: Equilibrative nucleoside transporter; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32700_c0_seq14.p1	Ec-06_006980.1	conserved unknown protein	GO:0016021;GO:0055085;n/a	PTHR23504:SF15: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR23504: ; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31726_c0_seq3.p3	Ec-06_007000.1	conserved unknown protein	n/a;n/a;n/a	PTHR31598: ; Coil: ; IPR000048: IQ motif, EF-hand binding site	NA
comp30441_c0_seq5.p3	Ec-06_007010.1	Ankyrin repeat-containing domain	n/a;GO:0005515	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR24181: ; SignalP-noTM: ; IPR020683: Ankyrin repeat-containing domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp28586_c0_seq1.p1	Ec-06_007020.1	HSP20-like chaperone	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR008978: HSP20-like chaperone; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002068: Alpha crystallin/Hsp20 domain; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp7257_c0_seq1.p1	Ec-06_007030.1	conserved unknown protein	n/a;GO:0005515	Coil: ; IPR000048: IQ motif, EF-hand binding site	NA
comp29403_c0_seq5.p2	Ec-06_007040.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34761_c0_seq1.p1	Ec-06_007080.1	conserved unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12809_c0_seq1.p2	Ec-06_007090.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp24289_c0_seq2.p1	Ec-06_007100.1	LETM1-like	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR14009: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; IPR011685: LETM1-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32938_c0_seq1.p1	Ec-06_007120.1	Ribokinase-like	n/a;n/a;n/a	IPR000631: ATP-dependent (S)-NAD(P)H-hydrate dehydratase; PTHR12592: ; IPR029056: Ribokinase-like	NA
comp19350_c0_seq1.p1	Ec-06_007160.1	Protein of unknown function DUF583	n/a;n/a;n/a	PTHR35024: ; PTHR35024:SF2: ; IPR007607: Protein of unknown function DUF583	NA
comp31754_c0_seq11.p1	Ec-06_007180.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp78800_c0_seq1.p1	Ec-06_007190.1	Armadillo-like helical	GO:0005488	IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold	NA
comp29982_c0_seq2.p1	Ec-06_007220.2	hypothetical protein	n/a;n/a;n/a	PTHR31477:SF1: ; PTHR31477: ; IPR029157: Centrosomal CEP44 domain	NA
comp12093_c0_seq1.p1	Ec-06_007250.1	Protein of unknown function DUF155	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003734: Protein of unknown function DUF155; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11860_c0_seq1.p1	Ec-06_007360.1	Major Facilitator Superfamily (MFS) protein domains	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020846: Major facilitator superfamily domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR23504: ; IPR011701: Major facilitator superfamily; G3DSA:1.20.1250.20: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31653_c0_seq4.p2	Ec-06_007370.1	conserved unknown protein	NA	IPR028978: Chorismate pyruvate-lyase/UbiC transcription regulator-associated domain	NA
comp31653_c0_seq4.p1	Ec-06_007380.1	Armadillo-type fold	GO:0005488	IPR011989: Armadillo-like helical; IPR019156: Ataxin-10 domain; IPR016024: Armadillo-type fold; PTHR13255:	NA
comp31271_c0_seq2.p2	Ec-06_007390.1	WD40-repeat-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp33800_c0_seq1.p1	Ec-06_007390.2	WD40-repeat-containing domain	GO:0005515	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31271_c0_seq2.p1	Ec-06_007400.1	WW domain	GO:0005515	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001202: WW domain; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:2.20.70.10:	NA
comp27712_c0_seq4.p1	Ec-06_007410.1	Rad4 beta-hairpin domain 2	GO:0003677;GO:0005634;GO:0006289;GO:0003684	IPR002931: Transglutaminase-like; IPR018328: Rad4 beta-hairpin domain 3; IPR018326: Rad4 beta-hairpin domain 1; SSF54001: ; IPR018325: Rad4/PNGase transglutaminase-like fold; IPR018327: Rad4 beta-hairpin domain 2; IPR004583: DNA repair protein Rad4	NA
comp29966_c0_seq3.p1	Ec-06_007450.1	C2 domain	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000008: C2 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp17766_c0_seq1.p1	Ec-06_007460.1	triose or hexose phosphate / phosphate translocator	n/a;n/a;n/a	IPR004853: Triose-phosphate transporter domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR11132: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF103481: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1441
comp31851_c2_seq1.p1	Ec-06_007470.1	NB-ARC	GO:0043531	IPR002182: NB-ARC; IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp31703_c0_seq2.p1	Ec-06_007480.2	Protein phosphatase 2C (PP2C)-like domain	GO:0003824	IPR000222: PPM-type phosphatase, divalent cation binding; IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C family; IPR029057: Phosphoribosyltransferase-like	NA
comp32614_c0_seq16.p1	Ec-06_007490.1	Threonine ammonia-lyase	GO:0006520;GO:0030170	G3DSA:3.40.1020.10: ; IPR005787: Threonine dehydratase, biosynthetic; SSF55021: ; IPR000634: Serine/threonine dehydratase, pyridoxal-phosphate-binding site; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001721: ACT-like domain; IPR001926: Tryptophan synthase beta subunit-like PLP-dependent enzyme; PTHR10314: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:3.40.50.1100:	KOG1250
comp12533_c0_seq1.p1	Ec-06_007510.1	Peptide methionine sulfoxide reductase	GO:0016020;GO:0055114;GO:0009765;GO:0016671;GO:0008113;GO:0019538	IPR028427: Peptide methionine sulfoxide reductase; IPR002569: Peptide methionine sulphoxide reductase MsrA	NA
comp24861_c0_seq1.p1	Ec-06_007520.1	Oxa1 or Cox18/Oxa2 homolog, mitochondrial integral inner membrane protein	GO:0016021;GO:0051205	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR028055: Membrane insertase YidC/Oxa1, C-terminal; IPR001708: Membrane insertase OXA1/ALB3/YidC; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	KOG1239
comp30571_c0_seq4.p1	Ec-06_007530.1	RNA recognition motif domain	GO:0003676;GO:0000166	PTHR24012: ; SSF54928: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp30938_c0_seq2.p1	Ec-06_007540.1	WD40-repeat-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; PTHR19862: ; IPR020472: G-protein beta WD-40 repeat	NA

comp32090_c1_seq28.p1	Ec-06_008540.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10360: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013083: Zinc finger, RING/FYVE/PHD-type; PF13920: Zinc finger, C3HC4 type (RING finger); Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32559_c1_seq16.p1	Ec-06_008550.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029058: Alpha/Beta hydrolase fold; PTHR42044:SF1: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR42044:	NA
comp35131_c0_seq1.p1	Ec-06_008570.1	PDZ-binding protein, CRIPT	n/a;n/a;n/a	IPR019367: PDZ-binding protein, CRIPT; PTHR11800:	NA
comp28788_c0_seq2.p1	Ec-06_008580.1	Creatinase/Aminopeptidase P, N-terminal	n/a;GO:0016787	IPR029149: Creatinase/Aminopeptidase P/Spt16, N-terminal; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000587: Creatinase, N-terminal; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR000994: Peptidase M24, structural domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10804: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR028980: Creatinase/Aminopeptidase P, N-terminal	NA
comp29248_c0_seq22.p2	Ec-06_008640.1	Protein kinase-like domain	GO:0006468;GO:0004672;GO:0016772	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; PTHR24362: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain	NA
comp24509_c0_seq1.p1	Ec-06_008650.1	Phosphoribosyltransferase-like	GO:0000287;GO:0004749;GO:0009165;GO:0016740	IPR005946: Ribose-phosphate diphosphokinase; PTHR10210: ; IPR029099: Ribose-phosphate pyrophosphokinase, N-terminal domain; IPR029057: Phosphoribosyltransferase-like	NA
comp29384_c0_seq3.p2	Ec-06_008660.1	WW domain, G-patch, C2H2 zinc finger	GO:0003676	IPR000467: G-patch domain; IPR007087: Zinc finger, C2H2; PTHR17614: ; G3DSA:2.20.70.10:	NA
comp69958_c0_seq1.p1	Ec-06_008670.1	Alpha/Beta hydrolase fold	GO:0031227;GO:0016788;GO:0006505;GO:0006886	IPR029058: Alpha/Beta hydrolase fold; IPR012908: GPI inositol-deacylase PGAP1-like	NA
comp32623_c0_seq5.p1	Ec-06_008700.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25187_c0_seq1.p1	Ec-06_008730.1	Leucyl-tRNA Synthetase (C-terminal region) Leucyl-tRNA Synthetase (Central region) Leucyl-tRNA Synth	GO:0004823;GO:0005524;GO:0006429;GO:0005737;GO:0006418;GO:0000166;GO:0004812	IPR001412: Aminoacyl-tRNA synthetase, class I, conserved site; PTHR11946: ; IPR009080: Aminoacyl-tRNA synthetase, class 1a, anticodon-binding; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; SSF52374: ; IPR013155: Methionyl/Valyl/Leucyl/Isoleucyl-tRNA synthetase, anticodon-binding; IPR009008: Valyl/Leucyl/Isoleucyl-tRNA synthetase, editing domain; IPR004493: Leucyl-tRNA synthetase, class Ia, archaeal/eukaryotic cytosolic; IPR002300: Aminoacyl-tRNA synthetase, class Ia; Coil:	KOG0437
comp28401_c0_seq3.p1	Ec-06_008740.1	Isoleucyl-tRNA Synthetase	GO:0005524;GO:0005737;GO:0004822;GO:0006428;GO:0006418;GO:0000166;GO:0006412;GO:0004812	IPR001412: Aminoacyl-tRNA synthetase, class I, conserved site; IPR023586: Isoleucine-tRNA ligase, type 2; PTHR11946: ; IPR002301: Isoleucine-tRNA ligase; IPR009080: Aminoacyl-tRNA synthetase, class 1a, anticodon-binding; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; SSF52374: ; IPR009008: Valyl/Leucyl/Isoleucyl-tRNA synthetase, editing domain; IPR013155: Methionyl/Valyl/Leucyl/Isoleucyl-tRNA synthetase, anticodon-binding; IPR002300: Aminoacyl-tRNA synthetase, class Ia	KOG0434
comp31811_c0_seq8.p1	Ec-06_008790.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp111013_c0_seq1.p1	Ec-06_008800.1	Tubulin-tyrosine ligase/Tubulin polyglutamylase	GO:0018095;GO:0006464	SSF56059: ; IPR004344: Tubulin-tyrosine ligase/Tubulin polyglutamylase; Coil: ; PTHR12241: ; IPR027748: Tubulin polyglutamylase TTLL-4	NA
comp32783_c6_seq6.p1	Ec-06_008810.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp28807_c0_seq1.p1	Ec-06_008820.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR24193: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020683: Ankyrin repeat-containing domain; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp30049_c0_seq2.p1	Ec-06_008830.2	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PTHR24361:SF408: ; G3DSA:1.10.510.10: ; PTHR24361: ; IPR011009: Protein kinase-like domain	NA
comp22175_c0_seq1.p1	Ec-06_008850.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25821_c1_seq1.p1	Ec-06_008860.1	Carbohydrate kinase, FGGY, N-terminal	GO:0008152;GO:0016773;GO:0003824;GO:0005975	PTHR10196: ; IPR013785: Aldolase-type TIM barrel; IPR000056: Ribulose-phosphate 3-epimerase-like; G3DSA:3.30.420.40: ; IPR018484: Carbohydrate kinase, FGGY, N-terminal; IPR018485: Carbohydrate kinase, FGGY, C-terminal; IPR011060: Ribulose-phosphate binding barrel; SSF53067:	NA
comp27637_c0_seq1.p1	Ec-06_008880.1	Pentatricopeptide repeat	GO:0006508;GO:0005515;GO:0004197	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002885: Pentatricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; IPR001478: PDZ domain; PTHR24015: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29010_c0_seq3.p1	Ec-06_008910.1	NAD(P)-binding domain	GO:0003995;GO:0006118;GO:0055114	PTHR10953: ; IPR009036: Molybdenum cofactor biosynthesis, MoeB; IPR016040: NAD(P)-binding domain	NA
comp33666_c0_seq1.p1	Ec-06_008920.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29878_c0_seq1.p1	Ec-06_008930.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; PTHR24345:	NA
comp11975_c0_seq1.p1	Ec-06_008940.1	Peptidase M20	GO:0008152;GO:0016787;GO:0006508	PTHR11014: ; IPR002933: Peptidase M20; IPR001160: Peptidase M20C, Xaa-His dipeptidase; SSF53187: ; G3DSA:3.40.630.10:	NA
comp27527_c0_seq3.p1	Ec-06_008950.3	Ankyrin repeat	GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; IPR002110: Ankyrin repeat	NA
comp31258_c0_seq8.p1	Ec-06_008960.1	DDT domain	n/a;n/a;n/a	IPR018501: DDT domain superfamily; IPR004022: DDT domain; Coil: ; IPR028935: WHIM3 domain; IPR028941: WHIM2 domain	NA
comp32736_c0_seq35.p1	Ec-06_009000.1	Dihydrolipoamide branched chain transacylase	GO:0008152;GO:0016746	PTHR23151: ; IPR004167: E3-binding domain; IPR011053: Single hybrid motif; SIGNAL_PEPTIDE: Signal peptide region; IPR000089: Biotin/lipoyl attachment; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR015761: Lipoamide Acyltransferase; SSF52777: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003016: 2-oxo acid dehydrogenase, lipoyl-binding site; G3DSA:2.40.50.100: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001078: 2-oxoacid dehydrogenase acyltransferase, catalytic domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023213: Chloramphenicol acetyltransferase-like domain	KOG0558
comp20451_c0_seq1.p2	Ec-06_009010.1	Branched chain alpha-keto acid dehydrogenase E1 beta subunit	NA	PTHR11624: ; IPR005476: Transketolase, C-terminal; IPR009014: Transketolase, C-terminal/Pyruvate-ferredoxin oxidoreductase, domain II; IPR005475: Transketolase-like, pyrimidine-binding domain; IPR029061: Thiamin diphosphate-binding fold; SignalP-TM:	KOG0525
comp24458_c0_seq1.p1	Ec-06_009020.1	Amidase	GO:0016884	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PIRSF001221: ; IPR023631: Amidase signature domain; IPR020556: Amidase, conserved site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000120: Amidase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28150_c1_seq2.p1	Ec-06_009100.1	diaminopimelate epimerase	GO:0008837;GO:0005737;GO:0009089	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001653: Diaminopimelate epimerase, DapF; IPR018510: Diaminopimelate epimerase, active site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SSF54506: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:3.10.310.10:	NA
comp24998_c0_seq1.p1	Ec-06_009110.1	60S ribosomal protein L35a	GO:0005840;GO:0006412;GO:0005622;GO:0003735	IPR001780: Ribosomal protein L35A; IPR018266: Ribosomal protein L35Ae, conserved site; IPR009000: Translation protein, beta-barrel domain	NA
comp45649_c0_seq1.p1	Ec-06_009130.2	Basic-leucine zipper and PAS domains	GO:0007165;GO:0004871	NA	NA
comp31958_c1_seq3.p1	Ec-06_009140.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30153_c0_seq1.p1	Ec-06_009150.3	EXS, C-terminal	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004342: EXS, C-terminal; PTHR10783:SF55: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10783:	NA
comp27266_c0_seq1.p1	Ec-06_009160.1	Protein kinase domain	GO:0005524;GO:0006468;GO:0004672	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; PTHR24343:	NA
comp28939_c0_seq2.p1	Ec-06_009180.1	Rubisco LSMT, substrate-binding domain	n/a;n/a;n/a	G3DSA:3.90.1410.10: ; SIGNAL_PEPTIDE: Signal peptide region; PTHR13271: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF82199: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015353: Rubisco LSMT, substrate-binding domain; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31876_c0_seq11.p1	Ec-06_009190.1	Hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30117_c0_seq3.p1	Ec-06_009270.1	Polycystin cation channel, PKD1/PKD2	n/a;GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR013122: Polycystin cation channel, PKD1/PKD2; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10877: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000048: IQ motif, EF-hand binding site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29934_c1_seq2.p1	Ec-06_009280.1	Ankyrin repeat Transient receptor potential channel	GO:0005216;GO:0006811;GO:0016020;GO:0055085	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10582: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005821: Ion transport domain; IPR020683: Ankyrin repeat-containing domain; PTHR10582:SF2: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002110: Ankyrin repeat	KOG3676
comp26671_c0_seq3.p1	Ec-06_009300.1	peptidase S8 and S53, subtilisin, kexin, sedolisin	NA	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000209: Peptidase S8/S53 domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR015500: Peptidase S8, subtilisin-related; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.10.8.10: ; IPR009060: UBA-like; IPR022398: Peptidase S8, subtilisin, His-active site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:2.60.120.380: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR015940: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote; SignalP-noTM: ; IPR023828: Peptidase S8, subtilisin, Ser-active site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24454_c0_seq1.p1	Ec-06_009310.1	Putative subunit of the Anaphase Promoting Complex	n/a;n/a;n/a	IPR026000: Anaphase-promoting complex subunit 5; PTHR12830: ; IPR011990: Tetratricopeptide-like helical domain; Coil:	KOG4322
comp22183_c0_seq2.p1	Ec-06_009340.1	HSP20-like chaperone	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR008978: HSP20-like chaperone; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002068: Alpha crystallin/Hsp20 domain; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30855_c0_seq3.p1	Ec-06_009360.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp28933_c0_seq2.p1	Ec-06_009430.1	Major facilitator superfamily domain	n/a;GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11360: ; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011701: Major facilitator superfamily; G3DSA:1.20.1250.20: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33215_c1_seq1.p1	Ec-06_009440.1	Zinc finger, RING-type	GO:0005515;GO:0008270	IPR001841: Zinc finger, RING-type; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12124_c0_seq1.p1	Ec-06_009490.1	DNA primase, small subunit, eukaryotic/archaeal	GO:0006269;GO:0003896	G3DSA:3.90.920.10: ; IPR002755: DNA primase, small subunit; Coil: ; IPR014052: DNA primase, small subunit, eukaryotic/archaeal; SSF56747:	NA
comp30472_c0_seq5.p1	Ec-06_009510.1	Phosphatidylinositol 4-kinase	GO:0004430;GO:0006661	G3DSA:3.30.1010.10: ; IPR000403: Phosphatidylinositol 3-/4-kinase, catalytic domain; SSF50729: ; IPR027003: Phosphatidylinositol 4-kinase; IPR001849: Pleckstrin homology domain; IPR011009: Protein kinase-like domain; IPR011993: Pleckstrin homology-like domain; IPR015433: Phosphatidylinositol Kinase; IPR018936: Phosphatidylinositol 3/4-kinase, conserved site	NA
comp25985_c0_seq1.p1	Ec-06_009520.1	RNA recognition motif domain	GO:0003676;GO:0000166	SSF54928: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp33729_c0_seq1.p1	Ec-06_009540.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32370_c1_seq1.p1	Ec-06_009570.1	START-like domain	n/a;n/a;n/a	PTHR12136: ; SSF55961: ; IPR002913: START domain; IPR023393: START-like domain	NA
comp33797_c0_seq1.p1	Ec-06_009580.1	Import inner membrane translocase subunit TIM44, mitochondrial precursor	GO:0005744;GO:0006886;GO:0015450	PTHR10721: ; IPR007379: Tim44-like domain; SSF54427: ; Coil: ; SignalP-TM:	KOG2580
comp31169_c0_seq7.p1	Ec-06_009590.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0016887	IPR003439: ABC transporter-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR026082: ABC transporter A, ABCA; PF12698: ABC-2 family transporter protein; IPR017871: ABC transporter, conserved site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32930_c0_seq2.p1	Ec-06_009600.1	Scramblase	n/a;n/a;n/a	IPR005552: Scramblase	NA
comp33774_c0_seq1.p1	Ec-06_009610.1	conserved unknown protein	n/a;n/a;n/a	PTHR36809:SF1: ; PTHR36809: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32886_c1_seq7.p2	Ec-06_009660.2	Hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25326_c0_seq2.p1	Ec-06_009670.1	Squalene Monooxygenase (N-terminal region)	GO:0050660;GO:0055114;GO:0008033;GO:0016021;GO:0004506	PTHR10835: ; IPR002218: Glucose-inhibited division protein A-related; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR013698: Squalene epoxidase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.50.50.60: ; SSF51905: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000420: Aromatic-ring hydroxylase (flavoprotein monooxygenase) signature	KOG1298
comp28817_c0_seq2.p1	Ec-06_009680.1	tRNA Pseudouridine Synthase D domain-containing protein	GO:0003723;GO:0001522;GO:0009451;GO:0009982	IPR020103: Pseudouridine synthase, catalytic domain; IPR001656: Pseudouridine synthase, TruD; Coil: ; IPR011760: Pseudouridine synthase, TruD, insertion domain	KOG2339
comp21282_c0_seq1.p1	Ec-06_009690.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29273_c0_seq1.p1	Ec-06_009700.1	Similar to 2-Epi-5-Epi-Valiolone Synthase (Sedoheptulose 7-Phosphate Cyclase)	GO:0003856;GO:0009073	G3DSA:1.20.1090.10: ; SSF56796: ; IPR030960: 3-dehydroquinate synthase domain; PTHR21090: ; G3DSA:3.40.50.1970:	KOG0692
comp20720_c0_seq1.p1	Ec-06_009720.1	Multi antimicrobial extrusion protein	GO:0016020;GO:0055085;GO:0015238;GO:0015297;GO:0006855	IPR002528: Multi antimicrobial extrusion protein; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11206: ; SignalP-noTM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20447_c0_seq1.p1	Ec-06_009730.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29273_c0_seq1.p2	Ec-06_009740.1	Thioredoxin-like fold	GO:0045454;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005746: Thioredoxin; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp2939_c0_seq1.p2	Ec-06_009760.1	Protein of unknown function DUF2723	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR16214: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR021280: Protein of unknown function DUF2723; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31500_c0_seq5.p1	Ec-06_009770.1	MATE efflux family protein	GO:0016020;GO:0055085;GO:0015238;GO:0015297;GO:0006855	IPR002528: Multi antimicrobial extrusion protein; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11206: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31500_c0_seq5.p2	Ec-06_009790.1	Tetratricopeptide repeat	GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; PTHR22904:	NA
comp11669_c0_seq1.p1	Ec-06_009800.1	Methyltransferase type 11	GO:0008152;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR12176: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013216: Methyltransferase type 11	NA
comp27957_c0_seq5.p1	Ec-06_009820.2	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp30321_c0_seq2.p1	Ec-06_009830.1	WW domain	GO:0005515	IPR013761: Sterile alpha motif/pointed domain; IPR001660: Sterile alpha motif domain; IPR001202: WW domain; PTHR11254:SF347: ; Coil: ; PTHR11254: ; G3DSA:2.20.70.10:	NA
comp25083_c0_seq2.p1	Ec-06_009840.1	UDP-sulfoquinovose: diacylglycerol alpha-sulfoquinovosyltransferase SQD2, C-terminal fragment, family GT4	GO:0009058	SSF53756: ; IPR001296: Glycosyl transferase, family 1; PTHR12526: ; G3DSA:3.40.50.2000:	KOG1111
comp31742_c0_seq2.p2	Ec-06_009880.1	C2 domain	GO:0005515	IPR000008: C2 domain	NA
comp31742_c0_seq2.p1	Ec-06_009890.1	PDZ domain	GO:0005515	PTHR13950: ; IPR001478: PDZ domain; IPR022033: RAVE complex protein Rav1 C-terminal	NA
comp10094_c0_seq1.p1	Ec-06_009900.1	Histidine kinase-like ATPase, C-terminal domain	GO:0005524	PTHR15600: ; IPR003594: Histidine kinase-like ATPase, C-terminal domain	NA
comp30861_c0_seq2.p1	Ec-06_009910.1	Histidine kinase-like ATPase, C-terminal domain	GO:0005524	IPR017907: Zinc finger, RING-type, conserved site; SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR15600: ; PF13920: Zinc finger, C3HC4 type (RING finger); IPR003594: Histidine kinase-like ATPase, C-terminal domain	NA
comp27136_c0_seq2.p1	Ec-06_009930.1	Histidine phosphatase superfamily, clade-1	GO:0006096;GO:0016868	IPR013078: Histidine phosphatase superfamily, clade-1; IPR001345: Phosphoglycerate/bisphosphoglycerate mutase, active site; IPR029033: Histidine phosphatase superfamily; IPR005952: Phosphoglycerate mutase 1	NA
comp24307_c0_seq1.p1	Ec-06_009940.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp11421_c0_seq1.p1	Ec-06_009950.1	hypothetical protein	n/a;n/a;n/a	Coil:	[illegible]
comp32279_c2_seq5.p1	Ec-06_009970.1	RuvB-like	GO:0043141	IPR010339: TIP49, C-terminal; IPR003593: AAA+ ATPase domain; IPR027238: RuvB-like; G3DSA:1.10.8.60: ; IPR027417: P-loop containing [illegible]	[illegible]
comp28780_c0_seq3.p1	Ec-06_009990.1	Sec16, central conserved domain	n/a;n/a;n/a	Coil: ; IPR024340: Sec16, central conserved domain; IPR024298: Ancestral coatomer element 1, Sec16/Sec31	[illegible]
comp26822_c0_seq1.p1	Ec-06_010000.1	Photosystem II oxygen evolution complex protein PsbP	GO:0005509;GO:0009523;GO:0009654;GO:0015979;GO:0019898	PTHR31407: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR016123: Mog1 [illegible]	[illegible]
comp18680_c0_seq1.p1	Ec-06_010010.1	Alkyl hydroperoxide reductase subunit C/ Thiol specific antioxidant	GO:0016209;GO:0016491;GO:0055114	IPR000866: Alkyl hydroperoxide reductase subunit C/ Thiol specific antioxidant; SIGNAL_PEPTIDE: Signal peptide region; [illegible]	[illegible]
comp25008_c0_seq1.p1	Ec-06_010020.1	Armadillo-type fold	GO:0005488	PTHR23316: ; IPR002652: Importin-alpha, importin-beta-binding domain; IPR011989: Armadillo-like helical; IPR000225: Armadillo; IPR024931: [illegible]	[illegible]
comp29972_c0_seq4.p1	Ec-06_010040.1	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	n/a;n/a;n/a	IPR000408: Regulator of chromosome condensation, RCC1; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal [illegible]	[illegible]
comp30988_c0_seq1.p1	Ec-06_010050.1	C2 domain protein	n/a;GO:0005515	PTHR10774: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; [illegible]	[illegible]
comp30988_c0_seq1.p2	Ec-06_010050.3	C2 domain protein	n/a;n/a;n/a	PTHR10774: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; [illegible]	[illegible]
comp12491_c0_seq1.p1	Ec-06_010060.1	DEAD box helicase	n/a;n/a;n/a	IPR014014: RNA helicase, DEAD-box type, Q motif; IPR011545: DEAD/DEAH box helicase domain; IPR027417: P-loop containing nucleoside [illegible]	[illegible]
comp19910_c0_seq1.p1	Ec-06_010070.1	Protein of unknown function DUF3353	n/a;n/a;n/a	IPR021788: Protein CHAPERONE-LIKE PROTEIN OF POR1-like; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound [illegible]	[illegible]
comp11755_c0_seq1.p1	Ec-06_010090.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; IPR002110: Ankyrin repeat	[illegible]
comp31147_c0_seq1.p3	Ec-06_010110.1	Prefoldin alpha-like	GO:0006457;GO:0016272;GO:0051082	IPR004127: Prefoldin alpha-like; IPR009053: Prefoldin; Coil:	[illegible]
comp31147_c0_seq1.p1	Ec-06_010120.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN [illegible]	[illegible]
comp33024_c5_seq2.p1	Ec-06_010130.1	Allantoicase domain	GO:0000256;GO:0004037	IPR005164: Allantoicase; IPR015908: Allantoicase domain; IPR008979: Galactose-binding domain-like; SignalP-TM:	[illegible]
comp34986_c0_seq1.p1	Ec-06_010220.1	ATP synthase O subunit, mitochondrial precursor	GO:0015986;GO:0046933	PTHR11910:SF1: ; IPR020781: ATPase, OSCP/delta subunit, conserved site; IPR026015: F1F0 ATP synthase OSCP/delta subunit, N-terminal domain; [illegible]	[illegible]
comp16531_c0_seq2.p1	Ec-06_010230.1	RNA recognition motif domain	GO:0003676	IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; PTHR18806: ; Coil: ; IPR002483: PWI domain	[illegible]
comp21123_c0_seq1.p1	Ec-06_010240.1	conserved unknown protein	n/a;n/a;n/a	SSF55961: ; SignalP-TM:	[illegible]
comp31851_c1_seq5.p2	Ec-06_010250.1	Mitochondrial substrate/solute carrier	GO:0005488;GO:0006810;GO:0016020	PTHR24089: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; [illegible]	[illegible]
comp12026_c0_seq1.p1	Ec-06_010260.1	Ribosomal protein L24e-related	GO:0003735;GO:0005622;GO:0005840;GO:0006412	IPR023441: Ribosomal protein L24e domain; SSF57716: ; IPR000988: Ribosomal protein L24e-related; Coil:	[illegible]
comp26970_c0_seq2.p1	Ec-06_010280.1	Alpha-mannosidase, family GH38	GO:0004559;GO:0005975	IPR027291: Glycoside hydrolase 38/57, N-terminal domain; IPR028995: Glycoside hydrolase, families 57/38, central domain; PTHR11607: ; SIGNAL_ [illegible]	[illegible]
comp25602_c1_seq1.p1	Ec-06_010280.2	Alpha-mannosidase, family GH38	GO:0004559;GO:0005975	IPR011013: Galactose mutarotase-like domain; PTHR11607:SF3: ; PTHR11607: ; IPR011682: Glycosyl hydrolase family 38, C-terminal; [illegible]	[illegible]
comp20696_c0_seq1.p1	Ec-06_010300.1	peptide chain release factor	GO:0006415;GO:0005737;GO:0016149	SIGNAL_PEPTIDE: Signal peptide region; G3DSA:1.20.58.410: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_ [illegible]	[illegible]
comp21225_c0_seq2.p1	Ec-06_010300.2	peptide chain release factor	GO:0005737;GO:0006415;GO:0016149	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_ [illegible]	[illegible]
comp32160_c0_seq14.p1	Ec-06_010310.1	hypothetical protein	n/a;n/a;n/a	SSF55753: ; IPR029006: ADF-H/Gelsolin-like domain	[illegible]
comp32160_c0_seq1.p1	Ec-06_010330.1	Protein-tyrosine phosphatase-like	GO:0008138;GO:0006470	IPR029021: Protein-tyrosine phosphatase-like; IPR000387: Protein-tyrosine/Dual specificity phosphatase; IPR024950: Dual specificity phosphatase; [illegible]	[illegible]
comp11979_c0_seq1.p1	Ec-06_010370.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0006470	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001932: [illegible]	[illegible]
comp32401_c0_seq1.p1	Ec-06_010380.1	Nucleoporin FG repeat	n/a;GO:0005643;GO:0006913	IPR024882: Nucleoporin p58/p45; IPR025574: Nucleoporin FG repeat; Coil: ; SignalP-TM:	[illegible]
comp30212_c0_seq1.p1	Ec-06_010400.1	Vacuolar (H+)-ATPase G subunit	GO:0016820;GO:0016471;GO:0015992	IPR005124: Vacuolar (H+)-ATPase G subunit; PF03179: Vacuolar (H+)-ATPase G subunit; Coil:	[illegible]
comp18704_c0_seq2.p1	Ec-06_010420.1	Short-chain dehydrogenase/reductase SDR	GO:0008152;GO:0016491	SSF51735: ; IPR020904: Short-chain dehydrogenase/reductase, conserved site; TMhelix: Region of a membrane-bound protein predicted to be embedded [illegible]	[illegible]
comp26310_c0_seq2.p1	Ec-06_010440.1	Peptidase T2, asparaginase 2	GO:0016787	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPT [illegible]	[illegible]
comp26310_c0_seq3.p1	Ec-06_010450.1	FKBP-type peptidyl-prolyl cis-trans isomerase 8	GO:0006457	SSF54534: ; G3DSA:3.10.50.40: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; [illegible]	[illegible]
comp32704_c0_seq11.p1	Ec-06_010460.1	Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain	GO:0000413;GO:0003755;GO:0006457	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR024936: Cyclophilin-type [illegible]	[illegible]
comp20361_c1_seq1.p1	Ec-06_010470.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp27640_c0_seq2.p1	Ec-06_010480.1	Protein of unknown function DUF3082	n/a;n/a;n/a	IPR021434: Protein of unknown function DUF3082; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein [illegible]	[illegible]
comp32840_c2_seq37.p1	Ec-06_010490.2	Heat Shock transcription factor	GO:0003700;GO:0005634;GO:0006355;GO:0043565	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR000232: Heat shock factor (HSF)-type, DNA-binding; IPR027725: Heat shock transcription [illegible]	[illegible]
comp30341_c2_seq1.p1	Ec-06_010520.1	Mitochondrial substrate/solute carrier	n/a;n/a;n/a	PTHR24089: ; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier	[illegible]
comp33883_c0_seq1.p1	Ec-06_010530.1	conserved unknown protein	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_P [illegible]	[illegible]
comp21101_c0_seq1.p1	Ec-06_010540.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp19839_c0_seq1.p1	Ec-06_010550.1	conserved unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; [illegible]	[illegible]
comp12037_c0_seq1.p1	Ec-06_010560.1	Nucleic acid-binding, OB-fold	GO:0003723;n/a	IPR012340: Nucleic acid-binding, OB-fold; IPR003029: Ribosomal protein S1, RNA-binding domain; SIGNAL_PEPTIDE: Signal peptide region; [illegible]	[illegible]
comp28557_c0_seq5.p1	Ec-06_010570.1	conserved unknown protein	n/a;n/a;n/a	NA	[illegible]
comp28685_c0_seq4.p1	Ec-06_010590.1	Hypothetical leucine rich repeat protein	GO:0005515	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001611: Leucine-rich repeat; IPR032675: Leucine-rich [illegible]	[illegible]
comp27285_c0_seq2.p1	Ec-06_010600.1	Enoyl coenzyme A hydratase	GO:0008152;GO:0003824	IPR029045: ClpP/crotonase-like domain; IPR014748: Crotonase, C-terminal; IPR001753: Crotonase superfamily; PTHR11941:	[illegible]
comp31561_c0_seq2.p1	Ec-06_010620.1	Zinc finger, PHD-finger	GO:0005515	IPR017956: AT hook, DNA-binding motif; IPR020478: AT hook-like; IPR019786: Zinc finger, PHD-type, conserved site; IPR001965: Zinc finger, PHD [illegible]	[illegible]
comp29465_c0_seq1.p1	Ec-06_010640.1	IFT27, Ras superfamily GTPase	GO:0005622;GO:0007264;GO:0005525	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR005225: Small GTP-binding [illegible]	[illegible]
comp100068_c0_seq1.p1	Ec-06_010650.1	FG-GAP repeat	n/a;n/a;n/a	IPR013519: Integrin alpha beta-propellor; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site [illegible]	[illegible]
comp12411_c0_seq1.p1	Ec-06_010670.1	Rab8D, RAB family GTPase	GO:0007165;GO:0006184;GO:0005622;GO:0003924;GO:0006886;GO:0006913;GO:0007264;GO:0005525	IPR002041: Ran GTPase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; [illegible]	[illegible]
comp21394_c0_seq1.p1	Ec-06_010680.1	Beta-lactamase-like	n/a;GO:0004416;GO:0008270;GO:0006750	SIGNAL_PEPTIDE: Signal peptide region; IPR001279: Beta-lactamase-like; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; [illegible]	[illegible]
comp32292_c0_seq6.p1	Ec-06_010700.1	expressed unknown protein	n/a;n/a;n/a	Coil:	[illegible]
comp25072_c0_seq2.p1	Ec-06_010710.1	Mog1/PsbP, alpha/beta/alpha sandwich	n/a;n/a;n/a	IPR007681: Ran-interacting Mog1 protein; IPR016123: Mog1/PsbP, alpha/beta/alpha sandwich; PTHR15837:	[illegible]
comp19794_c0_seq1.p1	Ec-06_010720.1	2Fe-2S ferredoxin-type domain	GO:0009055;GO:0051536	IPR001041: 2Fe-2S ferredoxin-type domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a [illegible]	[illegible]
comp31428_c0_seq4.p1	Ec-06_010750.1	conserved unknown protein	GO:0005506;GO:0005783;GO:0006633;GO:0016491;GO:0055114;n/a	PTHR11863:SF34: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide [illegible]	[illegible]
comp30688_c0_seq1.p1	Ec-06_010740.1	SR RNA splicing protein	GO:0000166	NA	[illegible]
comp33074_c3_seq15.p1	Ec-06_010760.1	Proteasome activator pa28, C-terminal domain	GO:0008537	IPR003186: Proteasome activator pa28, C-terminal domain; IPR009077: Proteasome activator pa28	[illegible]
comp29384_c0_seq3.p1	Ec-06_010770.2	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_P [illegible]	[illegible]
comp29600_c0_seq4.p1	Ec-06_010780.1	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp30455_c1_seq4.p1	Ec-06_010790.1	Zn-dependent peptidase, Cym1 homolog	GO:0003824;GO:0046872	PTHR11851: ; IPR007863: Peptidase M16, C-terminal domain; IPR011249: Metalloenzyme, LuxS/M16 peptidase-like; IPR011237: Peptidase M16 [illegible]	[illegible]
comp30455_c0_seq1.p1	Ec-06_010820.1	Metalloenzyme, LuxS/M16 peptidase-like	GO:0003824;GO:0046872	PTHR11851: ; IPR011249: Metalloenzyme, LuxS/M16 peptidase-like	[illegible]
comp33031_c0_seq13.p2	Ec-06_010830.1	flagellar associated protein, cobalamin adenosyltransferase-like protein	GO:0005524;GO:0008817;GO:0009236	IPR016030: Adenosylcobalamin biosynthesis, ATP:cob(I)alamin adenosyltransferase-like; IPR029499: ATP:cob(I)alamin adenosyltransferase, PduO-type [illegible]	[illegible]
comp33031_c0_seq17.p1	Ec-06_010840.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPT [illegible]	[illegible]
comp28362_c0_seq2.p1	Ec-06_010850.1	MEngA, mitochondrial EngA GTPase	GO:0005525	IPR031166: EngA-type guanine nucleotide-binding (G) domain; IPR016484: GTP-binding protein EngA; IPR027417: P-loop containing nucleoside [illegible]	[illegible]
comp31375_c0_seq8.p1	Ec-06_010870.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM [illegible]	[illegible]
comp31954_c0_seq2.p1	Ec-06_010890.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_P [illegible]	[illegible]
comp24533_c0_seq3.p1	Ec-06_010910.1	Alpha-ketoglutarate-dependent dioxygenase AlkB-like	GO:0016491;n/a	SSF51197: ; IPR005123: Oxoglutarate/iron-dependent dioxygenase; PTHR13069: ; IPR027450: Alpha-ketoglutarate-dependent dioxygenase AlkB-like	[illegible]
comp28075_c0_seq1.p1	Ec-06_010920.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR014014: RNA helicase, DEAD-box type, Q motif; IPR000629: ATP-dependent RNA helicase [illegible]	[illegible]
comp31954_c1_seq15.p1	Ec-06_010950.1	conserved unknown protein	n/a;n/a;n/a	Coil:	[illegible]
comp55212_c0_seq1.p1	Ec-06_010960.1	Sterile alpha motif/pointed domain	n/a;n/a;n/a	PTHR11255: ; IPR013761: Sterile alpha motif/pointed domain; IPR001660: Sterile alpha motif domain; IPR021129: Sterile alpha motif, type 1; Coil:	[illegible]
comp33924_c0_seq1.p1	Ec-06_010970.1	Leucine rich repeat protein	NA	G3DSA:3.80.10.10: ; PTHR23125: ; IPR006553: Leucine-rich repeat, cysteine-containing subtype; SSF52047: ; PF13516: Leucine Rich repeat	[illegible]
comp30917_c1_seq1.p1	Ec-06_010990.1	DENN domain	n/a;n/a;n/a	IPR001194: DENN domain; IPR001478: PDZ domain; PTHR12296:	[illegible]
comp27188_c0_seq1.p1	Ec-07_000010.1	Alpha/Beta hydrolase fold	GO:0008152;GO:0008415	PTHR22753: ; IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; IPR000073: Alpha/beta hydrolase fold-1; SIGNAL_ [illegible]	[illegible]
comp12923_c0_seq1.p1	Ec-07_000020.2	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp29821_c0_seq2.p1	Ec-07_000060.1	RecF/RecN/SMC, N-terminal	GO:0030915;GO:0005524;GO:0006281;GO:0005694;GO:0006259;GO:0000724	SSF90257: ; PTHR19306: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR003395: RecF/RecN/SMC, N-terminal; [illegible]	[illegible]
comp28383_c0_seq7.p1	Ec-07_000110.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_P [illegible]	[illegible]
comp32405_c0_seq8.p1	Ec-07_000120.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp30591_c0_seq1.p1	Ec-07_000160.1	ExV-1-7 domain protein	NA	NA	[illegible]
comp27742_c0_seq1.p1	Ec-07_000170.1	Hepatocellular carcinoma-associated antigen 59	n/a;n/a;n/a	IPR010756: Hepatocellular carcinoma-associated antigen 59	[illegible]
comp28033_c0_seq3.p1	Ec-07_000180.1	Mss4-like	GO:0003824;GO:0005488;GO:0008152	SSF51735: ; IPR002579: Peptide methionine sulphoxide reductase MrsB; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION [illegible]	[illegible]
comp32647_c0_seq10.p1	Ec-07_000190.1	ExV-1-163	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_P [illegible]	[illegible]
comp32374_c4_seq8.p1	Ec-07_000220.1	cyclin D2	GO:0031177	PTHR10177:SF203: ; IPR013763: Cyclin-like; IPR006671: Cyclin, N-terminal; PTHR10177:	[illegible]
comp50766_c0_seq1.p1	Ec-07_000260.1	WD40/YVTN repeat-like-containing domain	GO:0005515	IPR018247: EF-Hand 1, calcium-binding site; IPR019775: WD40 repeat, conserved site; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain [illegible]	[illegible]
comp32727_c1_seq6.p1	Ec-07_000280.1	Spondin, N-terminal	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR009465: Spondin, N-terminal; [illegible]	[illegible]
comp33239_c0_seq1.p1	Ec-07_000285.1	Spondin, N-terminal	n/a;n/a;n/a	SSF56672: ; PTHR11439:SF185: ; IPR013103: Reverse transcriptase, RNA-dependent DNA polymerase; PTHR11439:	[illegible]
comp28568_c0_seq4.p1	Ec-07_000310.1	Pseudouridine synthase, catalytic domain	GO:0003723;GO:0001522;GO:0009451;GO:0009982	IPR020103: Pseudouridine synthase, catalytic domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside [illegible]	[illegible]
comp33895_c0_seq1.p1	Ec-07_000320.1	Hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp26584_c0_seq2.p1	Ec-07_000340.1	hypothetical protein	n/a;n/a;n/a	Coil:	[illegible]
comp11714_c0_seq1.p1	Ec-07_000350.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp28442_c0_seq1.p1	Ec-07_000360.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp25809_c0_seq1.p1	Ec-07_000380.3	Phox homologous domain	GO:0035091	IPR001683: Phox homologous domain	[illegible]
comp32283_c2_seq1.p1	Ec-07_000390.3	Putative RING zinc finger of C3HC4-type	n/a;n/a;n/a	PF15227: zinc finger of C3HC4-type, RING; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, [illegible]	[illegible]
comp11974_c0_seq1.p1	Ec-07_000430.1	Smr protein/MutS2 C-terminal	n/a;n/a;n/a	SSF160443: ; IPR002885: Pentatricopeptide repeat; IPR002625: Smr protein/MutS2 C-terminal; Coil: ; PTHR24015: ; SignalP-TM:	[illegible]
comp31588_c0_seq8.p1	Ec-07_000440.1	conserved unknown protein	GO:0000166	Coil:	[illegible]
comp33458_c0_seq1.p2	Ec-07_000520.1	Histone H2A	GO:0003677;GO:0046982	NA	[illegible]
comp27540_c0_seq1.p1	Ec-07_000530.1	Smr protein/MutS2 C-terminal	n/a;n/a;n/a	SSF160443: ; SIGNAL_PEPTIDE: Signal peptide region; IPR002625: Smr protein/MutS2 C-terminal; PTHR13308: ; SIGNAL_PEPTIDE_N_REGION [illegible]	[illegible]
comp29886_c0_seq3.p1	Ec-07_000550.1	Dehydroquinase, class II	GO:0003855	IPR001874: Dehydroquinase, class II	[illegible]
comp32098_c0_seq2.p1	Ec-07_000670.1	Glycosyltransferase, family GT47	GO:0016020	IPR004263: Exostosin-like; PTHR11062:	[illegible]
comp11460_c0_seq2.p1	Ec-07_000690.1	Protein of unknown function DUF2358	n/a;n/a;n/a	IPR018790: Protein of unknown function DUF2358; SSF54427: ; G3DSA:3.10.450.50:	[illegible]
comp27526_c1_seq2.p1	Ec-07_000700.1	Pectin lyase fold/virulence factor	n/a;n/a;n/a	IPR011050: Pectin lyase fold/virulence factor; PF13229: Right handed beta helix region; Coil: ; IPR006626: Parallel beta-helix repeat; IPR012334: Pectin [illegible]	[illegible]
comp28977_c0_seq2.p1	Ec-07_000710.1	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	GO:0055114	IPR000103: Pyridine nucleotide-disulphide oxidoreductase, class-II; SIGNAL_PEPTIDE: Signal peptide region; PR00368: FAD-dependent pyridine [illegible]	[illegible]
comp32198_c0_seq8.p1	Ec-07_000730.1	F-box domain	GO:0005515	IPR001810: F-box domain; PTHR14289: ; G3DSA:1.20.1280.50: ; IPR007474: ApaG domain; SSF160631:	[illegible]
comp26804_c0_seq4.p1	Ec-07_000740.3	Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain	GO:0000413;GO:0003755;GO:0006457	IPR024936: Cyclophilin-type peptidyl-prolyl cis-trans isomerase; IPR002130: Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain; IPR029000: [illegible]	[illegible]
comp28857_c0_seq2.p1	Ec-07_000750.1	Dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichyl-alpha-1,6-mannosyltransferase, family GT22	GO:0006506;GO:0031227;GO:0016757	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp27000_c0_seq1.p1	Ec-07_000790.1	Zinc finger, CCCH-type	GO:0046872	IPR000571: Zinc finger, CCCH-type; IPR017907: Zinc finger, RING-type, conserved site; IPR001841: Zinc finger, RING-type; PTHR12930: ; PF1392 [illegible]	[illegible]
comp27550_c0_seq3.p1	Ec-07_000800.1	Ubiquitin-related domain	GO:0005515	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTID [illegible]	[illegible]
comp28327_c0_seq2.p1	Ec-07_000810.4	hypothetical protein	n/a;n/a;n/a	Coil:	[illegible]
comp32689_c0_seq1.p1	Ec-07_000820.1	Protein of unknown function DUF2009	GO:0005622;GO:0008270	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000315: Zinc finger, B-box; [illegible]	[illegible]
comp32920_c1_seq26.p3	Ec-07_000830.1	Amino acid transporter, transmembrane	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp30130_c0_seq1.p1	Ec-07_000840.1	polyunsaturated fatty acids delta-6-elongase	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003034: SAP domain; [illegible]	[illegible]
comp24752_c0_seq2.p1	Ec-07_000850.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noT [illegible]	[illegible]
comp30826_c0_seq2.p2	Ec-07_000880.1	BRCT domain	GO:0005622	SSF90209: ; IPR001876: Zinc finger, RanBP2-type; IPR001357: BRCT domain	[illegible]
comp21082_c0_seq1.p1	Ec-07_000910.1	conserved unknown protein	n/a;n/a;n/a	PTHR22069:	[illegible]
comp31569_c1_seq1.p1	Ec-07_000920.1	expressed unknown protein	n/a;n/a;n/a	Coil:	[illegible]
comp30901_c0_seq2.p1	Ec-07_000930.2	Histidine phosphatase superfamily, clade-2	GO:0003993	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR11567:SF110: ; NON [illegible]	[illegible]
comp19863_c0_seq1.p1	Ec-07_000970.1	Tetratricopeptide-like helical domain	GO:0005515;GO:0043531	PF13424: Tetratricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; IPR002182: NB-ARC; IPR027417: P-loop containing nucleoside [illegible]	[illegible]
comp13167_c1_seq1.p1	Ec-07_000990.1	expressed unknown protein	n/a;n/a;n/a	PTHR18895: ; PF13659: Methyltransferase domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR002052: DNA methylase, [illegible]	[illegible]
comp19606_c0_seq2.p1	Ec-07_001020.1	Dual-specificity protein kinase	GO:0007093;GO:0004712;GO:0051304;GO:0004672;GO:0006468	NA	[illegible]
comp20023_c0_seq1.p1	Ec-07_001030.1	Calcium-binding protein similar to Regucalin	n/a;n/a;n/a	NA	[illegible]
comp34089_c0_seq1.p1	Ec-07_001040.2	mRNA splicing factor, Cwf21	n/a;n/a;n/a	Coil: ; IPR013170: mRNA splicing factor Cwf21 domain	[illegible]
comp29623_c1_seq1.p1	Ec-07_001060.1	Zinc finger, FYVE/PHD-type	GO:0016773;GO:0005488	SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011009: Protein kinase-like domain; IPR000306: FYVE zinc finger; NON [illegible]	[illegible]
comp29623_c0_seq1.p1	Ec-07_001060.2	Zinc finger, FYVE/PHD-type	GO:0005488	Coil:	[illegible]
comp26770_c0_seq1.p1	Ec-07_001080.1	RNA helicase family protein	n/a;n/a;n/a	IPR007502: Helicase-associated domain; IPR011545: DEAD/DEAH box helicase domain; IPR011709: Domain of unknown function DUF1605; IPR014 [illegible]	[illegible]
comp31924_c0_seq5.p1	Ec-07_001070.1	Oxoglutarate/iron-dependent dioxygenase	GO:0055114;GO:0016706;GO:0016491	IPR006620: Prolyl 4-hydroxylase, alpha subunit; IPR005123: Oxoglutarate/iron-dependent dioxygenase; PTHR10869:	[illegible]
comp30080_c0_seq1.p1	Ec-07_001100.1	PsbB mRNA maturation factor Mbb1, chloroplast precursor	GO:0006396;GO:0005622;GO:0005515	SSF48452: ; PF13432: Tetratricopeptide repeat; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; PF13371: Tetratri [illegible]	[illegible]
comp24288_c0_seq1.p1	Ec-07_001140.1	Ovarian tumour, otubain	n/a;n/a;n/a	IPR003323: OTU domain; SSF54001:	[illegible]
comp26974_c0_seq2.p1	Ec-07_001150.1	Flotillin	NA	SSF117892: ; IPR027705: Flotillin family; IPR001107: Band 7 protein	[illegible]
comp12239_c0_seq1.p1	Ec-07_001170.4	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR22844: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containin [illegible]	[illegible]
comp32278_c0_seq11.p1	Ec-07_001180.1	Armadillo-type fold	GO:0005488	PTHR13387: ; IPR007205: Protein HGH1 N-terminal; IPR011989: Armadillo-like helical; IPR007206: Protein HGH1 C-terminal; IPR016024: Armadill [illegible]	[illegible]
comp26625_c0_seq1.p1	Ec-07_001230.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp31344_c0_seq1.p1	Ec-07_001250.3	Putative ATP-dependent RNA helicase, partial.	GO:0005622;GO:0008270	IPR007502: Helicase-associated domain; IPR011545: DEAD/DEAH box helicase domain; PTHR18934:SF145: ; IPR011709: Domain of unknown func [illegible]	[illegible]
comp20273_c0_seq1.p1	Ec-07_001260.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001594: Zinc finger, D [illegible]	[illegible]
comp31805_c0_seq9.p1	Ec-07_001270.2	S-adenosyl-L-methionine-dependent methyltransferase	GO:0003676;GO:0008168;GO:0032259;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR015507: Ribosomal RNA large subunit methyltransferase E; IPR022877: Ribos [illegible]	[illegible]
comp29441_c0_seq4.p1	Ec-07_001290.1	Ubiquinone Biosynthesis Monooxygenase COQ6 (C-terminal region) Ubiquinone Biosynthesis Monooxygenase	GO:0006744;GO:0016709;GO:0050660;GO:0055114	IPR010971: Ubiquinone biosynthesis hydroxylase UbiH/COQ6; IPR002938: Monooxygenase, FAD-binding; G3DSA:3.50.50.60: ; PTHR13789: ; SSF [illegible]	[illegible]
comp30299_c0_seq1.p1	Ec-07_001300.3	Hypothetical leucine rich repeat protein	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp31484_c0_seq3.p1	Ec-07_001310.2	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Re [illegible]	[illegible]
comp31484_c0_seq2.p1	Ec-07_001310.3	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Re [illegible]	[illegible]
comp31202_c1_seq3.p1	Ec-07_001360.1	Kelch-type beta propeller	GO:0005515	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF117281: [illegible]	[illegible]
comp22894_c0_seq1.p2	Ec-07_001400.1	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0006511;GO:0036459	SSF54001: ; IPR028889: Ubiquitin specific protease domain; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase	[illegible]
comp32626_c0_seq3.p1	Ec-07_001410.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noT [illegible]	[illegible]
comp28432_c0_seq2.p1	Ec-07_001420.1	Catalase	GO:0020037;GO:0055114;GO:0006979;GO:0004096	IPR018028: Catalase, mono-functional, haem-containing; IPR020835: Catalase-like domain; IPR002226: Catalase haem-binding site; IPR024708: Catalas [illegible]	[illegible]
comp32675_c5_seq1.p1	Ec-07_001500.1	PDZ domain	GO:0005515	IPR001478: PDZ domain	[illegible]
comp65298_c0_seq1.p1	Ec-07_001510.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PTHR24362: ; IPR011009: Protein kinase-like do [illegible]	[illegible]
comp33104_c0_seq5.p1	Ec-07_001530.1	Nucleoporin, Nup133/Nup155-like, C-terminal	GO:0005643;GO:0006913;GO:0017056	IPR014908: Nucleoporin, Nup133/Nup155-like, N-terminal; IPR004870: Nucleoporin, Nup155-like; IPR007187: Nucleoporin, Nup133/Nup155-like, C- [illegible]	[illegible]
comp12929_c0_seq2.p1	Ec-07_001560.1	Uncharacterised protein family UPF0642	n/a;n/a;n/a	IPR019434: Uncharacterised protein family UPF0642; Coil:	[illegible]
comp30781_c0_seq5.p1	Ec-07_001570.1	conserved unknown protein	n/a;n/a;n/a	NA	[illegible]
comp26362_c1_seq2.p1	Ec-07_001590.2	DNA polymerase delta/II small subunit family	GO:0003677;GO:0003887;GO:0005634;GO:0006260	IPR024826: DNA polymerase delta/II small subunit family; PTHR10416:SF0: ; IPR007185: DNA polymerase alpha/epsilon, subunit B	[illegible]
comp12878_c0_seq1.p1	Ec-07_001600.1	Ribosomal protein L28/L40, mitochondrial	n/a;n/a;n/a	IPR019192: Ribosomal protein L28/L40, mitochondrial	[illegible]
comp29287_c0_seq1.p1	Ec-07_001630.1	conserved unknown protein	n/a;n/a;n/a	PTHR31152:	[illegible]
comp20259_c0_seq2.p1	Ec-07_001680.1	cytochrome P450	GO:0020037;GO:0005506;GO:0055114;GO:0016705	IPR001128: Cytochrome P450; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal [illegible]	[illegible]
comp27736_c0_seq1.p1	Ec-07_001690.1	Impact, N-terminal	n/a;GO:0005515	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; IPR001498: Impact, N-terminal; IPR020568: Ribosomal protein S5 domain 2-type fold; IPR0235 [illegible]	[illegible]
comp32345_c0_seq2.p1	Ec-07_001720.1	hypothetical protein	GO:0005515	IPR001478: PDZ domain; Coil:	[illegible]
comp32176_c1_seq6.p1	Ec-07_001740.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_P [illegible]	[illegible]
comp27164_c0_seq1.p1	Ec-07_001750.1	Septum formation inhibitor MinC	GO:0000902;GO:0051726;GO:0000917	IPR005526: Septum formation inhibitor MinC, C-terminal; IPR013033: Septum formation inhibitor MinC; IPR016098: Cyclase-associated protein CAP/ [illegible]	[illegible]
comp19585_c0_seq1.p1	Ec-07_001760.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_P [illegible]	[illegible]
comp27248_c0_seq2.p1	Ec-07_001770.1	expressed unknown protein	n/a;n/a;n/a	Coil:	[illegible]
comp25728_c0_seq2.p1	Ec-07_001780.1	tRNA (guanine-N-7) methyltransferase, Trmb type	GO:0006400;GO:0008176	PTHR23417: ; IPR025763: tRNA (guanine-N-7) methyltransferase catalytic subunit Trm8, eukaryote; IPR029063: S-adenosyl-L-methionine-dependent [illegible]	[illegible]
comp32167_c0_seq5.p1	Ec-07_001790.1	Multi antimicrobial extrusion protein	GO:0006855;GO:0015238;GO:0015297;GO:0016020;GO:0055085	IPR002528: Multi antimicrobial extrusion protein; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_ [illegible]	[illegible]
comp30823_c2_seq3.p1	Ec-07_001800.1	ExV-1-7 domain protein	NA	NA	[illegible]
comp12388_c0_seq1.p1	Ec-07_001830.1	Peptidase M24, structural domain	GO:0004177;GO:0004239;GO:0006508;GO:0008235	IPR002893: Zinc finger, MYND-type; IPR000994: Peptidase M24, structural domain; IPR002467: Peptidase M24A, methionine aminopeptidase, subfam [illegible]	[illegible]
comp32839_c1_seq9.p1	Ec-07_001840.1	Zinc finger, RING-type	GO:0005515;GO:0008270	IPR001841: Zinc finger, RING-type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DO [illegible]	[illegible]
comp27659_c0_seq2.p1	Ec-07_001850.1	Beta-glucosidase, family GH1	GO:0003824;GO:0043169;GO:0005975	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PS51257: Proka [illegible]	[illegible]
comp30315_c1_seq1.p3	Ec-07_001860.1	Aspartic peptidase, DDI1-type	GO:0004190;GO:0006508	IPR019103: Aspartic peptidase, DDI1-type; IPR021109: Aspartic peptidase domain; PTHR12917:	[illegible]
comp47794_c0_seq1.p1	Ec-07_001910.3	hypothetical protein	n/a;n/a;n/a	Coil:	[illegible]
comp15893_c0_seq1.p1	Ec-07_001920.1	Longin-like domain	GO:0006810	IPR027156: AP-2 complex subunit sigma; IPR016635: Adaptor protein complex, sigma subunit; G3DSA:3.30.450.60: ; IPR011012: Longin-like domain [illegible]	[illegible]
comp30052_c0_seq2.p1	Ec-07_001940.3	Ubiquitin-conjugating enzyme/RWD-like	GO:0019787;GO:0043687;GO:0051246	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; SM00212: Ubiquitin-conjugating enzyme E2, catalytic domain homologues; IPR000608: Ubiquitin [illegible]	[illegible]
comp29470_c0_seq2.p1	Ec-07_001970.1	conserved unknown protein	n/a;n/a;n/a	PTHR10566: ; PTHR10566:SF86: ; G3DSA:3.90.1200.10: ; IPR002575: Aminoglycoside phosphotransferase; Coil: ; IPR011009: Protein kinase-like d [illegible]	[illegible]
comp21203_c0_seq1.p1	Ec-07_002010.1	FNIP	n/a;n/a;n/a	IPR008615: FNIP; PTHR32134: ; Coil:	[illegible]
comp30314_c0_seq1.p1	Ec-07_002030.3	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp29088_c0_seq2.p1	Ec-07_002040.1	Homeodomain-like	GO:0003677	PTHR10641: ; PF13921: Myb-like DNA-binding domain; IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; IPR017930: Myb domain [illegible]	[illegible]
comp21295_c0_seq1.p1	Ec-07_002070.1	Malic enzyme, NAD-binding	GO:0004470;GO:0004471;GO:0006108;GO:0051287;GO:0055114	IPR012302: Malic enzyme, NAD-binding; IPR001891: Malic oxidoreductase; IPR012301: Malic enzyme, N-terminal domain; SSF53223: ; PTHR23406 [illegible]	[illegible]
comp34102_c0_seq1.p1	Ec-07_002110.1	Glycosyltransferase, family GT47	GO:0016020;GO:0016021;GO:0015012	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPT [illegible]	[illegible]
comp29019_c0_seq1.p1	Ec-07_002120.3	ATP adenylyltransferase, C-terminal	GO:0003877	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp32437_c0_seq3.p1	Ec-07_002130.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13424: Tetratricopeptide repeat; PTHR19959: ; IPR011990: Tetratricopeptide-like helical domain; PF13374: Tetratricopeptide repeat; [illegible]	[illegible]
comp30026_c0_seq1.p1	Ec-07_002140.1	SCP / PR1-domain containing protein	NA	IPR013994: Carbohydrate-binding WSC, subgroup; SIGNAL_PEPTIDE: Signal peptide region; IPR001283: Cysteine-rich secretory protein, allergen V [illegible]	[illegible]
comp11761_c0_seq1.p1	Ec-07_002170.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noT [illegible]	[illegible]
comp23926_c0_seq1.p1	Ec-07_002180.1	Tweety	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp32610_c0_seq20.p1	Ec-07_002200.1	Hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp14454_c0_seq2.p1	Ec-07_002220.1	DNA recombination and repair protein Rad51, C-terminal	GO:0003677;GO:0005524;GO:0006259;GO:0008094	IPR020588: DNA recombination and repair protein RecA-like, ATP-binding domain; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop co [illegible]	[illegible]
comp29478_c0_seq3.p1	Ec-07_002230.2	Casein kinase (serine/threonine/tyrosine protein kinase)	GO:0016772	PTHR11909: ; PTHR11909:SF19: ; IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; [illegible]	[illegible]
comp33154_c1_seq16.p1	Ec-07_002240.1	expressed unknown protein	n/a;n/a;n/a	SSF101447: ; Coil:	[illegible]
comp45487_c0_seq1.p1	Ec-07_002280.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp31531_c2_seq1.p1	Ec-07_002290.1	Beta-(1,2)-xylosyltransferase	GO:0016757	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp30923_c0_seq1.p1	Ec-07_002300.1	Folylpolyglutamate synthetase	GO:0004326;GO:0005524;GO:0009396	PTHR11136:SF0: ; IPR018109: Folylpolyglutamate synthetase, conserved site; IPR013221: Mur ligase, central; IPR004101: Mur ligase, C-terminal; IPR [illegible]	[illegible]
comp4322_c0_seq1.p1	Ec-07_002310.2	EF-hand domain pair	GO:0005509	PTHR23056:SF4: ; IPR018247: EF-Hand 1, calcium-binding site; SIGNAL_PEPTIDE: Signal peptide region; IPR011992: EF-hand domain pair; IPR00 [illegible]	[illegible]
comp25551_c0_seq1.p1	Ec-07_002390.1	ribulose-phosphate 3-epimerase	GO:0008152;GO:0016857;GO:0003824;GO:0005975	IPR013785: Aldolase-type TIM barrel; IPR000056: Ribulose-phosphate 3-epimerase-like; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region [illegible]	[illegible]
comp20982_c0_seq1.p1	Ec-07_002400.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp25024_c0_seq3.p1	Ec-07_002410.1	flagellar associated protein, transcriptional coactivator-like protein	GO:0043565	IPR010982: Lambda repressor-like, DNA-binding domain; IPR001387: Cro/C1-type helix-turn-helix domain; IPR013729: Multiprotein bridging factor 1, [illegible]	[illegible]
comp30233_c0_seq3.p1	Ec-07_002420.1	Mtg1, mitochondrial YlqF-like GTPase	GO:0005622;GO:0005525	PTHR11089: ; IPR003593: AAA+ ATPase domain; IPR006073: GTP binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase [illegible]	[illegible]
comp24658_c1_seq2.p1	Ec-07_002430.1	SGNH hydrolase-type esterase domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp32990_c0_seq12.p1	Ec-07_002470.1	Mitochondrial import inner membrane translocase subunit TIM16 homolog	GO:0031072	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF03656: P [illegible]	[illegible]
comp31499_c0_seq1.p1	Ec-07_002490.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noT [illegible]	[illegible]
comp32014_c0_seq10.p1	Ec-07_002500.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp20968_c0_seq1.p1	Ec-07_002510.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_ [illegible]	[illegible]
comp16657_c0_seq1.p1	Ec-07_002520.1	Acetyltransferase (GNAT) domain protein	n/a;n/a;n/a	NA	[illegible]
comp22199_c0_seq3.p1	Ec-07_002530.1	Tyrosinase copper-binding domain	GO:0008152;GO:0016491	IPR002227: Tyrosinase copper-binding domain; IPR008922: Uncharacterised domain, di-copper centre	[illegible]
comp32167_c1_seq3.p1	Ec-07_002540.1	testis secretory pathway calcium transporting ATPase	GO:0005524;GO:0006754;GO:0006812;GO:0015662;GO:0016020	IPR023298: P-type ATPase, transmembrane domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR00 [illegible]	[illegible]
comp19923_c0_seq2.p2	Ec-07_002550.1	Non-haem dioxygenase N-terminal domain	GO:0016491;n/a	SSF51197: ; IPR027443: Isopenicillin N synthase-like; IPR005123: Oxoglutarate/iron-dependent dioxygenase; PTHR10209: ; IPR026992: Non-haem di [illegible]	[illegible]

comp33006_c1_seq16.p1	Ec-07_002600.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30971_c0_seq6.p1	Ec-07_002620.1	Hypothetical leucine rich repeat protein	NA	G3DSA:3.80.10.10: ; SSF52058: ; PTHR24420:	NA
comp27949_c0_seq1.p1	Ec-07_002730.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp87031_c0_seq1.p1	Ec-07_002750.3	hypothetical protein	n/a;n/a;n/a	NA	NA
comp24233_c0_seq2.p1	Ec-07_002760.1	Lipase maturation factor	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009613: Lipase maturation factor; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR14463:	NA
comp34113_c0_seq1.p1	Ec-07_002770.2	Ankyrin repeat	GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; IPR002110: Ankyrin repeat	NA
comp30318_c0_seq2.p1	Ec-07_002790.1	U3 small nucleolar ribonucleoprotein complex, subunit Mpp10p	GO:0005634;GO:0006364;GO:0030529	PTHR17039:SF0: ; IPR012173: U3 small nucleolar ribonucleoprotein complex, subunit Mpp10	NA
comp26741_c0_seq2.p1	Ec-07_002810.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp21603_c0_seq3.p1	Ec-07_002820.1	Domain of unknown function DUF4098	n/a;n/a;n/a	IPR025386: Domain of unknown function DUF4098	NA
comp30318_c0_seq2.p2	Ec-07_002830.1	Ribosomal protein S5, C-terminal	GO:0005840;GO:0003723;GO:0006412;GO:0003735	IPR014720: Double-stranded RNA-binding domain; IPR005324: Ribosomal protein S5, C-terminal; IPR020568: Ribosomal protein S5 domain 2-type fold; SSF54768: ; IPR000851: Ribosomal protein S5; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup; IPR013810: Ribosomal protein S5, N-terminal	NA
comp32231_c0_seq2.p1	Ec-07_002870.1	SDH4, succinate dehydrogenase subunit 4	GO:0005740;GO:0020037;GO:0005506;GO:0006118;GO:0006099;GO:0016021	SSF81343: ; PF05328: CybS; IPR007992: Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, CybS; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1300.10: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG4097
comp32424_c0_seq2.p1	Ec-07_002880.1	putative tyrosine kinase-like protein	GO:0004672;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; SIGNAL_PEPTIDE: Signal peptide region; IPR001245: Serine-threonine/tyrosine-protein kinase catalytic domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR23257: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000719: Protein kinase domain; SignalP-noTM: ; G3DSA:1.10.510.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26060_c0_seq3.p1	Ec-07_002900.1	Domain of unknown function DUF221	GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR13018: ; IPR003864: Domain of unknown function DUF221; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF13967: Late exocytosis, associated with Golgi transport	NA
comp32124_c1_seq2.p1	Ec-07_002910.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28372_c0_seq1.p1	Ec-07_002920.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21517_c0_seq3.p1	Ec-07_002930.1	Uncharacterised protein family UPF0118	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002549: Uncharacterised protein family UPF0118; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33835_c0_seq1.p1	Ec-07_002950.1	Uncharacterised protein family UPF0246	n/a;n/a;n/a	PTHR30283: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR005583: Uncharacterised protein family UPF0246; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12009_c0_seq1.p1	Ec-07_002960.1	FAM177 family	n/a;n/a;n/a	IPR028260: FAM177 family; Coil:	NA
comp12103_c0_seq1.p1	Ec-07_002970.1	Zinc finger, CCCH-type	GO:0046872;GO:0000166	SSF54928: ; IPR000571: Zinc finger, CCCH-type; PTHR14089: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; SSF90229:	NA
comp25355_c0_seq2.p1	Ec-07_002990.1	Chaperonin Cpn10	GO:0005737;GO:0006457	IPR020818: Chaperonin Cpn10; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011032: GroES (chaperonin 10)-like; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27276_c0_seq3.p1	Ec-07_003010.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp24925_c0_seq2.p1	Ec-07_003020.1	SET domain protein	GO:0005515	NA	NA
comp33074_c3_seq17.p1	Ec-07_003040.1	Flavodoxin-like fold	GO:0006118;GO:0009055;GO:0016491;GO:0050662	PTHR10204: ; IPR003680: Flavodoxin-like fold; IPR029039: Flavoprotein-like	NA
comp32621_c0_seq9.p2	Ec-07_003050.1	Putative subunit of the Anaphase Promoting Complex	n/a;n/a;n/a	PTHR11210: ; IPR024991: Anaphase-promoting complex subunit 11; SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type	KOG1493
comp12774_c0_seq1.p1	Ec-07_003070.1	ATPase, F1 complex, delta/epsilon subunit	GO:0045261;GO:0015986;GO:0046961;GO:0046933	IPR020546: ATPase, F1 complex, delta/epsilon subunit, N-terminal; IPR001469: ATPase, F1 complex, delta/epsilon subunit	NA
comp12791_c0_seq1.p1	Ec-07_003080.1	ATPase, F1 complex beta subunit/V1 complex, C-terminal	GO:0015078;GO:0015986;GO:0016469;GO:0016820;GO:0033178	IPR000793: ATPase, F1/V1/A1 complex, alpha/beta subunit, C-terminal; IPR004100: ATPase, F1 complex alpha/beta subunit, N-terminal domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; IPR020003: ATPase, alpha/beta subunit, nucleotide-binding domain, active site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000194: ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain; PIRSF039072: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:2.40.10.170: ; IPR005722: ATPase, F1 complex, beta subunit; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003593: AAA+ ATPase domain; PTHR15184: ; SignalP-noTM: ; IPR024034: ATPase, F1 complex beta subunit/V1 complex, C-terminal	NA
comp24151_c0_seq2.p1	Ec-07_003110.2	conserved unknown protein	NA	IPR011990: Tetratricopeptide-like helical domain; PTHR15696: ; Coil: ; PTHR15696:SF0: ; IPR018834: DNA/RNA-binding domain, Est1-type	NA
comp30445_c0_seq3.p1	Ec-07_003120.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp28385_c0_seq7.p1	Ec-07_003140.1	Uncharacterised protein family UPF0454	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR019352: Uncharacterised protein family UPF0454; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34351_c0_seq1.p1	Ec-07_003150.1	SR RNA splicing protein	GO:0003676;GO:0000166	NA	NA
comp28385_c0_seq7.p2	Ec-07_003160.1	CBS domain	n/a;n/a;n/a	G3DSA:3.10.580.10: ; IPR000644: CBS domain; SSF54631: ; PTHR11911: ; SignalP-TM:	NA
comp12922_c0_seq2.p1	Ec-07_003170.1	WD40-repeat-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR11024:	NA
comp30389_c2_seq2.p1	Ec-07_003200.1	Hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp33805_c0_seq1.p1	Ec-07_003240.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28088_c0_seq2.p2	Ec-07_003250.1	hypothetical protein	GO:0003677;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32779_c0_seq3.p1	Ec-07_003290.1	Protein of unknown function DUF389	n/a;n/a;n/a	PTHR20992: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR005240: Protein of unknown function DUF389; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30556_c0_seq2.p1	Ec-07_003330.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp17178_c0_seq2.p1	Ec-07_003350.1	TRAM/LAG1/CLN8 homology domain	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR016439: Ceramide synthase component Lag1/Lac1; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006634: TRAM/LAG1/CLN8 homology domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25721_c0_seq7.p1	Ec-07_003370.1	Zinc finger, RING-type	GO:0005515;GO:0008270	PTHR11224: ; IPR000571: Zinc finger, CCCH-type; IPR017907: Zinc finger, RING-type, conserved site; SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; SSF90229:	NA
comp24499_c1_seq1.p1	Ec-07_003390.1	Zinc finger, B-box	GO:0005622;GO:0008270	IPR018553: Protein of unknown function DUF2009; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR31560: ; IPR000315: Zinc finger, B-box	NA
comp27083_c0_seq1.p1	Ec-07_003400.1	KRR1 interacting protein 1	n/a;n/a;n/a	IPR018034: KRR1 interacting protein 1; IPR024626: Kri1-like, C-terminal; Coil:	NA
comp32507_c0_seq3.p1	Ec-07_003430.1	hypothetical protein	n/a;n/a;n/a	IPR031794: Hyaluronan-mediated motility receptor, C-terminal; Coil:	NA
comp32135_c1_seq8.p2	Ec-07_003470.1	PPPDE putative peptidase domain	n/a;n/a;n/a	PTHR12378: ; IPR008580: PPPDE putative peptidase domain	NA
comp32135_c1_seq8.p1	Ec-07_003480.1	putative aspartate carbamoyltransferase	GO:0004070;GO:0006207	IPR006132: Aspartate/ornithine carbamoyltransferase, carbamoyl-P binding; IPR006130: Aspartate/ornithine carbamoyltransferase; PTHR11405: ; IPR002082: Aspartate carbamoyltransferase; IPR006131: Aspartate/ornithine carbamoyltransferase, Asp/Orn-binding domain	KOG0370
comp32605_c1_seq5.p1	Ec-07_003490.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp20853_c0_seq2.p1	Ec-07_003530.1	WD40 repeat	GO:0005515	PTHR22847: ; IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp29147_c0_seq1.p1	Ec-07_003570.1	AGC family protein kinase	GO:0004672;GO:0005524;GO:0006468	PTHR24356: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR001849: Pleckstrin homology domain; IPR000961: AGC-kinase, C-terminal; IPR000719: Protein kinase domain; IPR011993: PH domain-like; G3DSA:1.10.510.10: ; Coil:	NA
comp28622_c0_seq2.p1	Ec-07_003580.1	Domain of unknown function DUF1336	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR12136: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009769: Domain of unknown function DUF1336; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp16330_c0_seq1.p1	Ec-07_003590.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020	PTHR24089: ; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023395: Mitochondrial carrier domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR018108: Mitochondrial substrate/solute carrier	NA
comp31986_c0_seq5.p1	Ec-07_003600.1	WD40 repeat	GO:0005515	PTHR14107:SF16: ; PTHR14107: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp30827_c0_seq13.p1	Ec-07_003620.1	C2H2 and CCCH zinc finger protein	GO:0046872	IPR015880: Zinc finger, C2H2-like; IPR000571: Zinc finger, CCCH-type; PTHR21354:SF0: ; PTHR21354: ; IPR007087: Zinc finger, C2H2	KOG4173
comp30576_c0_seq1.p1	Ec-07_003640.1	RNA polymerase, subunit H/Rpb5 C-terminal	GO:0003677;GO:0003899;GO:0006351	IPR020609: Archaeal RpoH /eukaryotic RPB5 RNA polymerase subunit; IPR005571: RNA polymerase, Rpb5, N-terminal; IPR000783: RNA polymerase, subunit H/Rpb5 C-terminal; IPR014381: DNA-directed RNA polymerase RPB5 subunit, eukaryote/virus; PTHR10535:	NA
comp11327_c0_seq2.p1	Ec-07_003650.1	Tim17/22-like protein	GO:0005743;GO:0008565;GO:0015031	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30249_c0_seq2.p1	Ec-07_003670.1	Polyketide Synthase III	GO:0008152;GO:0003824	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR016038: Thiolase-like, subgroup; IPR001099: Chalcone/stilbene synthase, N-terminal; IPR016039: Thiolase-like; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11877: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR012328: Chalcone/stilbene synthase, C-terminal	NA
comp26968_c0_seq1.p1	Ec-07_003680.1	Adenylate kinase/UMP-CMP kinase	GO:0005524;GO:0006139;GO:0019205	IPR018247: EF-Hand 1, calcium-binding site; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SSF47473: ; IPR000850: Adenylate kinase/UMP-CMP kinase; PF00406: Adenylate kinase; PF13833: EF-hand domain pair	NA
comp29138_c0_seq2.p3	Ec-07_003700.1	Beta-lactamase-like	n/a;n/a;n/a	PTHR36142:SF2: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001279: Metallo-beta-lactamase; PTHR36142: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13483: Beta-lactamase superfamily domain; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20512_c0_seq2.p1	Ec-07_003730.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp24282_c0_seq1.p1	Ec-07_003740.1	Ribosomal protein S5/S7, eukaryotic/archaeal	GO:0003735;GO:0006412;GO:0015935	IPR020606: Ribosomal protein S7, conserved site; IPR005716: Ribosomal protein S5/S7, eukaryotic/archaeal; IPR000235: Ribosomal protein S5/S7; IPR023798: Ribosomal protein S7 domain	NA
comp32777_c2_seq18.p1	Ec-07_003750.1	Major facilitator superfamily	GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24003: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; Coil: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25959_c0_seq1.p1	Ec-07_003760.2	Kelch-type beta propeller	GO:0005515	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF117281: ; SIGNAL_PEPTIDE: Signal peptide region; PF13418: Galactose oxidase, central domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR23244: ; PF13415: Galactose oxidase, central domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015915: Kelch-type beta propeller; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25095_c0_seq1.p1	Ec-07_003770.1	Isoprenylcysteine carboxyl methyltransferase	GO:0005783;GO:0016021;GO:0006481;GO:0004671	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR12714: ; IPR007269: Isoprenylcysteine carboxyl methyltransferase; IPR025770: Protein-S-isoprenylcysteine O-methyltransferase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27147_c0_seq1.p1	Ec-07_003800.1	Hypothetical inner membrane leucine rich repeat protein	GO:0005515;GO:0016021;GO:0019835	IPR005744: Hly-III; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF52047: ; IPR001611: Leucine-rich repeat; IPR032675: Leucine-rich repeat domain, L domain-like; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004254: AdipoR/Haemolysin-III-related; SM00368:	NA
comp29138_c0_seq2.p1	Ec-07_003810.1	DEAD box helicase	GO:0003676;GO:0005524	IPR014014: RNA helicase, DEAD-box type, Q motif; IPR011545: DEAD/DEAH box helicase domain; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001650: Helicase, C-terminal; PTHR24031:	KOG0347
comp87015_c0_seq1.p1	Ec-07_003830.1	MAPK related serine/threonine protein kinase	GO:0005524;GO:0006468;GO:0004672	PTHR24055: ; IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain	KOG0661
comp30928_c1_seq1.p2	Ec-07_003880.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp29211_c0_seq1.p1	Ec-07_003910.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp25666_c0_seq2.p1	Ec-07_003920.1	tRNA-splicing endonuclease, subunit Sen54, N-terminal	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR024336: tRNA-splicing endonuclease, subunit Sen54, N-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30896_c1_seq8.p2	Ec-07_003930.1	Dynein light chain, type 1/2	GO:0005875;GO:0007017	IPR019763: Dynein light chain, type 1/2, conserved site; SSF54648: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001372: Dynein light chain, type 1/2	NA
comp30896_c1_seq5.p1	Ec-07_003940.1	EF-hand domain pair	n/a;n/a;n/a	IPR011992: EF-hand domain pair; SSF47473:	NA
comp32177_c4_seq6.p2	Ec-07_003960.1	PQ-loop repeat	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006603: PQ-loop repeat; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27308_c0_seq2.p2	Ec-07_003990.1	PQ-loop repeat	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006603: PQ-loop repeat; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21138_c0_seq1.p1	Ec-07_004020.1	Ubiquitin/SUMO-activating enzyme E1	GO:0008641;GO:0006464	PTHR10953: ; IPR009036: Molybdenum cofactor biosynthesis, MoeB; IPR000594: UBA/THIF-type NAD/FAD binding fold; IPR016040: NAD(P)-binding domain; IPR000011: Ubiquitin/SUMO-activating enzyme E1	NA
comp34233_c0_seq1.p1	Ec-07_004030.1	DRG1, developmentally regulated GTPase 1	n/a;GO:0005622;GO:0005525	IPR031167: OBG-type guanine nucleotide-binding (G) domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR11702: ; IPR005225: Small GTP-binding protein domain; IPR012676: TGS-like; IPR004095: TGS; IPR006073: GTP binding domain; IPR006074: GTP1/OBG, conserved site; Coil:	NA
comp25491_c0_seq1.p1	Ec-07_004060.3	UBA-like	GO:0005515	G3DSA:1.10.8.10: ; IPR003892: Ubiquitin system component Cue; IPR009060: UBA-like	NA
comp32880_c0_seq9.p2	Ec-07_004070.1	S-phase kinase-associated protein 1-like	GO:0006511	IPR016897: S-phase kinase-associated protein 1; IPR016072: SKP1 component, dimerisation; PTHR11165: ; IPR001232: S-phase kinase-associated protein 1-like; IPR011333: BTB/POZ fold; G3DSA:3.30.710.10: ; IPR016073: SKP1 component, POZ domain	NA
comp31321_c0_seq11.p1	Ec-07_004090.2	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR22840: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp11839_c0_seq1.p1	Ec-07_004100.2	Acyl-CoA N-acyltransferase	n/a;n/a;n/a	IPR016181: Acyl-CoA N-acyltransferase	NA
comp20045_c0_seq1.p1	Ec-07_004110.1	Aminomethyltransferase	GO:0005960;GO:0006546;GO:0005737;GO:0004375;GO:0005515;GO:0004047	PTHR13847: ; SSF103025: ; IPR028896: Aminomethyltransferase/Dimethylsulfoniopropionate demethylase DmdA; IPR006222: Glycine cleavage T-protein-like, N-terminal; IPR027266: GTP-binding protein TrmE/Glycine cleavage system T protein, domain 1; G3DSA:3.30.70.1400: ; IPR006223: Glycine cleavage system T protein; IPR029043: Glycine cleavage T-protein/YgfZ, C-terminal domain; IPR013977: Glycine cleavage T-protein, C-terminal barrel domain	KOG2770
comp27520_c1_seq1.p1	Ec-07_004120.1	Glycine cleavage system H protein	GO:0005960;GO:0019464	G3DSA:2.40.50.100: ; IPR003016: 2-oxo acid dehydrogenase, lipoyl-binding site; IPR011053: Single hybrid motif; IPR000089: Biotin/lipoyl attachment; IPR002930: Glycine cleavage system H-protein; IPR017453: Glycine cleavage system H-protein, subgroup; SignalP-TM:	KOG3373
comp12529_c0_seq1.p1	Ec-07_004160.1	Tryptophan RNA-binding attenuator protein-like domain	n/a;n/a;n/a	IPR002838: Mitochondrial biogenesis protein AIM24; PTHR31801: ; PTHR31801:SF3: ; SignalP-TM: ; IPR016031: Tryptophan RNA-binding attenuator protein-like domain	NA
comp29837_c0_seq3.p1	Ec-07_004170.1	Hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31844_c0_seq2.p1	Ec-07_004190.1	Thioredoxin-like fold	n/a;n/a;n/a	PTHR21148:SF25: ; PTHR21148: ; Coil: ; IPR013766: Thioredoxin domain; IPR012336: Thioredoxin-like fold	NA
comp41197_c0_seq1.p1	Ec-07_004200.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR000048: IQ motif, EF-hand binding site	NA
comp20703_c0_seq2.p1	Ec-07_004220.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26124_c0_seq1.p3	Ec-07_004230.1	Oligosaccharyltransferase, DAD1 subunit (or epsilon subunit)	GO:0004579;GO:0008250;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR003038: DAD/Ost2; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1746
comp26124_c0_seq1.p1	Ec-07_004240.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp32196_c0_seq9.p1	Ec-07_004260.1	Ankyrin repeat-containing domain	n/a;GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020683: Ankyrin repeat-containing domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002110: Ankyrin repeat; PTHR24188: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28170_c0_seq2.p1	Ec-07_004270.1	Protein of unknown function DUF1294	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR010718: Protein of unknown function DUF1294; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27001_c0_seq2.p1	Ec-07_004310.1	hypothetical protein	GO:0005622;GO:0008270	SSF90209: ; IPR001876: Zinc finger, RanBP2-type	NA
comp28861_c0_seq1.p1	Ec-07_004320.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp31030_c0_seq5.p3	Ec-07_004340.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; PTHR24031:SF125: ; IPR000629: ATP-dependent RNA helicase DEAD-box, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR24031: ; IPR014014: RNA helicase, DEAD-box type, Q motif; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal	KOG0339
comp29893_c0_seq1.p1	Ec-07_004330.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp21438_c0_seq2.p1	Ec-07_004350.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21573_c0_seq2.p1	Ec-07_004360.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp29203_c1_seq2.p1	Ec-07_004370.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29203_c1_seq3.p1	Ec-07_004370.2	hypothetical protein	n/a;n/a;n/a	NA	NA
comp27740_c0_seq1.p1	Ec-07_004400.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp27257_c0_seq2.p1	Ec-07_004410.1	K Homology domain, type 1	GO:0003723	IPR004087: K Homology domain; IPR004088: K Homology domain, type 1; PTHR10288:	NA
comp21573_c0_seq4.p1	Ec-07_004420.1	eukaryotic initiation factor 4G	GO:0005515;GO:0016070	IPR003891: Initiation factor eIF-4 gamma, MA3; PTHR23253: ; IPR016024: Armadillo-type fold; IPR003890: MIF4G-like, type 3; IPR016021: MIF4G-like domain	NA
comp27982_c0_seq3.p1	Ec-07_004450.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp22783_c0_seq1.p1	Ec-07_004460.5	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30905_c0_seq3.p1	Ec-07_004480.1	Sodium/hydrogen exchanger family protein	GO:0055085;GO:0015299;GO:0006812;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018422: Cation/H+ exchanger, CPA1 family; IPR006153: Cation/H+ exchanger; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32203_c1_seq14.p1	Ec-07_004490.1	Beta-lactamase-like	n/a;n/a;n/a	IPR011108: RNA-metabolising metallo-beta-lactamase; IPR022712: Beta-Casp domain; PTHR11203: ; IPR001279: Beta-lactamase-like; IPR021718: Pre-mRNA 3'-end-processing endonuclease polyadenylation factor C-term	NA
comp26794_c0_seq1.p2	Ec-07_004540.1	Nicotinamide N-methyltransferase-like	n/a;n/a;n/a	PTHR23109: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR019410: Nicotinamide N-methyltransferase-like	NA
comp86616_c0_seq1.p1	Ec-07_004550.1	RmlC-like jelly roll fold	n/a;n/a;n/a	IPR000595: Cyclic nucleotide-binding domain; PTHR24353: ; IPR018488: Cyclic nucleotide-binding, conserved site; IPR018490: Cyclic nucleotide-binding-like; IPR014710: RmlC-like jelly roll fold	NA
comp32499_c0_seq4.p1	Ec-07_004610.1	carbonic anhydrase	GO:0008415;GO:0016740	PTHR13061: ; IPR011004: Trimeric LpxA-like; IPR001451: Bacterial transferase hexapeptide repeat; G3DSA:2.160.10.10:	NA
comp29862_c0_seq2.p1	Ec-07_004630.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28677_c0_seq1.p1	Ec-07_004640.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	IPR017907: Zinc finger, RING-type, conserved site; IPR001841: Zinc finger, RING-type; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR15860: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20900_c0_seq1.p1	Ec-07_004660.1	expressed unknown protein	GO:0006508;GO:0008237;GO:0008270	NA	NA
comp32361_c0_seq9.p1	Ec-07_004670.1	Armadillo-like helical	GO:0005524;GO:0005488;GO:0016887	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR022125: U3 small nucleolar RNA-associated protein 10; IPR011989: Armadillo-like helical; IPR012954: BP28, C-terminal domain; IPR016024: Armadillo-type fold; PTHR13457: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29684_c0_seq3.p1	Ec-07_004730.1	SET domain protein	GO:0005515	IPR001214: SET domain; G3DSA:2.170.270.10: ; PTHR12197: ; mobidb-lite: consensus disorder prediction; SSF82199:	NA
comp20310_c0_seq1.p1	Ec-07_004770.1	conserved unknown protein	GO:0005488	IPR019312: Protein of unknown function DUF2363	NA
comp19225_c0_seq2.p1	Ec-07_004780.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp37767_c0_seq1.p1	Ec-07_004800.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30824_c0_seq1.p1	Ec-07_004810.1	RNA binding protein, homologue of TOUGH	GO:0005622;GO:0003676	IPR011666: Domain of unknown function DUF1604; IPR000467: G-patch domain; PTHR13384:	NA
comp30824_c0_seq1.p2	Ec-07_004820.1	Stress-activated map kinase interacting 1	n/a;n/a;n/a	IPR008828: Stress-activated map kinase interacting 1	NA
comp32610_c0_seq6.p1	Ec-07_004830.2	CTP-phosphoethanolamine cytidylyltransferase	GO:0009058;GO:0016779	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; IPR004821: Cytidyltransferase-like domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF52374: ; Coil: ; PTHR10739: ; PTHR10739:SF23: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2803
comp26005_c0_seq1.p1	Ec-07_004840.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; PTHR14027: ; PF13374: Tetratricopeptide repeat; IPR031101: RNA polymerase-associated protein Ctr9; IPR013105: Tetratricopeptide TPR2; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; Coil: ; IPR019734: Tetratricopeptide repeat	NA
comp35071_c0_seq1.p1	Ec-07_004850.1	Modifier of rudimentary, Modr	n/a;n/a;n/a	PTHR13678: ; IPR009851: Modifier of rudimentary, Modr	NA
comp28018_c0_seq4.p1	Ec-07_004870.1	ESCRT-II complex, Vps25 subunit, N-terminal winged helix	n/a;n/a;n/a	PTHR13149:SF0: ; IPR011991: Winged helix-turn-helix DNA-binding domain; IPR014041: ESCRT-II complex, Vps25 subunit, N-terminal winged helix; IPR008570: ESCRT-II complex, vps25 subunit	NA
comp31870_c1_seq3.p1	Ec-07_004900.1	WD40 repeat	GO:0005515	IPR000409: BEACH domain; IPR001680: WD40 repeat; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR13743: ; IPR031570: Domain of unknown function DUF4704; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011993: PH domain-like; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR023362: PH-BEACH domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31870_c1_seq3.p2	Ec-07_004910.1	epimerase/dehydrogenase	GO:0003824;GO:0005488;GO:0008152	SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; PTHR15020: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PF13460: NAD(P)H-binding	KOG1203
comp29242_c0_seq3.p1	Ec-07_004930.3	Protein of unknown function DUF4281	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR34543: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR025461: Protein of unknown function DUF4281	NA
comp20279_c0_seq1.p2	Ec-07_004940.1	CTAG/Pcc1 family	n/a;n/a;n/a	PTHR31283: ; IPR015419: CTAG/Pcc1 family	NA
comp14935_c0_seq1.p1	Ec-07_004980.1	FK506-binding protein 3 (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase)	GO:0006457	SSF54534: ; G3DSA:3.10.50.40: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023566: Peptidyl-prolyl cis-trans isomerase, FKBP-type; IPR001179: Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0552
comp102136_c0_seq1.p1	Ec-07_004990.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp20768_c0_seq1.p1	Ec-07_005000.2	expressed unknown protein	GO:0005215;GO:0006810;GO:0016020;GO:0055085	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30557_c0_seq3.p1	Ec-07_005010.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30557_c0_seq3.p2	Ec-07_005020.1	TatD family	GO:0016888	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR018228: Deoxyribonuclease, TatD-related, conserved site; IPR001130: TatD family; SSF51556: ; G3DSA:3.20.20.140: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21415_c0_seq3.p1	Ec-07_005030.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31678_c0_seq5.p1	Ec-07_005040.1	Tryptophan RNA-binding attenuator protein-like domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR002838: Mitochondrial biogenesis protein AIM24; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR31801: ; IPR016031: Tryptophan RNA-binding attenuator protein-like domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30851_c0_seq1.p1	Ec-07_005050.1	Amidophosphoribosyltransferase	GO:0004044;GO:0009064	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR029057: Phosphoribosyltransferase-like; PTHR11907:SF0: ; IPR000836: Phosphoribosyltransferase domain; IPR005854: Amidophosphoribosyltransferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029055: Nucleophile aminohydrolases, N-terminal; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PF13522: Glutamine amidotransferase domain; IPR017932: Glutamine amidotransferase type 2 domain; PTHR11907:	KOG0572
comp33050_c0_seq1.p1	Ec-07_005060.1	GOLD	GO:0006810;GO:0016021	Coil: ; IPR009038: GOLD; PTHR22324:	NA
comp32862_c0_seq7.p1	Ec-07_005070.1	MORN motif	n/a;n/a;n/a	G3DSA:2.20.110.10: ; PTHR23084: ; PTHR23084:SF143: ; SSF82185: ; IPR003409: MORN motif	NA
comp33045_c1_seq11.p1	Ec-07_005080.1	Methyltransferase type 11	GO:0008152;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR10108: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013216: Methyltransferase type 11	NA
comp34106_c0_seq1.p1	Ec-07_005110.1	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	GO:0006457	SSF54534: ; G3DSA:3.10.50.40: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023566: Peptidyl-prolyl cis-trans isomerase, FKBP-type; IPR001179: Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0552
comp28983_c0_seq2.p1	Ec-07_005120.1	hypothetical protein	GO:0005488	IPR016024: Armadillo-type fold; Coil:	NA
comp12479_c0_seq1.p1	Ec-07_005130.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp20261_c0_seq2.p2	Ec-07_005140.1	PEra, plastid Era GTPase	GO:0005525;GO:0005622;n/a	IPR009019: K homology domain, prokaryotic type; SIGNAL_PEPTIDE: Signal peptide region; IPR005662: GTP-binding protein Era; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR030388: Era-type guanine nucleotide-binding (G) domain; IPR004044: K Homology domain, type 2; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005225: Small GTP-binding protein domain; IPR006073: GTP binding domain; SignalP-noTM: ; IPR015946: K homology domain-like, alpha/beta; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11649:	NA
comp20261_c0_seq2.p1	Ec-07_005150.1	RNA recognition motif domain	GO:0003676;GO:0000166	SSF54928: ; PTHR23236: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp29297_c0_seq6.p1	Ec-07_005160.1	alpha-tubulin folding cofactor	n/a;n/a;n/a	G3DSA:3.10.20.90: ; IPR029071: Ubiquitin-related domain; IPR000626: Ubiquitin-like; IPR000938: CAP Gly-rich domain; PTHR18916:	KOG3206
comp32965_c0_seq2.p3	Ec-07_005180.1	TMEM220 protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR029377: TMEM220 protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32965_c0_seq2.p1	Ec-07_005190.1	WD40 repeat	GO:0005515	PTHR22847: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; PTHR22847:SF412: ; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; IPR020472: G-protein beta WD-40 repeat	NA
comp26565_c0_seq1.p1	Ec-07_005200.1	Trans-2-enoyl-CoA reductase, mitochondrial precursor	GO:0055114;GO:0008270;GO:0016491	SSF51735: ; IPR011032: GroES (chaperonin 10)-like; IPR020843: Polyketide synthase, enoylreductase; IPR016040: NAD(P)-binding domain; IPR013154: Alcohol dehydrogenase GroES-like; IPR013149: Alcohol dehydrogenase, C-terminal; IPR002085: Alcohol dehydrogenase superfamily, zinc-type	NA
comp24641_c0_seq1.p1	Ec-07_005220.1	Histidine phosphatase superfamily, clade-1	n/a;GO:0005524;GO:0006000;GO:0003873	IPR013078: Histidine phosphatase superfamily, clade-1; IPR003094: Fructose-2,6-bisphosphatase; IPR029033: Histidine phosphatase superfamily; PIRSF000709: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR013079: 6-phosphofructo-2-kinase	NA
comp29485_c0_seq3.p1	Ec-07_005240.1	Beta-glucosidase, family GH1	GO:0003824;GO:0043169;GO:0005975	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR017853: Glycoside hydrolase superfamily; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001360: Glycoside hydrolase, family 1; SignalP-noTM: ; IPR018120: Glycoside hydrolase, family 1, active site; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013781: Glycoside hydrolase, catalytic domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0626
comp32836_c1_seq1.p1	Ec-07_005250.1	expressed unknown protein	n/a;n/a;n/a	SSF140860:	NA
comp33389_c0_seq1.p1	Ec-07_005280.1	Zinc finger, RING-type	GO:0005515;GO:0008270	IPR001841: Zinc finger, RING-type; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; PF13920: Zinc finger, C3HC4 type (RING finger)	NA
comp26345_c0_seq2.p1	Ec-07_005290.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp28219_c0_seq1.p1	Ec-07_005300.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp31031_c0_seq6.p1	Ec-07_005310.1	Endo-1,4-beta-xylanase, family GH10	GO:0003824;GO:0043169;GO:0005975	PTHR31490: ; IPR001000: Glycoside hydrolase, family 10; IPR017853: Glycoside hydrolase superfamily; IPR013781: Glycoside hydrolase, catalytic domain	NA
comp29471_c0_seq2.p1	Ec-07_005320.1	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	n/a;n/a;n/a	IPR000408: Regulator of chromosome condensation, RCC1; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR22870: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II; SignalP-noTM: ; PF13540: Regulator of chromosome condensation (RCC1) repeat; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20077_c0_seq1.p1	Ec-07_005330.1	conserved unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11951_c0_seq1.p1	Ec-07_005340.1	50S ribosomal protein L25	GO:0006412	IPR020057: Ribosomal protein L25, beta domain; IPR020056: Ribosomal protein L25/Gln-tRNA synthetase, beta-barrel domain; IPR029751: Ribosomal protein L25; IPR011035: Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain	NA
comp26084_c0_seq1.p1	Ec-07_005410.1	Digalactosyldiacylglycerol synthase, family GT4	NA	SSF53756: ; Coil: ; PTHR12526:	no relat
comp24685_c0_seq2.p1	Ec-07_005420.1	chloroplast clp protease P	GO:0004252;GO:0006508;GO:0008462	IPR029045: ClpP/crotonase-like domain; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; IPR018215: ClpP, active site; IPR001907: ATP-dependent Clp protease proteolytic subunit; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023562: Clp protease proteolytic subunit /Translocation-enhancing protein TepA	NA
comp55248_c0_seq1.p1	Ec-07_005430.2	Ankyrin repeat protein	GO:0005515	SSF57850: ; IPR003613: U box domain; IPR020683: Ankyrin repeat-containing domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR24198: ; IPR002110: Ankyrin repeat	NA
comp34476_c0_seq1.p1	Ec-07_005440.1	Choline transporter-like	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007603: Choline transporter-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp23197_c0_seq3.p1	Ec-07_005450.1	Nucleophile aminohydrolases, N-terminal	n/a;GO:0051603;GO:0004298;GO:0005839	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001353: Proteasome, subunit alpha/beta; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000426: Proteasome alpha-subunit, N-terminal domain; IPR029055: Nucleophile aminohydrolases, N-terminal; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11599:	NA
comp31397_c0_seq6.p1	Ec-07_005460.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp28183_c0_seq1.p1	Ec-07_005470.1	Alpha/beta hydrolase fold-1	GO:0016787	IPR029058: Alpha/Beta hydrolase fold; IPR000073: Alpha/beta hydrolase fold-1; PTHR10992:	NA
comp27114_c0_seq3.p1	Ec-07_005490.1	cyclin D3	NA	IPR013763: Cyclin-like; IPR006671: Cyclin, N-terminal; PTHR10177:	KOG0653
comp3846_c0_seq1.p1	Ec-07_005520.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp12639_c0_seq1.p1	Ec-07_005530.1	expressed unknown protein	GO:0009523;GO:0016021;GO:0019684	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28011_c0_seq2.p1	Ec-07_005540.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-noTM: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp26330_c0_seq1.p1	Ec-07_005560.3	Arginine biosynthesis bifunctional protein ArgJ	NA	IPR002813: Arginine biosynthesis protein ArgJ; SIGNAL_PEPTIDE: Signal peptide region; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR23100:SF0: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PD004193: ACETYLTRANSFERASE ORNITHINE ARGININE BIOSYNTHESIS ARGJ GLUTAMATE N-ACETYLTRANSFERASE TRANSFERASE ACY; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR016117: ArgJ-like domain	KOG2786
comp33361_c0_seq1.p1	Ec-07_005600.1	Short-chain dehydrogenase/reductase SDR	GO:0008152;GO:0016491	SSF51735: ; PTHR24322: ; IPR020904: Short-chain dehydrogenase/reductase, conserved site; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32484_c0_seq2.p1	Ec-07_005620.1	mRNA decapping complex protein	NA	PTHR16290:SF0: ; IPR011993: PH domain-like; Coil: ; IPR010334: mRNA-decapping enzyme subunit 1	NA
comp32869_c0_seq4.p1	Ec-07_005640.1	Tyrosinase copper-binding domain	GO:0008152;GO:0016491	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR008922: Uncharacterised domain, di-copper centre; IPR002227: Tyrosinase copper-binding domain; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31875_c0_seq1.p1	Ec-07_005660.1	Saccharopine dehydrogenase	GO:0003824;GO:0004753;GO:0005488;GO:0006553;GO:0008152	SSF51735: ; IPR005097: Saccharopine dehydrogenase / Homospermidine synthase; IPR016040: NAD(P)-binding domain; PTHR12286:	KOG2733
comp28172_c0_seq1.p1	Ec-07_005670.1	Light harvesting complex protein	GO:0005524;GO:0009765;GO:0016020;GO:0016887	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR022796: Chlorophyll A-B binding protein; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023329: Chlorophyll a/b binding protein domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001344: Chlorophyll A-B binding protein, plant; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26757_c0_seq4.p1	Ec-07_005740.1	Cyclin-like	n/a;n/a;n/a	IPR013763: Cyclin-like; IPR006671: Cyclin, N-terminal; PTHR10177:	NA
comp45055_c0_seq1.p1	Ec-07_005760.1	RIB43A	n/a;n/a;n/a	Coil: ; IPR008805: RIB43A	NA
comp28711_c0_seq2.p1	Ec-07_005770.1	riboflavin biosynthesis protein	GO:0008835;GO:0008703;GO:0009231;GO:0055114	G3DSA:3.40.140.10: ; PTHR11079: ; SIGNAL_PEPTIDE: Signal peptide region; IPR024072: Dihydrofolate reductase-like domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR004794: Riboflavin biosynthesis protein RibD; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002125: Cytidine and deoxycytidylate deaminases, zinc-binding; IPR016193: Cytidine deaminase-like; IPR016192: APOBEC/CMP deaminase, zinc-binding; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31805_c0_seq4.p2	Ec-07_005800.1	Homologue of the meiosis-specific protein HOP1	GO:0007067	IPR003511: HORMA domain	KOG4652
comp31805_c0_seq4.p1	Ec-07_005810.1	Nicotinamide N-methyltransferase-like	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR019410: Nicotinamide N-methyltransferase-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR14614:	NA
comp19576_c0_seq1.p1	Ec-07_005820.1	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR22889: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp21379_c0_seq2.p1	Ec-07_005830.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31805_c0_seq4.p3	Ec-07_005840.1	PfkB-type carbohydrate kinase	GO:0004747;GO:0016773;GO:0006014	IPR011611: Carbohydrate kinase PfkB; IPR002139: Ribokinase; IPR002173: Carbohydrate/puine kinase, PfkB, conserved site; PTHR10584: ; IPR029056: Ribokinase-like	NA
comp32220_c0_seq3.p1	Ec-07_005850.1	Protein of unknown function DUF4539	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR028045: Protein of unknown function DUF4539; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30267_c0_seq5.p1	Ec-07_005880.1	HAD-like domain	GO:0005524;GO:0006754;GO:0006810;GO:0015662;GO:0016020	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF12710: haloacid dehalogenase-like hydrolase; IPR008250: P-type ATPase, A domain; IPR023299: P-type ATPase, cytoplasmic domain N; SSF81653: ; PTHR24093: ; IPR023214: HAD-like domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001757: P-type ATPase; SSF81665: ; Coil: ; IPR018303: P-type ATPase, phosphorylation site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29703_c1_seq3.p1	Ec-07_005890.1	serine hydroxymethyltransferase 2	GO:0003824;GO:0016740;GO:0030170	IPR015424: Pyridoxal phosphate-dependent transferase; IPR019798: Serine hydroxymethyltransferase, pyridoxal phosphate binding site; IPR001085: Serine hydroxymethyltransferase; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	NA
comp30544_c0_seq2.p2	Ec-07_005900.1	Histidine phosphatase superfamily, clade-1	GO:0003824;GO:0008152	IPR013078: Histidine phosphatase superfamily, clade-1; IPR001345: Phosphoglycerate/bisphosphoglycerate mutase, active site; IPR029033: Histidine phosphatase superfamily; PTHR23029:	NA
comp30544_c0_seq2.p1	Ec-07_005910.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp19660_c0_seq1.p1	Ec-07_005920.1	Zinc finger, RING/FYVE/PHD-type	GO:0008270	PTHR24007: ; IPR001607: Zinc finger, UBP-type; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; Coil:	NA
comp31273_c0_seq2.p1	Ec-07_005930.1	DNA ligase, ATP-dependent, N-terminal	GO:0003677;GO:0006281;GO:0005524;GO:0003910;GO:0071897;GO:0006310	IPR012340: Nucleic acid-binding, OB-fold; IPR012308: DNA ligase, ATP-dependent, N-terminal; IPR012310: DNA ligase, ATP-dependent, central; IPR016059: DNA ligase, ATP-dependent, conserved site; PTHR10459: ; G3DSA:3.30.470.30: ; Coil: ; IPR012309: DNA ligase, ATP-dependent, C-terminal; G3DSA:3.30.1490.70: ; IPR000977: DNA ligase, ATP-dependent; SSF56091:	NA
comp32721_c4_seq7.p1	Ec-07_005960.1	EF-hand domain pair	GO:0005509	IPR018247: EF-Hand 1, calcium-binding site; PTHR10891: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF47473: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003675: CAAX amino terminal protease; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32721_c4_seq7.p2	Ec-07_005970.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; IPR002110: Ankyrin repeat	NA
comp32721_c4_seq7.p5	Ec-07_005980.1	Nucleic acid-binding, OB-fold	GO:0000049	IPR012340: Nucleic acid-binding, OB-fold; IPR002547: tRNA-binding domain; PTHR11586:	NA
comp32721_c4_seq7.p6	Ec-07_006000.1	PDZ domain	GO:0005515	IPR001478: PDZ domain; Coil:	NA
comp33944_c0_seq1.p1	Ec-07_006010.1	Prolyl 4-hydroxylase, alpha subunit	GO:0005506;GO:0031418;GO:0055114;GO:0016705;GO:0016706;GO:0016491	IPR006620: Prolyl 4-hydroxylase, alpha subunit; IPR005123: Oxoglutarate/iron-dependent dioxygenase; PTHR10869:	NA
comp12391_c0_seq2.p1	Ec-07_006020.1	NUDIX hydrolase domain-like	GO:0016787	SIGNAL_PEPTIDE: Signal peptide region; IPR020084: NUDIX hydrolase, conserved site; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015797: NUDIX hydrolase domain-like; PTHR22769: ; IPR020476: NUDIX hydrolase; IPR003563: 7,8-dihydro-8-oxoguanine triphosphatase; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR000086: NUDIX hydrolase domain	NA
comp28056_c0_seq1.p1	Ec-07_006030.1	conserved hypothetical protei	n/a;n/a;n/a	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12391_c0_seq2.p2	Ec-07_006040.2	conserved unknown protein	n/a;n/a;n/a	PTHR12868:SF0: ; PTHR12868:	NA
comp34643_c0_seq1.p1	Ec-07_006050.1	Ribosomal protein L10e/L16	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR001197: Ribosomal protein L10e; PTHR11726: ; IPR016180: Ribosomal protein L10e/L16; IPR018255: Ribosomal protein L10e, conserved site	NA
comp32812_c0_seq3.p2	Ec-07_006060.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; Coil: ; IPR002110: Ankyrin repeat	NA
comp31820_c0_seq2.p1	Ec-07_006100.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PTHR24361: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10:	NA
comp28056_c0_seq1.p2	Ec-07_006150.1	FKBP-type peptidyl-prolyl cis-trans isomerase 11	GO:0006457	G3DSA:3.10.50.40: ; SSF54534: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023566: Peptidyl-prolyl cis-trans isomerase, FKBP-type; IPR001179: Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR000774: Peptidyl-prolyl cis-trans isomerase, FKBP-type, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0544
comp19540_c0_seq1.p1	Ec-07_006170.1	Cycloartenol synthase	GO:0003824	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11764: ; IPR018333: Squalene cyclase; IPR008930: Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR001330: Prenyltransferase/squalene oxidase	NA
comp34652_c0_seq1.p1	Ec-07_006200.1	Ribosomal protein S2, flavodoxin-like domain	GO:0015935;GO:0006412;GO:0003735	IPR001865: Ribosomal protein S2; IPR023591: Ribosomal protein S2, flavodoxin-like domain; IPR018130: Ribosomal protein S2, conserved site; PTHR12534: ; IPR005707: Ribosomal protein S2, eukaryotic/archaeal; IPR027498: Ribosomal protein S2, eukaryotic; G3DSA:3.40.50.10490:	NA
comp29579_c0_seq1.p1	Ec-07_006210.1	Pumilio RNA-binding repeat protein	GO:0005488	IPR001313: Pumilio RNA-binding repeat; IPR012959: CPL; IPR011989: Armadillo-like helical; PTHR13389: ; IPR016024: Armadillo-type fold; Coil:	NA
comp12532_c0_seq1.p1	Ec-07_006220.1	Coatomer protein complex, gamma sub-unit	GO:0030117;GO:0030130;GO:0005515;GO:0006461;GO:0006886;GO:0016192	IPR008152: Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdomain; IPR017107: Adaptor protein complex AP-1, gamma subunit; IPR011989: Armadillo-like helical; IPR008153: Clathrin adaptor, gamma-adaptin, appendage; PTHR22780: ; IPR002553: Clathrin/coatomer adaptor, adaptin-like, N-terminal; IPR016024: Armadillo-type fold; IPR013041: Coatomer/clathrin adaptor appendage, Ig-like subdomain	KOG1062
comp21989_c0_seq1.p1	Ec-07_006270.1	Homeodomain-like	GO:0003677	IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; IPR017877: Myb-like domain	NA
comp30719_c0_seq3.p1	Ec-07_006280.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp14623_c0_seq1.p1	Ec-07_006290.1	Vesicle transport protein, Use1	n/a;n/a;n/a	PTHR13050: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR019150: Vesicle transport protein, Use1; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:1.20.5.110: ; Coil: ; SSF58038: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29677_c0_seq1.p1	Ec-07_006310.1	SANT/Myb domain	GO:0003682	PTHR10641: ; IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; PTHR10641:SF221: ; Coil: ; IPR017930: Myb domain	NA
comp12576_c0_seq1.p1	Ec-07_006350.2	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp29338_c0_seq2.p1	Ec-07_006370.1	hypothetical protein	GO:0005515;GO:0005524;GO:0005737;GO:0006457;GO:0044267	PTHR22929:	NA
comp30164_c0_seq1.p1	Ec-07_006390.1	Hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp27205_c0_seq3.p1	Ec-07_006410.1	Adrenodoxin	GO:0009055;GO:0051537	IPR001041: 2Fe-2S ferredoxin-type domain; IPR001055: Adrenodoxin; IPR012675: Beta-grasp domain; PTHR23426:	NA
comp28877_c0_seq2.p1	Ec-07_006420.1	Atg6/Beclin	GO:0006914	Coil: ; IPR007243: Atg6/Beclin	NA
comp24143_c0_seq1.p1	Ec-07_006430.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp27146_c1_seq2.p1	Ec-07_006440.1	Translocation protein Sec62	GO:0008565;GO:0016021;GO:0015031	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR011991: Winged helix-turn-helix DNA-binding domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004728: Translocation protein Sec62; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28734_c0_seq3.p1	Ec-07_006470.2	Ankyrin repeat-containing domain	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp12173_c0_seq1.p1	Ec-07_006500.1	60S ribosomal protein L3	NA	IPR000597: Ribosomal protein L3; PTHR11363: ; IPR019926: Ribosomal protein L3, conserved site; G3DSA:2.40.30.10: ; IPR009000: Translation protein, beta-barrel domain; G3DSA:3.30.1430.10:	NA
comp28994_c0_seq2.p1	Ec-07_006520.1	ABC transporter-like	GO:0005524;GO:0016887	IPR003439: ABC transporter-like; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003593: AAA+ ATPase domain; PTHR24220: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31896_c0_seq3.p1	Ec-07_006530.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32933_c0_seq9.p1	Ec-07_006540.1	oxidoreductase, NAD-binding, myo-inositol 2-dehydrogenase	GO:0003824;GO:0005488;GO:0008152	IPR000683: Oxidoreductase, N-terminal; SSF51735: ; IPR004104: Oxidoreductase, C-terminal; G3DSA:3.30.360.10: ; IPR016040: NAD(P)-binding domain; PTHR22604: ; IPR030827: Inositol 2-dehydrogenase; SSF55347:	NA
comp27179_c0_seq1.p1	Ec-07_006560.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp32434_c0_seq8.p1	Ec-07_006570.1	Casein kinase substrate, phosphoprotein PP28	GO:0003676	PTHR22055: ; IPR003034: SAP domain; IPR019380: Casein kinase substrate, phosphoprotein PP28; Coil: ; SSF68906:	NA
comp26086_c0_seq2.p1	Ec-07_006590.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp30900_c0_seq1.p1	Ec-07_006630.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30790_c0_seq7.p1	Ec-07_006640.1	SNF2 helicase	n/a;n/a;n/a	IPR019786: Zinc finger, PHD-type, conserved site; IPR001841: Zinc finger, RING-type; IPR001965: Zinc finger, PHD-type; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR000330: SNF2-related; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR011011: Zinc finger, FYVE/PHD-type; IPR001650: Helicase, C-terminal; PTHR10799: ; Coil:	KOG0298
comp27821_c0_seq1.p1	Ec-07_006650.1	TerD domain	GO:0006950	G3DSA:2.60.60.30: ; IPR003325: TerD domain	NA
comp25245_c0_seq3.p1	Ec-07_006670.1	Alpha/beta hydrolase fold-1	GO:0016787	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029058: Alpha/Beta hydrolase fold; SignalP-noTM: ; IPR000073: Alpha/beta hydrolase fold-1; PTHR10992: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26313_c0_seq3.p1	Ec-07_006680.1	Protein of unknown function DUF501	n/a;n/a;n/a	IPR007511: Protein of unknown function DUF501	NA
comp18215_c0_seq1.p1	Ec-07_006690.2	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp18384_c0_seq1.p1	Ec-07_006700.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp31132_c0_seq1.p1	Ec-07_006720.1	K Homology domain, type 1	GO:0003723	IPR013761: Sterile alpha motif/pointed domain; IPR001660: Sterile alpha motif domain; SIGNAL_PEPTIDE: Signal peptide region; IPR021129: Sterile alpha motif, type 1; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR004087: K Homology domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004088: K Homology domain, type 1; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR10288:	NA
comp24296_c0_seq1.p1	Ec-07_006740.1	Protein of unknown function DUF726	NA	IPR029058: Alpha/Beta hydrolase fold; IPR007941: Protein of unknown function DUF726; Coil:	NA
comp28999_c0_seq2.p1	Ec-07_006750.1	Pseudouridine synthase I, TruA	GO:0001522;GO:0003723;GO:0009451;GO:0009982	IPR020103: Pseudouridine synthase, catalytic domain; IPR020097: Pseudouridine synthase I, TruA, alpha/beta domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020094: Pseudouridine synthase I, TruA, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020095: Pseudouridine synthase I, TruA, C-terminal; Coil: ; PTHR11142:SF5: ; IPR001406: Pseudouridine synthase I, TruA; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28326_c0_seq1.p3	Ec-07_006760.1	cytochrome c oxidase subunit VIa	GO:0005740;GO:0004129;GO:0006118;GO:0005743;GO:0005751	IPR001349: Cytochrome c oxidase, subunit VIa; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3469
comp26596_c0_seq3.p1	Ec-07_006790.1	Glycyl-tRNA Synthetase (N-terminal region)	GO:0004820;GO:0005524;GO:0006426;GO:0005737;GO:0000166;GO:0006418;GO:0004812	IPR002314: Aminoacyl-tRNA synthetase, class II (G/ H/ P/ S), conserved domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR006195: Aminoacyl-tRNA synthetase, class II; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF55681: ; IPR027031: Glycyl-tRNA synthetase/DNA polymerase subunit gamma-2; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002315: Glycyl-tRNA synthetase; G3DSA:3.30.930.10: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2298
comp30563_c0_seq2.p1	Ec-07_006800.1	putative c-myb-like transcription factor	NA	PTHR10641: ; IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; IPR017930: Myb domain	NA
comp33888_c0_seq1.p1	Ec-07_006830.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp25036_c0_seq1.p1	Ec-07_006840.1	vacuolar ATP synthase subunit B	GO:0005524;GO:0005737;GO:0015988;GO:0015986;GO:0016820;GO:0008553;GO:0033180	IPR000793: ATPase, F1/V1/A1 complex, alpha/beta subunit, C-terminal; IPR004100: ATPase, F1 complex alpha/beta subunit, N-terminal domain; IPR022879: V-type ATP synthase regulatory subunit B/beta; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR005723: ATPase, V1 complex, subunit B; IPR020003: ATPase, alpha/beta subunit, nucleotide-binding domain, active site; PTHR15184: ; IPR000194: ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain	NA
comp20068_c0_seq1.p3	Ec-07_006850.1	Concanavalin A-like lectin/glucanase domain	n/a;GO:0005515	IPR001870: B30.2/SPRY domain; IPR013320: Concanavalin A-like lectin/glucanase domain; IPR003877: SPRY domain	NA
comp29498_c0_seq2.p1	Ec-07_006870.1	Cupin-like domain protein	n/a;n/a;n/a	NA	NA
comp12118_c0_seq1.p1	Ec-07_006880.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008168;GO:0032259;GO:0003676	NA	NA
comp28366_c0_seq1.p1	Ec-07_006900.1	actin related protein 2/3 complex, subunit 5	GO:0005856;GO:0030833;GO:0005885;GO:0034314;GO:0015629	PR01217: Proline rich extensin signature; IPR006789: Actin-related protein 2/3 complex subunit 5	NA
comp20490_c0_seq2.p1	Ec-07_006910.2	Mitochondrial Processing Peptidase alpha subunit	GO:0003824;GO:0046872	PTHR11851: ; IPR007863: Peptidase M16, C-terminal; IPR011765: Peptidase M16, N-terminal; IPR011249: Metalloenzyme, LuxS/M16 peptidase-like; IPR011237: Peptidase M16 domain	KOG2067
comp24784_c0_seq1.p1	Ec-07_006920.1	Metallo-dependent phosphatase-like	GO:0016787	IPR029052: Metallo-dependent phosphatase-like; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; IPR006186: Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase; PTHR11668:	NA
comp32662_c0_seq12.p1	Ec-07_006930.1	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase, family GT54	GO:0016020;GO:0016758;GO:0005975	IPR006759: Glycosyl transferase family 54	NA
comp34712_c0_seq1.p1	Ec-07_006940.1	ADP-ribose pyrophosphatase	GO:0016787	SIGNAL_PEPTIDE: Signal peptide region; IPR020084: NUDIX hydrolase, conserved site; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR015797: NUDIX hydrolase domain-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22769: ; IPR020476: NUDIX hydrolase; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR000086: NUDIX hydrolase domain	NA
comp29120_c0_seq1.p1	Ec-07_006950.1	conserved unknown protein	NA	IPR007946: A1 cistron-splicing factor, AAR2	NA
comp29120_c0_seq3.p1	Ec-07_006950.2	conserved unknown protein	NA	NA	NA
comp26328_c0_seq1.p1	Ec-07_007020.1	N-acetylglucosaminephosphotransferase	GO:0008963;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000715: Glycosyl transferase, family 4; PTHR10571: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2788
comp33202_c2_seq7.p1	Ec-07_007040.1	20S proteasome beta 5 subunit	GO:0004175;GO:0005839;GO:0006511;GO:0051603	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR11599:SF63: ; IPR001353: Proteasome, subunit alpha/beta; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR023333: Proteasome B-type subunit; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016050: Proteasome beta-type subunit, conserved site; IPR029055: Nucleophile aminohydrolases, N-terminal; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR000243: Peptidase T1A, proteasome beta-subunit; PTHR11599:	NA
comp28028_c0_seq4.p1	Ec-07_007060.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008168;GO:0003676;GO:0032259	PTHR18895: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PF13659: Methyltransferase domain; IPR002052: DNA methylase, N-6 adenine-specific, conserved site	NA
comp21251_c0_seq1.p1	Ec-07_007070.1	Alanyl-tRNA Synthetase	GO:0003676;GO:0004813;GO:0005524;GO:0005737;GO:0006412;GO:0006419	IPR002318: Alanine-tRNA ligase, class IIc; IPR018163: Threonyl/alanyl tRNA synthetase, class II-like, putative editing domain; IPR023033: Alanine-tRNA ligase, eukaryota/bacteria; IPR018162: Alanine-tRNA ligase, class IIc, anti-codon-binding domain; PTHR11777: ; IPR018165: Alanyl-tRNA synthetase, class IIc, core domain; IPR012947: Threonyl/alanyl tRNA synthetase, SAD; IPR018164: Alanyl-tRNA synthetase, class IIc, N-terminal; SSF55681: ; IPR003156: DHHA1 domain; G3DSA:3.30.930.10: ; IPR009000: Translation protein, beta-barrel domain	KOG0188
comp11690_c0_seq1.p1	Ec-07_007080.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.5.110: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR12380: ; SSF58038: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3202
comp28985_c0_seq1.p1	Ec-07_007090.1	Ubiquitin-conjugating enzyme/RWD-like	GO:0019787;GO:0043687;GO:0051246	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; PTHR24067: ; SM00212: Ubiquitin-conjugating enzyme E2, catalytic domain homologues; IPR000608: Ubiquitin-conjugating enzyme E2; IPR023313: Ubiquitin-conjugating enzyme, active site	NA
comp31389_c0_seq3.p1	Ec-07_007130.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp24763_c0_seq1.p1	Ec-07_007140.1	Pleckstrin homology domain	n/a;n/a;n/a	SSF50729: ; IPR011993: Pleckstrin homology-like domain; IPR001849: Pleckstrin homology domain	NA
comp31463_c0_seq2.p1	Ec-07_007150.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp14923_c0_seq2.p1	Ec-07_007170.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp11934_c0_seq1.p1	Ec-07_007190.1	Zinc/iron permease	GO:0016020;GO:0055085;GO:0046873;GO:0030001	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11065: ; IPR003689: Zinc/iron permease; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2474
comp12710_c0_seq1.p1	Ec-07_007200.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006603: PQ-loop repeat; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21133_c0_seq2.p1	Ec-07_007220.1	nucleotidyltransferase	GO:0009058;GO:0016779	IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; SSF52374: ; PTHR31285: ; G3DSA:3.40.50.2300:	NA
comp20068_c0_seq1.p2	Ec-07_007230.1	Nucleoside phosphorylase domain	GO:0003824;GO:0009116	IPR000845: Nucleoside phosphorylase domain; PTHR21234:SF16: ; IPR018017: Nucleoside phosphorylase	NA
comp29638_c0_seq1.p1	Ec-07_007240.1	conserved unknown protein	NA	G3DSA:3.10.580.10: ; PTHR12320: ; IPR001932: PPM-type phosphatase domain; IPR000644: CBS domain; SSF54631:	NA
comp33836_c0_seq1.p1	Ec-07_007250.1	WD40 repeat	GO:0005515	IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR013979: Translation initiation factor, beta propellor-like domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR22839:	NA
comp32344_c0_seq19.p1	Ec-07_007260.2	cytochrome P450	GO:0005506;GO:0016705;GO:0020037;GO:0055114	IPR001128: Cytochrome P450; Coil: ; PTHR24286:	NA
comp32736_c0_seq12.p2	Ec-07_007290.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	PF12847: Methyltransferase domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR12176:	NA
comp32736_c0_seq12.p1	Ec-07_007300.1	Biotin/lipoyl attachment	n/a;n/a;n/a	PTHR23151: ; G3DSA:2.40.50.100: ; IPR003016: 2-oxo acid dehydrogenase, lipoyl-binding site; IPR011053: Single hybrid motif; IPR000089: Biotin/lipoyl attachment	NA
comp30517_c0_seq1.p1	Ec-07_007310.1	SDH2, succinate dehydrogenase subunit 2	GO:0009055;GO:0055114;GO:0006099;GO:0016491	PF13534: 4Fe-4S dicluster domain; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:1.10.1060.10: ; IPR001041: 2Fe-2S ferredoxin-type domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012675: Beta-grasp domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR025192: Succinate dehydogenase/fumarate reductase N-terminal; PTHR11921: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017900: 4Fe-4S ferredoxin, iron-sulphur binding, conserved site; IPR006058: 2Fe-2S ferredoxin, iron-sulphur binding site; IPR017896: 4Fe-4S ferredoxin-type, iron-sulphur binding domain; IPR009051: Alpha-helical ferredoxin; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR004489: Succinate dehydrogenase/fumarate reductase iron-sulphur protein	KOG3049
comp30517_c1_seq2.p1	Ec-07_007320.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29646_c0_seq1.p1	Ec-07_007390.1	tRNA methyltransferase TrmK	GO:0016429	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR006901: tRNA methyltransferase TrmK; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp34485_c0_seq1.p1	Ec-07_007410.3	Peptidyl-tRNA hydrolase, PTH2	GO:0004045	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002833: Peptidyl-tRNA hydrolase, PTH2; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR12649: ; IPR023476: Peptidyl-tRNA hydrolase II domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12807_c0_seq1.p1	Ec-07_007420.1	Isopenicillin N synthase-like	n/a;n/a;n/a	IPR027443: Isopenicillin N synthase-like; SSF51197:	NA
comp12531_c0_seq1.p1	Ec-07_007470.1	Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain	GO:0003824;GO:0055114;GO:0009396;GO:0004488	IPR020631: Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain; PTHR10025: ; SSF51735: ; SSF53223: ; IPR016040: NAD(P)-binding domain; IPR020630: Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain; G3DSA:3.40.192.10:	NA
comp12217_c0_seq1.p1	Ec-07_007490.1	delta-1-pyrroline-5-carboxylate synthase	GO:0006561;GO:0016620;GO:0008152;GO:0055114;GO:0017084;GO:0016491	IPR001057: Glutamate/acetylglutamate kinase; IPR016161: Aldehyde/histidinol dehydrogenase; IPR019797: Glutamate 5-kinase, conserved site; IPR001048: Aspartate/glutamate/uridylate kinase; PTHR11063: ; IPR016162: Aldehyde dehydrogenase N-terminal domain; IPR016163: Aldehyde dehydrogenase, C-terminal	KOG1154

comp20272_c0_seq2.p1	Ec-07_007540.1	DNA repair protein XRCC4, C-terminal	GO:0003677;GO:0006302;GO:0006310
comp24265_c0_seq1.p1	Ec-07_007550.1	Nicotinamide N-methyltransferase-like	n/a;n/a;n/a
comp34820_c0_seq1.p2	Ec-07_007560.1	expressed unknown protein	n/a;n/a;n/a
comp12070_c0_seq1.p1	Ec-07_007590.1	SGNH hydrolase-type esterase domain	n/a;n/a;n/a
comp22164_c0_seq1.p1	Ec-07_007600.2	hypothetical protein	n/a;n/a;n/a
comp30320_c0_seq4.p1	Ec-07_007630.1	Sulfatase	GO:0008152;GO:0008484
comp17070_c0_seq1.p1	Ec-07_007710.1	Adenylate cyclase-associated CAP, N-terminal	GO:0003779;GO:0007010
comp31530_c0_seq3.p1	Ec-07_007720.1	Peptidyl-tRNA hydrolase, PTH2	GO:0004045
comp28770_c0_seq1.p1	Ec-07_007730.1	expressed unknown protein	n/a;n/a;n/a
comp28631_c0_seq3.p1	Ec-07_007790.1	Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain	GO:0055114;GO:0016491
comp28333_c0_seq1.p1	Ec-07_007800.1	Pentatricopeptide repeat	n/a;n/a;n/a
comp19717_c0_seq1.p2	Ec-07_007810.1	Hypothetical protein	n/a;n/a;n/a
comp20540_c0_seq1.p1	Ec-07_007840.1	Autophagy-related protein 11	GO:0016757;GO:0008152
comp32812_c2_seq6.p1	Ec-07_007860.1	Ankyrin Repeat Transient Receptor Potential Channel	GO:0016020;GO:0055085;GO:0006811;GO:0005216;GO:0005515
comp33610_c0_seq1.p1	Ec-07_007870.1	Acyl-CoA N-acyltransferase	n/a;GO:0004379
comp32338_c0_seq2.p1	Ec-07_007890.2	Transcription initiation factor TFIID subunit 1, domain of unknown function	n/a;n/a;n/a
comp30494_c2_seq1.p1	Ec-07_007920.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp24353_c0_seq1.p1	Ec-08_000050.1	Nucleic acid-binding, OB-fold	GO:0003723;GO:0005215;GO:0005524;GO:0005622;GO:0006396;GO:0006810;GO:0016820;GO:0043190
comp30625_c0_seq1.p1	Ec-08_000080.3	Hypothetical protein	n/a;n/a;n/a
comp30625_c0_seq2.p1	Ec-08_000080.4	Hypothetical protein	n/a;n/a;n/a
comp28844_c0_seq1.p1	Ec-08_000090.1	DnaJ homologue	GO:0031072
comp27105_c0_seq3.p1	Ec-08_000130.1	Rossmann-like alpha/beta/alpha sandwich fold	GO:0008152;GO:0016740;n/a
comp32174_c0_seq1.p1	Ec-08_000140.1	hypothetical protein	n/a;n/a;n/a
comp34664_c0_seq1.p1	Ec-08_000200.1	Hypothetical UPF0043 protein slr0305	GO:0016021
comp21490_c0_seq2.p1	Ec-08_000250.1	Radial spoke 3	n/a;n/a;n/a
comp12463_c0_seq1.p1	Ec-08_000260.1	ABC transporter-like	GO:0016020;GO:0005524;GO:0016887
comp29585_c0_seq4.p1	Ec-08_000270.1	Single-stranded nucleic acid binding R3H	GO:0003676
comp34486_c0_seq1.p1	Ec-08_000280.1	Protein of unknown function DUF2103, metal-binding	n/a;n/a;n/a
comp33056_c0_seq3.p1	Ec-08_000290.1	Glycosyltransferase, family GT8	NA
comp33056_c2_seq1.p1	Ec-08_000300.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp33056_c2_seq1.p2	Ec-08_000310.1	Ribosomal protein S19e	GO:0005840;GO:0005622;GO:0006412;GO:0003735
comp20861_c0_seq1.p1	Ec-08_000360.1	Protein kinase domain	GO:0005524;GO:0006468;GO:0004672
comp25269_c0_seq2.p1	Ec-08_000370.1	conserved unknown protein	n/a;n/a;n/a
comp30710_c0_seq1.p1	Ec-08_000400.1	Armadillo-like helical	n/a;GO:0005488
comp28903_c0_seq1.p1	Ec-08_000410.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a
comp20126_c0_seq1.p1	Ec-08_000440.1	Sec62/63 complex, subunit Sec66	n/a;n/a;n/a
comp28488_c0_seq1.p1	Ec-08_000470.1	Kelch repeat type 1	GO:0005515
comp12074_c0_seq1.p1	Ec-08_000490.1	flagellar associated protein	n/a;n/a;n/a
comp33161_c2_seq1.p1	Ec-08_000500.1	triosephosphate isomerase/glyceraldehyde-3-phosphate dehydrogenase	GO:0016620;GO:0008152;GO:0004807;GO:0055114
comp28495_c0_seq1.p1	Ec-08_000550.1	RNA-binding S4 domain	GO:0003723;GO:0001522;GO:0016866;GO:0009451
comp28495_c0_seq2.p1	Ec-08_000580.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp29176_c0_seq3.p1	Ec-08_000590.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a
comp33527_c0_seq1.p1	Ec-08_000600.1	expressed unknown protein	n/a;n/a;n/a
comp30601_c0_seq4.p1	Ec-08_000610.1	conserved unknown protein	n/a;n/a;n/a
comp31317_c0_seq1.p1	Ec-08_000630.1	Mitochondrial carrier protein	GO:0055085
comp27684_c0_seq2.p1	Ec-08_000660.1	Bromodomain	GO:0005515;GO:0005524
comp29047_c0_seq2.p1	Ec-08_000690.1	Prolyl 4-hydroxylase, alpha subunit	GO:0005506;GO:0031418;GO:0055114;GO:0016705;GO:0016706;GO:0016491
comp24348_c0_seq1.p1	Ec-08_000700.1	PsbB mRNA maturation factor Mbb1	GO:0005515
comp19422_c0_seq1.p1	Ec-08_000710.1	putative FKBP-type peptidyl-prolyl cis-trans isomerase 2	GO:0006457
comp31800_c0_seq1.p1	Ec-08_000720.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp24129_c0_seq1.p1	Ec-08_000760.1	Bromodomain	GO:0005515
comp21237_c0_seq4.p1	Ec-08_000770.1	WD40-repeat-containing domain	GO:0005515
comp30999_c0_seq4.p1	Ec-08_000790.1	Alpha/Beta hydrolase fold	GO:0016787
comp20784_c0_seq2.p1	Ec-08_000810.1	26S proteasome complex ubiquitin receptor, subunit Rpn13	GO:0005634;GO:0005737
comp24663_c0_seq2.p1	Ec-08_000830.1	GTP1/OBG domain	GO:0000287;GO:0003924;GO:0005525
comp28670_c0_seq3.p1	Ec-08_000870.3	expressed unknown protein	n/a;n/a;n/a
comp33234_c0_seq19.p1	Ec-08_000930.1	Pectin lyase fold	n/a;n/a;n/a
comp33234_c0_seq47.p2	Ec-08_000950.1	EF-hand domain pair	GO:0005509
comp11967_c0_seq2.p1	Ec-08_001020.1	expressed unknown protein	n/a;n/a;n/a
comp20804_c0_seq1.p1	Ec-08_001030.1	Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	GO:0006457
comp33024_c4_seq5.p1	Ec-08_001040.1	DEAD box helicase	n/a;n/a;n/a
comp12836_c0_seq1.p1	Ec-08_001060.1	hypothetical protein	NA
comp28840_c0_seq2.p1	Ec-08_001070.1	Helicase superfamily 1/2, ATP-binding domain	n/a;n/a;n/a
comp32873_c2_seq1.p1	Ec-08_001100.1	EF2, translation elongation factor 2	GO:0005525
comp28947_c0_seq2.p1	Ec-08_001110.2	conserved unknown protein	n/a;n/a;n/a
comp30545_c1_seq1.p1	Ec-08_001120.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270
comp12472_c0_seq1.p1	Ec-08_001130.1	tetrapyrrole-binding protein	n/a;n/a;n/a
comp32504_c1_seq8.p1	Ec-08_001140.1	Hypothetical protein	n/a;n/a;n/a
comp30720_c0_seq4.p1	Ec-08_001180.1	Folate-biopterin transporter	GO:0006810;GO:0016021
comp33186_c2_seq1.p1	Ec-08_001190.1	cytochrome b-561 domain protein	n/a;n/a;n/a
comp29675_c0_seq1.p1	Ec-08_001230.1	potential Allene oxide cyclase, partial	GO:0009507;GO:0016853
comp28304_c0_seq1.p1	Ec-08_001250.1	Arf GTPase activating protein	GO:0005096;GO:0005515;GO:0008060;GO:0008270;GO:0032312
comp28470_c0_seq6.p1	Ec-08_001270.1	RNA polymerase, N-terminal	GO:0003677;GO:0006351;GO:0003899
comp28556_c0_seq4.p1	Ec-08_001280.1	Telomere length regulation protein, conserved domain	GO:0005509
comp20446_c0_seq1.p1	Ec-08_001300.1	Cyclophilin-like domain	GO:0006457;GO:0003755;GO:0005622;GO:0008270
comp26020_c0_seq2.p1	Ec-08_001320.1	conserved unknown protein	n/a;n/a;n/a
comp31444_c0_seq6.p1	Ec-08_001340.1	EsV-1-7 domain protein	NA
comp29783_c0_seq2.p1	Ec-08_001370.1	Mitochondrial import receptor, Tom70 homolog	GO:0005515
comp26286_c0_seq2.p1	Ec-08_001400.1	Major facilitator superfamily domain	GO:0016020;n/a;GO:0055085;GO:0022891
comp33158_c0_seq4.p1	Ec-08_001420.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a
comp30422_c0_seq1.p1	Ec-08_001460.1	DNA topoisomerase IV subunit B	GO:0005524;GO:0003918
comp31983_c0_seq5.p1	Ec-08_001470.1	coproporphyrinogen oxidase, putative chloroplast precursor	GO:0055114;GO:0006779;GO:0004109
comp26151_c0_seq1.p1	Ec-08_001540.1	Ubiquitin-conjugating enzyme/RWD-like	GO:0019787;GO:0043687;GO:0051246
comp19726_c0_seq1.p1	Ec-08_001560.1	hypothetical protein	n/a;n/a;n/a
comp31890_c0_seq3.p1	Ec-08_001580.1	Zinc finger, PHD-type	GO:0005515;GO:0008270
comp23636_c0_seq2.p1	Ec-08_001600.3	hypothetical protein	n/a;n/a;n/a
comp29132_c0_seq3.p1	Ec-08_001630.1	Ribosomal protein L37, mitochondrial	n/a;n/a;n/a
comp32216_c0_seq10.p1	Ec-08_001650.1	Calponin homology domain	GO:0005515
comp30876_c1_seq1.p1	Ec-08_001660.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a
comp26049_c0_seq1.p1	Ec-08_001670.1	Streptomyces cyclase/dehydrase	n/a;n/a;n/a
comp28869_c0_seq4.p1	Ec-08_001690.1	Alkyl hydroperoxide reductase subunit C/ Thiol specific antioxidant	GO:0016209;GO:0016491;GO:0055114
comp31587_c1_seq2.p1	Ec-08_001700.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270
comp21568_c0_seq1.p1	Ec-08_001750.1	conserved unknown protein	n/a;n/a;n/a
comp32583_c0_seq31.p1	Ec-08_001760.1	hypothetical protein	n/a;n/a;n/a
comp33053_c0_seq4.p1	Ec-08_001760.2	hypothetical protein	n/a;n/a;n/a
comp31983_c0_seq5.p2	Ec-08_001770.1	hypothetical conserved protein	NA
comp32297_c0_seq6.p1	Ec-08_001810.1	TIC 20 plastid import protein	GO:0005509
comp30422_c0_seq1.p2	Ec-08_001830.1	HNH endonuclease	GO:0003676;GO:0004519
comp24290_c0_seq2.p1	Ec-08_001840.1	Histone H3-K79 methyltransferase	GO:0005634;GO:0051726;GO:0034729;GO:0031151
comp11780_c0_seq1.p1	Ec-08_001880.1	Tetratricopeptide-like helical domain	GO:0005515
comp12236_c0_seq1.p1	Ec-08_001920.1	protein phosphatase 5, catalytic subunit variant	GO:0016787
comp30688_c1_seq1.p1	Ec-08_001950.1	Btz domain	n/a;n/a;n/a
comp31689_c0_seq8.p1	Ec-08_001960.1	Cilia/flagella-associated protein 20	n/a;n/a;n/a
comp34714_c0_seq1.p1	Ec-08_001970.1	Conserved Cys-containing small protein	n/a;n/a;n/a
comp34196_c0_seq1.p1	Ec-08_001990.1	Vacuolar protein sorting protein 26 related	GO:0007034;GO:0030904
comp28696_c0_seq2.p1	Ec-08_002000.1	hypothetical protein	n/a;n/a;n/a
comp32376_c0_seq6.p1	Ec-08_002020.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468
comp32943_c0_seq7.p1	Ec-08_002030.1	conserved protein	GO:0005488
comp32323_c0_seq8.p1	Ec-08_002040.2	Methyltransferase type 11	GO:0008152;GO:0008168
comp12196_c0_seq1.p1	Ec-08_002050.1	DnaJ Cysteine-Rich Domain-Containing Protein	GO:0031072;GO:0051082
comp25023_c0_seq4.p2	Ec-08_002060.1	Imp1 homolog, Inner Membrane Peptidase complex subunit 1	GO:0008236;GO:0009003;GO:0016021
comp30148_c0_seq7.p1	Ec-08_002070.1	UAA transporter	GO:0055085
comp25023_c0_seq4.p1	Ec-08_002100.1	20S proteasome beta subunit	GO:0051603;GO:0004298;GO:0005839;GO:0006511
comp30148_c0_seq7.p2	Ec-08_002110.1	Putative GTP-binding controlling metal-binding domain	n/a;GO:0003725
comp32256_c0_seq5.p1	Ec-08_002120.1	expressed unknown protein	GO:0003676;GO:0008270;n/a
comp31704_c1_seq9.p1	Ec-08_002130.1	Protein of unknown function DUF3067	n/a;n/a;n/a
comp20097_c0_seq1.p1	Ec-08_002140.1	Sec1-like protein	GO:0006904;GO:0016192
comp34907_c0_seq1.p1	Ec-08_002150.1	Domain of unknown function DUF4149	n/a;n/a;n/a
comp26875_c0_seq3.p2	Ec-08_002170.1	Prolyl 4-hydroxylase, alpha subunit	GO:0005506;GO:0031418;GO:0055114;GO:0016705;GO:0016706;GO:0016491
comp26875_c0_seq3.p1	Ec-08_002210.1	MutS protein homolog 2B	GO:0005524;GO:0006298;GO:0030983
comp89862_c0_seq1.p1	Ec-08_002220.1	Ubiquitin-conjugating enzyme E2	GO:0019787;GO:0043687;GO:0051246
comp20386_c0_seq1.p1	Ec-08_002240.2	Microtubule-associated protein, MAP65/Ase1/PRC1	GO:0000226;GO:0000910;GO:0008017
comp26324_c0_seq1.p1	Ec-08_002250.1	conserved unknown protein	GO:0005524;GO:0006468;GO:0004672
comp20919_c0_seq1.p2	Ec-08_002260.1	Ccc1 family	n/a;n/a;n/a
comp20919_c0_seq1.p1	Ec-08_002270.1	COX10 homolog, cytochrome c oxidase assembly protein	GO:0004659;GO:0016021
comp28914_c0_seq1.p1	Ec-08_002280.1	Putative enoyl-CoA-hydratase	GO:0008152;GO:0003824
comp29157_c0_seq2.p1	Ec-08_002290.1	conserved unknown protein	n/a;n/a;n/a
comp20905_c0_seq2.p1	Ec-08_002300.1	NAD-dependent epimerase/dehydratase, N-terminal domain	GO:0003824;GO:0050662
comp26691_c0_seq6.p1	Ec-08_002310.1	Kelch-type beta propeller	GO:0005515
comp19417_c0_seq4.p1	Ec-08_002330.1	conserved unknown protein	n/a;n/a;n/a
comp13618_c0_seq1.p1	Ec-08_002340.1	WD40-repeat-containing domain	GO:0005515
comp24965_c0_seq5.p1	Ec-08_002360.1	Serine-tRNA ligase, type1	GO:0005524;GO:0004828;GO:0006434;GO:0005737;GO:0000166;GO:0006418;GO:0004812
comp24965_c0_seq5.p2	Ec-08_002370.1	Pyridoxamine 5'-phosphate oxidase-related	GO:0055114;GO:0010181;GO:0016491
comp28790_c0_seq2.p1	Ec-08_002390.1	SAC domain	GO:0042578
comp21430_c1_seq1.p1	Ec-08_002400.1	phosphoglycerate kinase	GO:0006096;GO:0004618
comp24813_c0_seq1.p1	Ec-08_002420.2	expressed unknown protein	n/a;n/a;n/a
comp24813_c0_seq1.p2	Ec-08_002430.1	Snf7 family	GO:0007034
comp32622_c0_seq30.p1	Ec-08_002440.1	Putative sodium calcium exchanger	GO:0016021;GO:0055085
comp30845_c1_seq1.p1	Ec-08_002460.1	Kelch-type beta propeller	GO:0005515
comp34017_c0_seq1.p1	Ec-08_002470.1	MND1 family	n/a;n/a;n/a
comp12773_c0_seq1.p1	Ec-08_002490.1	Nuclear protein DGCR14	n/a;n/a;n/a
comp32562_c1_seq2.p1	Ec-08_002500.1	Galactose-3-O-sulfotransferase	GO:0001733;GO:0005794;GO:0009058;GO:0016021
comp26121_c0_seq1.p1	Ec-08_002510.1	P-loop containing nucleoside triphosphate hydrolase	GO:0001733;GO:0005794;GO:0009058;GO:0016021;n/a
comp33074_c3_seq25.p1	Ec-08_002540.1	Serine/threonine-protein kinase CTR1	GO:0004672;GO:0005524;GO:0006468
comp28068_c0_seq2.p1	Ec-08_002560.1	Serine/threonine-protein kinase CTR1	GO:0016772
comp34007_c0_seq1.p1	Ec-08_002570.1	Heat shock factor binding 1	n/a;n/a;n/a
comp9997_c0_seq1.p1	Ec-08_002590.1	Dpy-30 motif	n/a;n/a;n/a
comp20278_c0_seq1.p1	Ec-08_002600.1	Protein-tyrosine phosphatase-like	n/a;GO:0004725;GO:0016791;GO:0004721;GO:0016311
comp28841_c0_seq1.p1	Ec-08_002610.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524
comp25967_c0_seq1.p1	Ec-08_002650.2	CGI121/TPRKB	n/a;n/a;n/a
comp31767_c0_seq12.p1	Ec-08_002680.1	SNF2-related	GO:0003677;GO:0005524
comp20191_c0_seq1.p1	Ec-08_002700.1	Ran-GTPase activating protein	NA
comp29616_c0_seq1.p1	Ec-08_002720.2	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase, family GT13	GO:0008375;GO:0006486;GO:0003827;GO:0006487;GO:0000139
comp27611_c0_seq2.p1	Ec-08_002730.1	Fructosamine/Ketosamine-3-kinase	n/a;n/a;n/a
comp27011_c0_seq1.p1	Ec-08_002740.1	WD40/YVTN repeat-like-containing domain	GO:0005515
comp29260_c0_seq2.p1	Ec-08_002770.1	Proteasome component (PCI) domain	GO:0005515
comp30500_c0_seq13.p1	Ec-08_002800.1	Extradiol ring-cleavage dioxygenase, class III enzyme, subunit B	GO:0006725;GO:0016491;GO:0008198
comp31125_c0_seq1.p1	Ec-08_002820.1	Ankyrin repeat	GO:0005515
comp29627_c0_seq1.p1	Ec-08_002900.1	Actin family	GO:0005515;GO:0009055;GO:0045454
comp12616_c0_seq2.p1	Ec-08_002930.1	Protein of unknown function DUF3054	n/a;n/a;n/a
comp31576_c1_seq2.p1	Ec-08_002950.1	Peroxiredoxin or Alkyl hydroperoxide reductase/ Thiol specific antioxidant	GO:0016209;GO:0016491;GO:0055114
comp31556_c0_seq1.p2	Ec-08_002980.1	Domain of unknown function DUF1995	n/a;n/a;n/a
comp31556_c0_seq1.p1	Ec-08_002990.1	Hydroxymethylglutaryl-CoA reductase (NADPH)	GO:0004420;GO:0055114
comp24224_c0_seq3.p2	Ec-08_003000.1	conserved unknown protein	n/a;n/a;n/a
comp31931_c0_seq1.p2	Ec-08_003010.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0005524;GO:0006468;GO:0004672
comp29997_c0_seq3.p1	Ec-08_003020.1	Bifunctional Indole-3-Glycerol Phosphate Synthase/Phosphoribosylanthranilate Isomerase (C-terminal)	GO:0004425
comp19036_c0_seq2.p1	Ec-08_003040.1	ubiquinol cytochrome c reductase subunit QCR7	GO:0005750;GO:0006122
comp28192_c0_seq5.p1	Ec-08_003090.1	conserved unknown protein	n/a;n/a;n/a
comp14129_c0_seq2.p1	Ec-08_003110.1	N-acyl-phosphatidylethanolamine-hydrolysing phospholipase D	GO:0008270;GO:0070290
comp32886_c0_seq1.p1	Ec-08_003150.1	Pseudouridine synthase I, TruA, alpha/beta domain	GO:0003723;GO:0001522;GO:0009451;GO:0009982
comp31858_c0_seq1.p1	Ec-08_003160.1	TB2/DP1/HVA22-related protein	n/a;n/a;n/a
comp28359_c0_seq1.p1	Ec-08_003170.1	conserved unknown protein	n/a;n/a;n/a
comp29483_c0_seq1.p1	Ec-08_003190.1	SECIS binding protein 2	GO:0000166
comp12243_c0_seq1.p1	Ec-08_003210.1	flagellar associated protein	GO:0016020
comp32764_c5_seq13.p1	Ec-08_003230.1	Tuf1, mitochondrial translation elongation factor EF-Tu	GO:0005525
comp31225_c0_seq1.p1	Ec-08_003250.1	ATP-binding cassette transporter, subfamily B, member 4, group TAP protein PpABCB4 MET type	GO:0006810;GO:0005524;GO:0042626;GO:0016021;GO:0016887
comp30390_c0_seq1.p1	Ec-08_003260.1	DDHD domain-containing protein	GO:0046872
comp12927_c0_seq1.p1	Ec-08_003290.1	Light harvesting complex protein	GO:0009765;GO:0016020
comp20570_c0_seq1.p1	Ec-08_003320.1	radial spoke protein 10	n/a;n/a;n/a
comp24482_c0_seq1.p1	Ec-08_003330.1	carnitine/acylcarnitine carrier protein	GO:0005215;GO:0005743;GO:0006810;GO:0055085
comp31661_c0_seq1.p1	Ec-08_003340.1	DNA topoisomerase I	GO:0003677;GO:0003917;GO:0006265
comp29355_c0_seq3.p1	Ec-08_003360.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a
comp24770_c0_seq1.p1	Ec-08_003370.1	expressed unknown protein	n/a;n/a;n/a
comp20148_c0_seq1.p1	Ec-08_003390.1	BSD	n/a;n/a;n/a
comp26824_c0_seq1.p1	Ec-08_003410.2	Peptidase C19, ubiquitin-specific peptidase, DUSP domain	GO:0004843
comp29486_c1_seq1.p1	Ec-08_003430.1	Helicase, C-terminal	n/a;GO:0005515
comp20166_c0_seq1.p1	Ec-08_003450.1	hypothetical protein	n/a;n/a;n/a
comp33019_c1_seq5.p1	Ec-08_003470.1	hypothetical protein	n/a;n/a;n/a
comp31966_c2_seq2.p1	Ec-08_003500.1	hypothetical protein	n/a;n/a;n/a
comp33299_c0_seq1.p1	Ec-08_003510.1	dioxygenase	GO:0005506;GO:0016491;GO:0055114
comp29233_c0_seq3.p1	Ec-08_003530.1	expressed unknown protein	GO:0005634
comp31209_c2_seq7.p1	Ec-08_003540.1	Ribose-5-phosphate isomerase	GO:0009052;GO:0004751
comp25041_c0_seq1.p1	Ec-08_003550.1	TspO/MBR-related protein	GO:0016021
comp19851_c0_seq2.p1	Ec-08_003580.1	Coatomer protein complex, beta sub-unit	GO:0006886;GO:0016192;GO:0030131
comp27444_c0_seq2.p1	Ec-08_003590.1	Superoxide dismutase, Destroys radicals which are normally produced within the cells and which are t	GO:0006801;GO:0004784;GO:0055114;GO:0046872
comp19851_c0_seq2.p2	Ec-08_003600.1	Ubiquitin-conjugating enzyme E2	GO:0019787;GO:0043687;GO:0051246
comp12486_c0_seq2.p1	Ec-08_003610.1	SAP domain	n/a;n/a;n/a
comp31747_c0_seq4.p1	Ec-08_003630.1	expressed unknown protein	n/a;n/a;n/a
comp21267_c0_seq1.p2	Ec-08_003650.1	EF-hand domain pair	GO:0005509
comp32175_c0_seq2.p1	Ec-08_003660.1	expressed unknown protein	n/a;n/a;n/a
comp19769_c0_seq2.p1	Ec-08_003680.1	hypothetical protein	n/a;n/a;n/a
comp12033_c0_seq1.p1	Ec-08_003710.1	SUN domain	n/a;n/a;n/a
comp12414_c0_seq1.p1	Ec-08_003750.1	hypothetical protein	GO:0005515;GO:0008270;n/a
comp31895_c2_seq13.p1	Ec-08_003770.1	YLP motif-containing protein 1	GO:0005634
comp32530_c0_seq48.p1	Ec-08_003780.1	conserved unknown protein	n/a;n/a;n/a
comp31596_c0_seq7.p1	Ec-08_003810.1	expressed unknown protein	n/a;n/a;n/a
comp31612_c0_seq7.p1	Ec-08_003820.1	ankyrin repeat protein	n/a;n/a;n/a
comp29804_c0_seq2.p1	Ec-08_003830.1	Protein kinase-like domain	GO:0016772
comp29804_c0_seq2.p2	Ec-08_003840.1	Predicted unusual protein kinase (ISS)	n/a;n/a;n/a
comp32549_c0_seq5.p1	Ec-08_003850.1	Streptomyces cyclase/dehydrase	n/a;n/a;n/a
comp32530_c0_seq26.p1	Ec-08_003860.4	Kinesin motor domain	GO:0003777;GO:0005524;GO:0007018;GO:0008017
comp29475_c0_seq1.p1	Ec-08_003870.1	conserved unknown protein	GO:0003723
comp27135_c0_seq1.p1	Ec-08_003880.1	methylenetetrahydrofolate reductase	GO:0006555;GO:0004489;GO:0055114
comp27135_c0_seq2.p1	Ec-08_003890.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a
comp31587_c3_seq9.p1	Ec-08_003900.1	Replication factor C, C-terminal domain	GO:0003677;GO:0003689;GO:0005524;GO:0005663;GO:0006260
comp30183_c0_seq2.p1	Ec-08_003920.1	Ankyrin Repeat Transient Receptor Potential Channel	n/a;GO:0005515
comp31587_c3_seq13.p1	Ec-08_003940.1	conserved unknown protein	n/a;n/a;n/a
comp28998_c0_seq2.p1	Ec-08_003970.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020
comp40050_c0_seq1.p1	Ec-08_004010.1	Butirosin biosynthesis, BtrG-like	n/a;n/a;n/a
comp79645_c0_seq1.p1	Ec-08_004020.1	expressed unknown protein	n/a;n/a;n/a
comp20568_c0_seq1.p1	Ec-08_004080.1	conserved unknown protein	n/a;n/a;n/a
comp29248_c0_seq4.p2	Ec-08_004100.1	FKBP-type peptidyl-prolyl cis-trans isomerase 7	GO:0006457
comp28646_c0_seq1.p1	Ec-08_004110.1	Rad9/Ddc1	GO:0006281;GO:0000077;GO:0030896;GO:0000075
comp32882_c1_seq4.p1	Ec-08_004130.1	expressed unknown protein	n/a;n/a;n/a
comp32882_c1_seq6.p1	Ec-08_004210.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp33642_c0_seq1.p1	Ec-08_004210.2	Ankyrin repeat-containing domain	n/a;n/a;n/a
comp19357_c0_seq1.p1	Ec-08_004230.4	NB-ARC and TPR repeat-containig protein	NA
comp32157_c0_seq15.p1	Ec-08_004250.1	Ca2+/calmodulin-dependent protein kinase I-like protein	n/a;n/a;n/a
comp34654_c0_seq1.p2	Ec-08_004260.1	Protein of unknown function DUF2039	n/a;n/a;n/a
comp12918_c0_seq2.p1	Ec-08_004270.1	Plastid lipid-associated protein/fibrillin conserved domain	n/a;n/a;n/a
comp34605_c0_seq1.p1	Ec-08_004280.1	GDP-fucose protein O-fucosyltransferase	n/a;n/a;n/a
comp28211_c0_seq2.p1	Ec-08_004300.1	RAI1-like	n/a;n/a;n/a
comp27226_c0_seq1.p1	Ec-08_004310.1	DNA polymerase subunit Cdc27	GO:0005634;GO:0006260
comp28425_c0_seq2.p1	Ec-08_004320.1	Amidinotransferase	GO:0005737;GO:0016813
comp33138_c0_seq15.p1	Ec-08_004330.1	expressed unknown protein	n/a;n/a;n/a
comp20711_c0_seq3.p1	Ec-08_004340.1	expressed unknown protein	n/a;n/a;n/a
comp32353_c2_seq18.p1	Ec-08_004350.1	Proteasome, subunit alpha/beta	GO:0051603;GO:0004298;GO:0005839
comp30414_c1_seq2.p1	Ec-08_004360.1	RNA recognition motif domain, eukaryote	GO:0003676
comp30069_c0_seq3.p1	Ec-08_004370.1	Glycosyl transferase, family 31	GO:0016020;GO:0006486;GO:0008378
comp26349_c0_seq1.p1	Ec-08_004380.1	hypothetical protein	n/a;n/a;n/a
comp30259_c0_seq1.p1	Ec-08_004390.1	EF-hand domain pair	n/a;n/a;n/a
comp29393_c0_seq3.p1	Ec-08_004400.1	WD40-repeat-containing domain	GO:0005515
comp32932_c0_seq4.p1	Ec-08_004410.4	von Willebrand factor, type A	n/a;n/a;n/a
comp33673_c0_seq1.p1	Ec-08_004480.1	Valine--tRNA ligase,	GO:0005524;GO:0006418;GO:0000166;GO:0004812
comp30257_c2_seq1.p1	Ec-08_004510.1	Mannosyl-oligosaccharide 1,2-alpha-mannosidase, family GH47	GO:0004571;GO:0005509;GO:0005515;GO:0016020
comp31684_c1_seq1.p1	Ec-08_004520.1	HAMP linker domain	GO:0004871;GO:0007165;GO:0016021
comp12483_c0_seq1.p1	Ec-08_004540.1	Arfaptin homology (AH) domain/BAR domain	n/a;n/a;n/a
comp26470_c1_seq1.p1	Ec-08_004550.1	FNIP	n/a;n/a;n/a
comp32583_c0_seq36.p1	Ec-08_004590.1	conserved unknown protein	GO:0016020;n/a
comp32583_c0_seq22.p1	Ec-08_004600.1	hypothetical protein	n/a;n/a;n/a
comp12811_c0_seq2.p1	Ec-08_004630.1	HAD-like domain	GO:0003824;GO:0008152
comp21248_c0_seq1.p1	Ec-08_004640.1	protein required for templated centriole assembly	n/a;n/a;n/a
comp12788_c0_seq1.p2	Ec-08_004650.1	Glycoside hydrolase/deacetylase, beta/alpha-barrel	GO:0003824;GO:0005975;GO:0016810
comp20630_c0_seq1.p1	Ec-08_004660.2	conserved unknown protein	n/a;n/a;n/a
comp31892_c1_seq21.p1	Ec-08_004670.1	Zinc finger, RING-type	GO:0005515;GO:0008270
comp31131_c0_seq3.p1	Ec-08_004690.1	Pentatricopeptide repeat	n/a;n/a;n/a
comp12292_c0_seq1.p1	Ec-08_004700.1	peptide chain release factor 1	GO:0006415;GO:0005737;GO:0016149
comp30095_c0_seq1.p1	Ec-08_004710.1	Winged helix-turn-helix DNA-binding domain	n/a;n/a;n/a
comp12424_c0_seq1.p1	Ec-08_004730.1	Sorting and Assembly Machinery 35kDa protein	NA
comp18488_c0_seq1.p1	Ec-08_004750.1	conserved unknown protein	n/a;n/a;n/a
comp27106_c0_seq3.p1	Ec-08_004770.1	Zinc finger, PHD-finger	GO:0005515
comp61508_c0_seq1.p1	Ec-08_004780.3	hypothetical protein	n/a;n/a;n/a
comp28410_c0_seq1.p1	Ec-08_004790.1	WD40 repeat	GO:0005515
comp29270_c0_seq1.p1	Ec-08_004800.1	1,3-beta-glucan synthase, family GT48	GO:0000148;GO:0003843;GO:0006075;GO:0016020
comp32905_c0_seq33.p1	Ec-00_010800.1	Mannuronan C-5-epimerase	n/a;n/a;n/a

comp27536_c0_seq5.p1	Ec-08_004860.1	expressed unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27536_c0_seq4.p1	Ec-08_004860.2	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32408_c2_seq24.p1	Ec-08_004820.1	Mannuronan C-5-epimerase	NA	PF13229: Right handed beta helix region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012334: Pectin lyase fold; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR022441: Parallel beta-helix repeat-2; IPR011050: Pectin lyase fold/virulence factor; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR006626: Parallel beta-helix repeat	NA
comp30203_c0_seq4.p1	Ec-08_004890.1	Heat shock protein DnaJ, cysteine-rich domain	GO:0031072;GO:0051082	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR001305: Heat shock protein DnaJ, cysteine-rich domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp21482_c0_seq2.p1	Ec-08_004940.2	phospholipidmethyltransferase	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24761_c0_seq2.p1	Ec-08_004950.1	P-loop containing nucleoside triphosphate hydrolase	GO:0045454;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR21343: ; IPR012336: Thioredoxin-like fold; IPR013766: Thioredoxin domain; PF13500: AAA domain	NA
comp27503_c0_seq1.p1	Ec-08_004980.7	autophagy-related protein 5	GO:0005737;GO:0006914	PTHR13040:SF2: ; IPR007239: Autophagy-related protein 5	NA
comp29797_c0_seq1.p1	Ec-08_004990.1	TLDc domain	n/a;n/a;n/a	IPR006571: TLDc domain; IPR011992: EF-hand domain pair; PTHR23354:	NA
comp33089_c0_seq4.p1	Ec-08_005000.1	Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote	n/a;GO:0005515	IPR000449: Ubiquitin-associated domain/translation elongation factor EF-Ts, N-terminal; IPR013536: WLM; G3DSA:3.10.20.90: ; IPR015940: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote; G3DSA:1.10.8.10: ; IPR019954: Ubiquitin conserved site; IPR029071: Ubiquitin-related domain; IPR018997: PUB domain; IPR006567: PUG domain; IPR000626: Ubiquitin-like; PTHR23153: ; SSF143503: ; IPR009060: UBA-like	NA
comp32266_c0_seq2.p1	Ec-08_005010.1	Transient Receptor Potential Channel	GO:0005216;GO:0006811;GO:0016020;GO:0055085	NA	KOG3609
comp20393_c0_seq2.p1	Ec-08_005070.1	Protein of unknown function DUF4079	n/a;n/a;n/a	IPR025067: Protein of unknown function DUF4079; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32145_c4_seq3.p1	Ec-08_005150.2	Checkpoint protein Rad17/Rad24	GO:0005634;GO:0006281;GO:0007049	NA	NA
comp20985_c0_seq2.p1	Ec-08_005160.1	Probable membrane-associated 30 kDa protein, chloroplast precursor	n/a;n/a;n/a	IPR007157: PspA/IM30; PTHR31088: ; Coil:	NA
comp20059_c0_seq2.p1	Ec-08_005180.1	Acetyltransferase (GNAT) domain protein	n/a;n/a;n/a	NA	NA
comp26003_c0_seq1.p1	Ec-08_005190.1	DEAD box helicase	n/a;n/a;n/a	IPR014014: RNA helicase, DEAD-box type, Q motif; IPR011545: DEAD/DEAH box helicase domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; PTHR24031: ; SignalP-TM:	KOG0335
comp34096_c0_seq1.p1	Ec-08_005200.1	SEP domain	n/a;n/a;n/a	G3DSA:3.10.20.90: ; IPR001012: UBX domain; IPR029071: Ubiquitin-related domain; IPR012989: SEP domain; PTHR23333:	NA
comp28478_c0_seq1.p1	Ec-08_005210.1	Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote	n/a;GO:0005515	IPR006636: Heat shock chaperonin-binding; IPR000449: Ubiquitin-associated domain/translation elongation factor EF-Ts, N-terminal; G3DSA:3.10.20.90: ; IPR015940: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote; IPR019954: Ubiquitin conserved site; G3DSA:1.10.8.10: ; IPR029071: Ubiquitin-related domain; IPR015496: Ubiquilin; IPR000626: Ubiquitin-like; IPR009060: UBA-like	NA
comp12872_c0_seq1.p1	Ec-08_005220.1	sperm flagellar energy carrier protein	GO:0006810;GO:0055085;GO:0005743;GO:0005215	PTHR24089: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002067: Mitochondrial carrier protein; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023395: Mitochondrial carrier domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR018108: Mitochondrial substrate/solute carrier; IPR002113: Adenine nucleotide translocator 1	NA
comp33807_c0_seq1.p2	Ec-08_005250.1	EF-hand domain pair	GO:0005509	IPR018247: EF-Hand 1, calcium-binding site; SIGNAL_PEPTIDE: Signal peptide region; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF47473: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26463_c0_seq2.p1	Ec-08_005260.1	Fibronectin type III	GO:0005515	IPR013783: Immunoglobulin-like fold; IPR020683: Ankyrin repeat-containing domain; IPR003961: Fibronectin type III; Coil: ; PTHR24193: ; IPR002110: Ankyrin repeat	NA
comp26021_c0_seq1.p1	Ec-08_005270.1	trehalose-6-phosphate phosphatase	n/a;GO:0005992;GO:0003824	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023214: HAD-like domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR003337: Trehalose-phosphatase; PTHR10788:	KOG1050
comp29011_c0_seq2.p1	Ec-08_005290.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp26253_c0_seq1.p1	Ec-08_005300.2	WD40 repeat	GO:0005515	PTHR19932:SF10: ; IPR022100: Minichromosome loss protein Mcl1, middle region; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR19932: ; Coil:	NA
comp25260_c0_seq1.p3	Ec-08_005320.1	Ubiquitin-conjugating enzyme E2	GO:0019787;GO:0043687;GO:0051246	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; PTHR24067: ; SM00212: Ubiquitin-conjugating enzyme E2, catalytic domain homologues; IPR000608: Ubiquitin-conjugating enzyme E2; IPR023313: Ubiquitin-conjugating enzyme, active site	NA
comp15104_c0_seq1.p1	Ec-08_005330.1	2Fe-2S ferredoxin-type domain	GO:0009055;GO:0051536	PTHR19370: ; IPR001041: 2Fe-2S ferredoxin-type domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012675: Beta-grasp domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26643_c0_seq1.p1	Ec-08_005340.1	CRAL-TRIO domain	n/a;n/a;n/a	IPR001251: CRAL-TRIO domain; PTHR23324:	NA
comp28763_c0_seq1.p1	Ec-08_005370.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	NA	NA
comp28194_c0_seq2.p1	Ec-08_005410.1	Major facilitator superfamily	GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; PTHR16172: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29528_c0_seq2.p1	Ec-08_005420.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31342_c3_seq1.p2	Ec-08_005440.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20290_c0_seq1.p1	Ec-08_005450.1	NADH dehydrogenase (ubiquinone)	GO:0055114;GO:0016491	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; G3DSA:3.50.50.60: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR22915: ; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	KOG2495
comp31366_c0_seq2.p1	Ec-08_005460.1	Tetratricopeptide-like helical domain	GO:0005515	IPR011717: Tetratricopeptide TPR-4; PF14559: Tetratricopeptide repeat; IPR013105: Tetratricopeptide repeat 2; IPR011990: Tetratricopeptide-like helical domain; PTHR14699: ; PTHR14699:SF0: ; IPR013026: Tetratricopeptide repeat-containing domain; Coil: ; IPR019734: Tetratricopeptide repeat	NA
comp20652_c0_seq1.p1	Ec-08_005470.1	ATP-dependent protease, HslV subunit	GO:0004298;GO:0009376;GO:0006508	PTHR32194: ; IPR029055: Nucleophile aminohydrolases, N-terminal; IPR022281: ATP-dependent protease, HslV subunit; Coil: ; IPR001353: Proteasome, subunit alpha/beta; IPR023333: Proteasome B-type subunit	NA
comp30354_c0_seq2.p1	Ec-08_005480.1	tubulin folding cofactor D	GO:0005488	NA	KOG1943
comp63706_c0_seq1.p1	Ec-08_005490.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0006470	IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C	NA
comp31222_c0_seq4.p2	Ec-08_005510.1	HAD-like domain	n/a;n/a;n/a	PTHR15157: ; Coil: ; IPR023214: HAD-like domain	NA
comp33638_c0_seq1.p1	Ec-08_005550.1	expressed unknown protein	n/a;GO:0006812;GO:0008324	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006667: SLC41 divalent cation transporters, integral membrane domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24411_c0_seq1.p1	Ec-08_005570.2	Proline--tRNA ligase	GO:0000166;GO:0004827;GO:0005524;GO:0005737;GO:0006412;GO:0006433	NA	KOG4163
comp33766_c0_seq1.p1	Ec-08_005580.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33079_c1_seq1.p1	Ec-08_005590.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008168;GO:0006400;GO:0008176	PTHR23417: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR003358: tRNA (guanine-N-7) methyltransferase, Trmb type	NA
comp15237_c0_seq2.p1	Ec-08_005600.2	Zinc finger, A20-type	GO:0003677;GO:0008270	IPR000058: Zinc finger, AN1-type; SSF118310: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10634: ; SSF57716: ; IPR002653: Zinc finger, A20-type; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32704_c0_seq33.p1	Ec-08_005610.1	P-loop containing nucleoside triphosphate hydrolase	GO:0016020;n/a;GO:0005524;GO:0016887	IPR003439: ABC transporter-like; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR017871: ABC transporter, conserved site; IPR013525: ABC-2 type transporter; PTHR19241: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30381_c0_seq1.p1	Ec-08_005620.1	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR005135: Endonuclease/exonuclease/phosphatase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR000300: Inositol polyphosphate-related phosphatase; PTHR11200: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30025_c0_seq4.p1	Ec-08_005640.1	Response receiver	GO:0000160	PTHR26402: ; IPR011006: CheY-like superfamily; IPR001789: Signal transduction response regulator, receiver domain; G3DSA:3.40.50.2300:	NA
comp30724_c2_seq2.p1	Ec-08_005660.1	Transcription factor IIS, N-terminal	GO:0003677;GO:0005634;GO:0006351	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30724_c2_seq3.p2	Ec-08_005660.2	Transcription factor IIS, N-terminal	GO:0003677;GO:0005634;GO:0006351	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29377_c0_seq2.p1	Ec-08_005700.1	EsV-1-7 domain protein	GO:0009055;GO:0016020;GO:0006118	IPR003439: ABC transporter-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013525: ABC-2 type transporter; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR19241: ; IPR017871: ABC transporter, conserved site	NA
comp33651_c0_seq1.p1	Ec-08_005700.2	EsV-1-7 domain protein	GO:0009055;GO:0006118	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR003439: ABC transporter-like; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013525: ABC-2 type transporter; IPR017871: ABC transporter, conserved site; PTHR19241:	NA
comp24791_c0_seq2.p1	Ec-08_005710.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; Coil: ; IPR002110: Ankyrin repeat	NA
comp32377_c0_seq3.p1	Ec-08_005720.1	NIN-like transcription factor	n/a;n/a;n/a	NA	NA
comp16909_c0_seq1.p1	Ec-08_005750.1	Novel protein containing IQ calmodulin-binding motif	n/a;GO:0035735	PTHR31540: ; Coil: ; IPR030465: Centrosomal protein of 131 kDa	NA
comp18107_c0_seq1.p1	Ec-08_005760.1	Ribosomal protein L1, 2-layer alpha/beta-sandwich	GO:0003723	IPR002143: Ribosomal protein L1; IPR023674: Ribosomal protein L1-like; PTHR23105: ; IPR016095: Ribosomal protein L1, 3-layer alpha/beta-sandwich; IPR028364: Ribosomal protein L1/ribosomal biogenesis protein; IPR016094: Ribosomal protein L1, 2-layer alpha/beta-sandwich	NA
comp32302_c1_seq28.p1	Ec-08_005770.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; PTHR22967: ; IPR011009: Protein kinase-like domain	NA
comp30876_c0_seq2.p1	Ec-08_005780.1	Protein of unknown function DUF1295	GO:0005737;GO:0006629;GO:0016021;GO:0016627	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001104: 3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal; PTHR32251: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR010721: Protein of unknown function DUF1295; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31021_c0_seq4.p1	Ec-08_005800.1	DDHD domain-containing protein	GO:0003824;GO:0046872	IPR004177: DDHD; IPR029058: Alpha/Beta hydrolase fold; PTHR15457:	KOG2308
comp25706_c0_seq1.p1	Ec-08_005810.1	conserved unknown protein	GO:0003824;GO:0008152	SignalP-TM:	NA
comp64145_c0_seq1.p1	Ec-08_005830.1	conserved unknown protein	n/a;n/a;n/a	PTHR23050: ; Coil:	NA
comp29411_c0_seq30.p2	Ec-08_005840.1	putative phosphatase	GO:0016791;n/a	NA	KOG3120
comp29411_c0_seq30.p1	Ec-08_005850.1	Alpha/Beta hydrolase fold	GO:0016787	IPR029058: Alpha/Beta hydrolase fold; IPR000639: Epoxide hydrolase-like; IPR000073: Alpha/beta hydrolase fold-1; PTHR10992: ; SignalP-TM:	NA
comp33643_c0_seq1.p1	Ec-08_005860.1	TB2/DP1/HVA22-related protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; IPR004345: TB2/DP1/HVA22-related protein; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32203_c1_seq9.p1	Ec-08_005870.1	Tryptophan--tRNA ligase	GO:0005524;GO:0005737;GO:0006418;GO:0000166;GO:0006412;GO:0004812	G3DSA:1.10.240.10: ; IPR001412: Aminoacyl-tRNA synthetase, class I, conserved site; IPR018163: Threonyl/alanyl tRNA synthetase, class II-like, putative editing domain; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; SSF52374: ; IPR002306: Tryptophan-tRNA ligase; IPR002305: Aminoacyl-tRNA synthetase, class Ic	KOG2145
comp33294_c0_seq6.p1	Ec-08_005880.2	hypothetical protein	n/a;n/a;n/a	PF14223: gag-polypeptide of LTR copia-type; PTHR11439:SF185: ; IPR001584: Integrase, catalytic core; IPR012337: Ribonuclease H-like domain; PTHR11439: ; Coil:	NA
comp21319_c0_seq1.p1	Ec-08_005930.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp13012_c0_seq1.p1	Ec-08_005940.1	Ribosomal protein L15e	GO:0005840;GO:0006412;GO:0003735	IPR000439: Ribosomal protein L15e; IPR012678: Ribosomal protein L23/L15e core domain; IPR024794: Ribosomal protein L15e core domain	NA
comp11682_c0_seq1.p1	Ec-08_005950.1	Ubiquitin-conjugating enzyme/RWD-like	GO:0019787;GO:0043687;GO:0051246	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; PTHR24067: ; SM00212: Ubiquitin-conjugating enzyme E2, catalytic domain homologues; IPR000608: Ubiquitin-conjugating enzyme E2	NA
comp33688_c0_seq1.p1	Ec-08_005960.1	Acetyltransferase (GNAT) domain protein	GO:0008080	NA	NA
comp26825_c0_seq1.p1	Ec-08_005990.1	mitogen-activated protein kinase putative serine/threonine protein kinase	GO:0004672;GO:0005524;GO:0006468	PTHR24055: ; SSF50729: ; IPR017441: Protein kinase, ATP binding site; G3DSA:3.30.200.20: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; IPR008271: Serine/threonine-protein kinase, active site; IPR001849: Pleckstrin homology domain; IPR011009: Protein kinase-like domain; IPR003527: Mitogen-activated protein (MAP) kinase, conserved site; IPR000719: Protein kinase domain; IPR011993: Pleckstrin homology-like domain; G3DSA:1.10.510.10:	KOG0660
comp31906_c0_seq1.p1	Ec-08_006010.1	ATP-NAD kinase, PpnK-type, all-beta	GO:0003951;GO:0008152;GO:0019674	IPR017438: Inorganic polyphosphate/ATP-NAD kinase, domain 1; IPR016064: NAD kinase/diacylglycerol kinase-like domain; IPR002504: NAD kinase; IPR017437: ATP-NAD kinase, PpnK-type, all-beta	NA
comp24618_c0_seq2.p1	Ec-08_006020.2	BAX inhibitor motif-containing protein	GO:0004601;GO:0006118;GO:0006979;GO:0020037	NA	NA
comp31307_c0_seq2.p2	Ec-08_006030.1	Hypothetical protein	n/a;n/a;n/a	PTHR31849:SF1: ; IPR018785: Cysteine-rich domain, DPF-motif; PTHR31849:	NA
comp26998_c0_seq1.p1	Ec-08_006070.1	Elongated TPR repeat-containing domain	GO:0006457	SSF48452: ; IPR023114: Elongated TPR repeat-containing domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023566: Peptidyl-prolyl cis-trans isomerase, FKBP-type; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13414: TPR repeat; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19599_c0_seq1.p1	Ec-08_006080.1	G10 protein	GO:0005634	IPR001748: G10 protein; Coil:	NA
comp19599_c0_seq1.p4	Ec-08_006090.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp26641_c0_seq2.p2	Ec-08_006110.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28176_c0_seq2.p1	Ec-08_006140.2	F-box domain	GO:0005515	NA	NA
comp24322_c0_seq1.p1	Ec-08_006160.1	Zinc finger C2HC domain-containing protein	GO:0005622;GO:0008270;n/a	IPR026319: Zinc finger C2HC domain-containing protein; PF13913: zinc-finger of a C2HC-type	NA
comp19880_c0_seq1.p4	Ec-08_006170.1	Ribonuclease P/MRP protein subunit	GO:0008033;GO:0004540	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF160350: ; PTHR15441: ; IPR002759: Ribonuclease P/MRP protein subunit; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19880_c0_seq1.p1	Ec-08_006180.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32982_c0_seq20.p1	Ec-08_006220.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32408_c2_seq3.p1	Ec-08_006230.3	hypothetical protein	n/a;n/a;n/a	NA	NA
comp28776_c0_seq2.p1	Ec-08_006340.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp24875_c1_seq2.p1	Ec-08_006350.1	Ribonuclease P/MRP, subunit p29	GO:0003723;GO:0006364;GO:0008033;GO:0000172;GO:0030677;GO:0006379;GO:0004540	IPR023534: Rof/RNase P-like; IPR002730: Ribonuclease P/MRP, subunit p29; PTHR13348:	NA
comp30966_c0_seq2.p1	Ec-08_006360.1	PIH1 family	n/a;n/a;n/a	IPR012981: PIH1 family; Coil:	NA
comp35060_c0_seq1.p1	Ec-08_006370.1	ADP-ribosylation factor-like 2-binding protein, domain	n/a;n/a;n/a	IPR023379: ADP-ribosylation factor-like 2-binding protein, domain	NA
comp29189_c0_seq1.p1	Ec-08_006390.1	acyl-CoA dehydrogenase	GO:0016627;GO:0055114;GO:0003995	IPR013786: Acyl-CoA dehydrogenase/oxidase, N-terminal; IPR009100: Acyl-CoA dehydrogenase/oxidase, N-terminal and middle domain; IPR006091: Acyl-CoA oxidase/dehydrogenase, central domain; IPR006089: Acyl-CoA dehydrogenase, conserved site; G3DSA:1.20.140.10: ; IPR009075: Acyl-CoA dehydrogenase/oxidase C-terminal; PTHR10909:	KOG0139
comp14064_c0_seq1.p1	Ec-08_006420.1	Eukaryotic initiation factor 3 d subunit	GO:0005737;GO:0003743;GO:0005852	IPR007783: Eukaryotic translation initiation factor 3 subunit D	NA
comp31906_c1_seq7.p1	Ec-08_006490.1	putative: Beta-tubulin folding cofactor C	GO:0000902	IPR006599: CARP motif; IPR027684: Tubulin-specific chaperone C; IPR016098: Cyclase-associated protein CAP/septum formation inhibitor MinC, C-terminal; IPR017901: C-CAP/cofactor C-like domain; IPR012945: Tubulin binding cofactor C-like domain	KOG2512
comp27723_c0_seq1.p1	Ec-08_006590.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp31879_c0_seq3.p1	Ec-08_006600.1	NCAIR mutase (PurE)-related proteins	GO:0006189	PTHR23046: ; IPR000031: Phosphoribosylaminoimidazole carboxylase PurE domain	KOG1691
comp27927_c0_seq4.p1	Ec-08_006620.1	UbiE/COQ5 methyltransferase	GO:0008168	IPR023576: UbiE/COQ5 methyltransferase, conserved site; IPR004033: UbiE/COQ5 methyltransferase; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; PTHR10108: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31879_c0_seq3.p2	Ec-08_006630.1	Protein atp11, mitochondrial precursor	GO:0005739;GO:0006461	IPR010591: ATP11; SignalP-TM:	NA
comp32378_c0_seq1.p1	Ec-08_006640.2	Ankyrin repeat-containing domain	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp30152_c0_seq1.p1	Ec-08_006650.2	RNA recognition motif domain	GO:0003676	PTHR24012: ; PTHR24012:SF348: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp24257_c1_seq3.p1	Ec-08_006660.1	Homeodomain-like	GO:0003677	PTHR10641: ; PF13921: Myb-like DNA-binding domain; IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; Coil: ; IPR017877: Myb-like domain; IPR017930: Myb domain	NA
comp29836_c0_seq1.p1	Ec-08_006670.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26876_c0_seq1.p1	Ec-08_006680.1	double HA-tagged mitogen activated protein kinase 2 mitogen-activated protein kinase	GO:0004707;GO:0005524;GO:0006468;n/a	SSF50729: ; PTHR24055: ; IPR017441: Protein kinase, ATP binding site; G3DSA:3.30.200.20: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR001849: Pleckstrin homology domain; IPR003527: Mitogen-activated protein (MAP) kinase, conserved site; IPR000719: Protein kinase domain; IPR011993: Pleckstrin homology-like domain; G3DSA:1.10.510.10:	KOG0660
comp27927_c0_seq1.p1	Ec-08_006690.1	Thioredoxin-like fold	n/a;GO:0045454	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR18929: ; IPR012336: Thioredoxin-like fold; PF13848: Thioredoxin-like domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29650_c0_seq1.p1	Ec-08_006710.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29650_c1_seq1.p1	Ec-08_006720.1	PSP1, C-terminal	n/a;n/a;n/a	PTHR21600: ; Coil: ; IPR007557: PSP1, C-terminal	NA
comp20998_c0_seq1.p1	Ec-09_000010.1	signal peptide peptidase	GO:0008233;GO:0006508	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029045: ClpP/crotonase-like domain; IPR002142: Peptidase S49; IPR004635: Peptidase S49, SppA; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28906_c0_seq1.p1	Ec-09_000030.1	Peptidase M20, dimerisation domain	GO:0016787;GO:0046983	PTHR11014: ; IPR002933: Peptidase M20; SSF53187: ; G3DSA:3.40.630.10: ; IPR011650: Peptidase M20, dimerisation domain	NA
comp12904_c0_seq1.p1	Ec-09_000040.1	conserved unknown protein	n/a;n/a;n/a	PTHR12436: ; PTHR12436:SF3: ; IPR005062: SAC3/GANP/THP3	NA
comp33730_c0_seq1.p1	Ec-09_000050.1	Glyoxalase I	GO:0004462;GO:0046872	PTHR10374: ; IPR029068: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase; SIGNAL_PEPTIDE: Signal peptide region; IPR018146: Glyoxalase I, conserved site; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR004361: Glyoxalase I; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR004360: Glyoxalase/fosfomycin resistance/dioxygenase domain	NA
comp29618_c0_seq3.p1	Ec-09_000060.2	Nucleotide-binding alpha-beta plait domain	GO:0000166	PTHR24012: ; IPR000504: RNA recognition motif domain; IPR029123: Splicing factor RBM39, linker; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp24664_c0_seq3.p1	Ec-09_000080.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	IPR001841: Zinc finger, RING-type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:3.50.30.30: ; IPR003137: Protease-associated domain, PA; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; PTHR22765: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27677_c0_seq1.p1	Ec-09_000090.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp18005_c0_seq1.p1	Ec-09_000100.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp59512_c0_seq1.p1	Ec-09_000110.1	Galactose-binding domain-like	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR008979: Galactose-binding domain-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26744_c0_seq4.p1	Ec-09_000120.1	Tubulin/FtsZ, GTPase domain	GO:0051258;GO:0043234;GO:0006184;GO:0005525;GO:0003924	SIGNAL_PEPTIDE: Signal peptide region; IPR000158: Cell division protein FtsZ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR30314: ; IPR003008: Tubulin/FtsZ, GTPase domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR008280: Tubulin/FtsZ, C-terminal; IPR024757: Cell division protein FtsZ, C-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017975: Tubulin, conserved site; IPR020805: Cell division protein FtsZ, conserved site; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR018316: Tubulin/FtsZ, 2-layer sandwich domain	NA
comp21640_c0_seq2.p1	Ec-09_000140.1	Peptidase A22B, signal peptide peptidase	GO:0004190;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR006639: Presenilin/signal peptide peptidase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR007369: Peptidase A22B, signal peptide peptidase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34772_c0_seq1.p1	Ec-09_000150.1	Lin-54 family	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR028307: Lin-54 family	NA
comp33241_c0_seq11.p1	Ec-09_000180.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp31178_c0_seq3.p1	Ec-09_000190.1	Protein of unknown function DUF1688	n/a;n/a;n/a	PTHR31687: ; IPR012469: Protein of unknown function DUF1688	NA
comp17229_c0_seq1.p1	Ec-09_000200.1	Trypsin domain protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24695_c0_seq1.p1	Ec-09_000230.1	Zinc finger, C3HC4 RING-type	GO:0005515;GO:0008270;GO:0046872	SSF57850: ; IPR001841: Zinc finger, RING-type; cd00162: RING; IPR018957: Zinc finger, C3HC4 RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR12983: ; Coil:	NA
comp29060_c0_seq3.p2	Ec-09_000240.1	Mitochondrial substrate/solute carrier	GO:0005488;GO:0006810;GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12317_c0_seq1.p1	Ec-09_000250.2	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp29060_c0_seq3.p1	Ec-09_000290.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020	PTHR24089: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29497_c0_seq1.p1	Ec-09_000300.1	Mannitol dehydrogenase, N-terminal	GO:0008152;GO:0003824;GO:0055114;GO:0016491	PTHR30562: ; SSF51735: ; IPR013118: Mannitol dehydrogenase, C-terminal; IPR008927: 6-phosphogluconate dehydrogenase C-terminal domain-like; IPR013328: 6-phosphogluconate dehydrogenase, domain 2; IPR013131: Mannitol dehydrogenase, N-terminal; IPR016040: NAD(P)-binding domain; IPR000669: Mannitol dehydrogenase	NA
comp22605_c0_seq2.p1	Ec-09_000320.1	Snf7 family	GO:0007034	IPR005024: Snf7 family; PTHR22761: ; Coil:	NA
comp19557_c0_seq1.p1	Ec-09_000370.1	Tetratricopeptide repeat	GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat	NA
comp16557_c0_seq2.p1	Ec-09_000380.1	fatty acid desaturase	GO:0020037;GO:0046914	IPR005804: Fatty acid desaturase, type 1; IPR001199: Cytochrome b5-like heme/steroid binding domain; PTHR19353:	KOG4232
comp20623_c0_seq1.p1	Ec-09_000390.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR000629: ATP-dependent RNA helicase DEAD-box, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR24031: ; IPR014014: RNA helicase, DEAD-box type, Q motif; IPR014001: Helicase superfamily 1/2, ATP-binding domain; Coil: ; IPR001650: Helicase, C-terminal	KOG0338
comp33900_c0_seq1.p1	Ec-09_000410.2	WD40-repeat-containing domain	GO:0005515	PTHR22847:SF413: ; PTHR22847: ; IPR017986: WD40-repeat-containing domain; IPR011989: Armadillo-like helical; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; IPR007148: Small-subunit processome, Utp12	NA
comp12540_c0_seq1.p1	Ec-09_000420.1	SGNH hydrolase-type esterase domain	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013830: SGNH hydrolase-type esterase domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31153_c0_seq2.p1	Ec-09_000460.3	Ankyrin repeat-containing domain	n/a;n/a;n/a	SSF109993: ; IPR031968: Domain of unknown function DUF4782; PTHR24158: ; PF13637: Ankyrin repeats (many copies); PF13857: Ankyrin repeats (many copies); IPR003123: VPS9 domain; IPR020683: Ankyrin repeat-containing domain; Coil: ; IPR002110: Ankyrin repeat	NA
comp31681_c0_seq10.p1	Ec-09_000490.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; PTHR24058: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10:	NA
comp12740_c0_seq1.p1	Ec-09_000510.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30224_c0_seq3.p1	Ec-09_000640.1	hypothetical protein	GO:0006807;GO:0004356;GO:0006542	Coil:	NA
comp12065_c0_seq1.p1	Ec-09_000650.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; IPR002110: Ankyrin repeat	NA
comp30695_c0_seq1.p1	Ec-09_000660.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp32906_c0_seq13.p1	Ec-09_000670.1	Protein kinase-like domain	GO:0016772	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; PTHR24056:	KOG0594
comp15839_c0_seq1.p1	Ec-09_000680.1	Domain of unknown function DUF4496	n/a;n/a;n/a	Coil: ; IPR028034: Domain of unknown function DUF4496	NA
comp29840_c0_seq3.p1	Ec-09_000720.1	HECT	GO:0004842	IPR000569: HECT; G3DSA:3.30.2160.10: ; PTHR11254:	NA
comp31385_c0_seq1.p1	Ec-09_000740.1	Protein of unknown function DUF1665	n/a;n/a;n/a	IPR012459: Protein of unknown function DUF1665	NA
comp30916_c0_seq2.p1	Ec-09_000750.1	GPI transamidase component PIG-T	GO:0016255;GO:0042765	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR007245: GPI transamidase component PIG-T; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12098_c0_seq1.p1	Ec-09_000770.1	Acyl-CoA N-acyltransferase	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR016181: Acyl-CoA N-acyltransferase; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007434: Protein of unknown function DUF482; SignalP-noTM: ; PTHR31384: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20858_c0_seq1.p1	Ec-09_000780.1	Mitochondrial transcription termination factor	GO:0003690;GO:0005739;GO:0006355	PTHR13068: ; IPR003690: Mitochondrial transcription termination factor	NA
comp33825_c0_seq1.p1	Ec-09_000810.1	Ribophorin I (Oligosaccharyltransferase, alpha subunit)	GO:0006486;GO:0005783;GO:0004579;GO:0016021	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR007676: Ribophorin I; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2291
comp24274_c0_seq1.p1	Ec-09_000830.1	Mitochondrial carrier domain	GO:0008152;GO:0016491	PTHR24089: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR023395: Mitochondrial carrier domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR018108: Mitochondrial substrate/solute carrier	NA
comp20836_c0_seq1.p1	Ec-09_000840.3	Protein kinase-like domain	GO:0016772	IPR017441: Protein kinase, ATP binding site; IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; PTHR24348: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site	NA
comp27968_c0_seq1.p1	Ec-09_000850.3	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp30193_c0_seq1.p1	Ec-09_000860.3	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp20184_c0_seq1.p1	Ec-09_000870.1	Ribosomal protein L6, chloroplast	GO:0005840;GO:0006412;GO:0003735;GO:0019843;GO:0009507	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020526: Ribosomal protein L6, chloroplast; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30278_c0_seq3.p1	Ec-09_000880.1	Protein kinase-like domain	GO:0016772	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; PTHR24361: ; Coil: ; IPR011009: Protein kinase-like domain	NA
comp30916_c0_seq1.p1	Ec-09_000890.1	HAD-like domain	n/a;n/a;n/a	G3DSA:3.10.20.90: ; IPR029071: Ubiquitin-related domain; IPR011943: HAD-superfamily hydrolase, subfamily IIID; IPR004274: NLI interacting factor; IPR023214: HAD-like domain; PTHR32054:	NA
comp30683_c0_seq2.p1	Ec-09_000950.1	Ankyrin repeat-containing domain	n/a;GO:0005515	SSF50729: ; PF13637: Ankyrin repeats (many copies); IPR001849: Pleckstrin homology domain; PTHR23180: ; IPR001164: Arf GTPase activating protein; SSF103657: ; IPR020683: Ankyrin repeat-containing domain; IPR011993: Pleckstrin homology-like domain; Coil: ; SSF57863: ; IPR002110: Ankyrin repeat	NA
comp31664_c1_seq8.p1	Ec-09_000960.1	molybdopterin biosynthesis protein MoeB	n/a;n/a;n/a	IPR001763: Rhodanese-like domain; PTHR10953: ; IPR009036: Molybdenum cofactor biosynthesis, MoeB; IPR000594: UBA/THIF-type NAD/FAD binding fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR016040: NAD(P)-binding domain; IPR007901: MoeZ/MoeB	NA
comp31900_c0_seq1.p1	Ec-09_000990.1	Mitochondrial transcription termination factor	GO:0003690;GO:0005739;GO:0006355	PTHR13068: ; IPR003690: Mitochondrial transcription termination factor	NA
comp31664_c1_seq8.p2	Ec-09_001000.1	Mitochondrial transcription termination factor	GO:0006355;GO:0003690;GO:0005739	IPR003690: Mitochondrial transcription termination factor; PTHR13068:	NA
comp20078_c0_seq1.p1	Ec-09_001020.1	Glucose/ribitol dehydrogenase	GO:0008152;GO:0016491	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24320: ; IPR002347: Glucose/ribitol dehydrogenase; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002198: Short-chain dehydrogenase/reductase SDR; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24797_c0_seq1.p3	Ec-09_001030.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; IPR002110: Ankyrin repeat; PTHR24193:	NA
comp28543_c0_seq1.p1	Ec-09_001070.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR019748: FERM central domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR13140: ; IPR000857: MyTH4 domain; IPR000048: IQ motif, EF-hand binding site; IPR019749: Band 4.1 domain; IPR011993: PH domain-like; IPR001609: Myosin head, motor domain; Coil: ; IPR000299: FERM domain	NA
comp26240_c0_seq2.p2	Ec-09_001080.1	expressed unknown protein	n/a;n/a;n/a	IPR026939: At2g23090-like; PTHR21213:SF5:	NA
comp33270_c0_seq26.p1	Ec-09_001090.1	Cyclin-like	n/a;n/a;n/a	IPR015429: Cyclin C/H/T/L; IPR013763: Cyclin-like; IPR006671: Cyclin, N-terminal	NA
comp30330_c0_seq1.p1	Ec-09_001140.1	DEP domain	GO:0035556	IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; IPR000008: C2 domain; IPR000591: DEP domain	NA
comp23061_c0_seq2.p1	Ec-09_001160.1	GAF domain	GO:0005515	PTHR11347: ; IPR029016: GAF domain-like; IPR003018: GAF domain	NA
comp23061_c0_seq1.p1	Ec-09_001160.2	GAF domain	GO:0005515	NA	NA
comp12010_c0_seq1.p1	Ec-09_001210.1	General substrate transporter	GO:0055085;GO:0016021;GO:0022857	IPR005828: General substrate transporter; IPR003663: Sugar/inositol transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; PTHR24063: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24182_c0_seq2.p1	Ec-09_001220.1	Mpv17/PMP22	GO:0016021	IPR007248: Mpv17/PMP22; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24320_c0_seq2.p1	Ec-09_001240.1	Kelch-type beta propeller	GO:0005515	IPR006652: Kelch repeat type 1; SSF117281: ; IPR011333: BTB/POZ fold; PF13418: Galactose oxidase, central domain; PTHR23244: ; PF13415: Galactose oxidase, central domain; IPR015916: Galactose oxidase, beta-propeller; IPR013069: BTB/POZ; IPR000210: BTB/POZ-like; G3DSA:3.30.710.10: ; IPR015915: Kelch-type beta propeller; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily	NA
comp30380_c0_seq1.p1	Ec-09_001310.2	RNA-binding S4 domain	GO:0003723	SSF55174: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002942: RNA-binding S4 domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA

comp21349_c0_seq1.p1	Ec-09_003530.1	PPPDE putative peptidase domain	n/a;n/a;n/a
comp31267_c0_seq1.p1	Ec-09_003540.2	expressed unknown protein	GO:0005509
comp31267_c0_seq3.p1	Ec-09_003540.3	expressed unknown protein	GO:0005509
comp12076_c0_seq1.p1	Ec-09_003600.1	expressed unknown protein	n/a;n/a;n/a
comp27976_c1_seq2.p1	Ec-09_003610.2	Mx1, Mx-like dynamin-related GTPase	GO:0005515
comp31923_c0_seq8.p1	Ec-09_003630.1	Protein kinase-like domain	GO:0006468;GO:0004672;GO:0016772
comp32323_c1_seq2.p1	Ec-09_003640.1	Tissue inhibitor of metalloproteinases-like, OB-fold	NA
comp33139_c0_seq7.p1	Ec-09_003650.1	Nucleotide cyclase	GO:0007242;GO:0009190;GO:0016849
comp27212_c0_seq1.p1	Ec-09_003660.1	Thioesterase superfamily	n/a;n/a;n/a
comp32301_c0_seq2.p1	Ec-09_003680.1	GDP-fucose protein O-fucosyltransferase, family GT65	NA
comp12001_c0_seq1.p1	Ec-09_003710.1	Actin-related protein 2/3 complex subunit ARPC2 or p34-Arc (Arp2/3 complex 34 kDa subunit)	GO:0030833;GO:0005885;GO:0034314;GO:0015629
comp30150_c0_seq2.p1	Ec-09_003730.1	conserved unknown protein	n/a;n/a;n/a
comp26569_c0_seq4.p1	Ec-09_003740.1	DEAD box helicase	GO:0005622;GO:0003676
comp19358_c0_seq1.p1	Ec-09_003750.1	conserved unknown protein	NA
comp35410_c0_seq1.p1	Ec-09_003770.1	expressed unknown protein	n/a;n/a;n/a
comp26227_c0_seq1.p1	Ec-09_003790.1	K Homology domain, type 1	GO:0003723
comp27838_c0_seq1.p2	Ec-09_003800.1	Ammonium/urea transporter	GO:0006810;GO:0008519;GO:0016020;n/a
comp26165_c0_seq1.p1	Ec-09_003830.1	Flavinator of succinate dehydrogenase	n/a;n/a;n/a
comp31457_c0_seq4.p1	Ec-09_003840.1	Rab18, RAB family GTPase	GO:0007165;GO:0006184;GO:0003924;GO:0006886;GO:0006913;GO:0007264;GO:0005525;GO:0015031
comp28826_c0_seq1.p1	Ec-09_003870.1	Protein kinase-like domain	GO:0016772
comp24152_c0_seq4.p1	Ec-09_003880.1	Pseudouridine synthase II	GO:0006396
comp24152_c0_seq2.p2	Ec-09_003890.1	tRNA pseudouridine synthase II, TruB	GO:0003723;GO:0001522;GO:0009451;GO:0009982
comp28259_c0_seq2.p1	Ec-09_003920.1	Zinc finger, FYVE/PHD-type	GO:0005515;GO:0008270
comp31947_c0_seq1.p1	Ec-09_003930.1	EsV-1-7 domain protein	GO:0005874;GO:0007017;GO:0005525
comp28661_c0_seq1.p2	Ec-09_003960.1	START-like domain	n/a;n/a;n/a
comp30818_c0_seq3.p1	Ec-09_003990.1	ENTH/VHS	n/a;n/a;n/a
comp30659_c1_seq1.p1	Ec-09_004000.1	UAA transporter	GO:0055085
comp73931_c0_seq1.p1	Ec-09_004020.1	WD40 repeat protein flagellar associated protein	GO:0005515
comp24983_c0_seq2.p2	Ec-09_004030.1	PDZ domain	GO:0005515
comp24983_c0_seq2.p1	Ec-09_004040.1	conserved unknown protein	n/a;n/a;n/a
comp26179_c0_seq4.p1	Ec-09_004080.1	WD40-repeat-containing domain	GO:0005515
comp16029_c0_seq1.p1	Ec-09_004090.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0005524;GO:0006468;GO:0004672
comp74458_c0_seq1.p1	Ec-09_004100.1	hypothetical protein	n/a;n/a;n/a
comp58835_c0_seq1.p1	Ec-09_004110.1	hypothetical protein	n/a;n/a;n/a
comp33783_c0_seq1.p1	Ec-09_004120.1	50S ribosomal protein L28	GO:0005840;GO:0005622;GO:0006412;GO:0003735
comp32103_c0_seq28.p1	Ec-09_004130.1	Pectin lyase fold/virulence factor	n/a;n/a;n/a
comp31926_c0_seq3.p1	Ec-09_004160.1	hypothetical protein	n/a;n/a;n/a
comp33563_c0_seq1.p1	Ec-09_004180.1	hypothetical protein	n/a;n/a;n/a
comp24873_c0_seq1.p1	Ec-09_004200.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0031072
comp32130_c0_seq8.p1	Ec-09_004210.1	MORN motif	n/a;n/a;n/a
comp24742_c0_seq1.p1	Ec-09_004220.1	expressed unknown protein	n/a;n/a;n/a
comp31549_c0_seq1.p1	Ec-09_004230.3	Pectin lyase fold	n/a;n/a;n/a
comp21564_c0_seq2.p1	Ec-09_004270.1	P-loop containing nucleoside triphosphate hydrolase	GO:0016020;n/a
comp26034_c0_seq2.p1	Ec-09_004280.1	Rieske [2Fe-2S] iron-sulphur domain	GO:0051537;GO:0055114;GO:0016491
comp32857_c0_seq6.p1	Ec-09_004300.1	JAB1/MPN/MOV34 metalloenzyme domain	GO:0005515
comp25964_c0_seq1.p1	Ec-09_004320.1	SKP1 component, POZ domain	GO:0006511
comp29781_c0_seq1.p1	Ec-09_004330.1	Forkhead-associated (FHA) domain	GO:0005515
comp12546_c0_seq2.p1	Ec-09_004340.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	GO:0016020;GO:0005515
comp20314_c0_seq1.p1	Ec-09_004350.1	carboxyl-terminal protease	GO:0008236;GO:0006508
comp26616_c0_seq1.p1	Ec-09_004460.1	BTB/POZ-like	GO:0005515
comp28421_c0_seq2.p1	Ec-09_004470.2	hypothetical protein	n/a;n/a;n/a
comp31682_c1_seq5.p1	Ec-09_004520.1	hypothetical protein	n/a;n/a;n/a
comp33046_c1_seq2.p1	Ec-09_004530.1	eIF-2alpha kinase GCN2 similar to Eukaryotic translation initiation factor 2-alpha kinase 4	GO:0005515
comp31450_c0_seq10.p2	Ec-09_004540.1	nicotianamide aminotransferase A	GO:0003824;GO:0030170
comp31450_c0_seq5.p1	Ec-09_004550.3	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a
comp14232_c0_seq2.p1	Ec-09_004560.1	Uncharacterised protein family UPF0546	n/a;n/a;n/a
comp34707_c0_seq1.p1	Ec-09_004580.1	Proteasome Alpha Subunit family member	GO:0004298;GO:0005839;GO:0051603;n/a
comp27648_c1_seq1.p1	Ec-09_004590.1	Thioredoxin-like fold	n/a;n/a;n/a
comp27648_c0_seq1.p1	Ec-09_004600.1	Protein of unknown function DUF2358	n/a;n/a;n/a
comp25272_c0_seq3.p3	Ec-09_004610.1	Ankyrin repeat-containing domain	n/a;n/a;n/a
comp31520_c0_seq1.p1	Ec-09_004620.1	TPR repeat-containing protein	GO:0005515
comp30024_c0_seq2.p2	Ec-09_004630.1	expressed unknown protein	GO:0005515;n/a
comp30024_c0_seq2.p1	Ec-09_004640.1	Transient Receptor Potential Channel Fragment	n/a;n/a;n/a
comp21533_c0_seq1.p1	Ec-09_004650.1	Peptidase A22B, signal peptide peptidase	GO:0004190;GO:0016021
comp31851_c0_seq4.p1	Ec-09_004660.1	hypothetical protein	n/a;n/a;n/a
comp29395_c0_seq1.p1	Ec-09_004670.2	hypothetical protein	n/a;n/a;n/a
comp29704_c1_seq2.p1	Ec-09_004680.1	Glutathione peroxidase	GO:0004602;GO:0006979;GO:0055114;n/a
comp29704_c1_seq3.p1	Ec-09_004690.1	groES chaperonin, plastidal	GO:0005524;GO:0005737;GO:0006457
comp27525_c0_seq2.p1	Ec-09_004720.1	expressed unknown protein	GO:0005351;GO:0006810;GO:0009401
comp12431_c0_seq1.p2	Ec-09_004730.1	Protein of unknown function DUF583	GO:0005525;GO:0005874;GO:0007017
comp30503_c2_seq2.p1	Ec-09_004740.1	Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote	n/a;n/a;n/a
comp32617_c2_seq13.p1	Ec-09_004750.1	ubiquitin-activating enzyme E1	GO:0006464;GO:0006512;GO:0008641
comp25238_c0_seq1.p1	Ec-09_004770.1	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0006511;GO:0036459
comp29382_c0_seq3.p1	Ec-09_004790.1	conserved unknown protein	GO:0003824;GO:0046872
comp20560_c0_seq1.p1	Ec-09_004800.1	RHD3/Sey1	NA
comp29791_c1_seq2.p1	Ec-09_004820.1	axonemal 1-beta dynein heavy chain dynein heavy chain	n/a;n/a;n/a
comp32482_c0_seq2.p1	Ec-09_004830.1	Ankyrin repeat-containing domain	n/a;n/a;n/a
comp30605_c1_seq3.p1	Ec-09_004840.1	RNA recognition motif domain, eukaryote	GO:0003676
comp43260_c0_seq1.p1	Ec-10_000020.1	expressed unknown protein	n/a;n/a;n/a
comp34019_c0_seq1.p1	Ec-10_000030.1	Succinate--CoA ligase (GDP-forming), alpha subunit	GO:0004776;GO:0045244
comp30133_c0_seq8.p1	Ec-10_000040.2	hypothetical protein	n/a;n/a;n/a
comp30650_c0_seq2.p1	Ec-10_000050.1	Protein of unknown function DUF602	n/a;n/a;n/a
comp30304_c0_seq3.p2	Ec-10_000060.2	expressed unknown protein	n/a;n/a;n/a
comp20406_c0_seq1.p1	Ec-10_000110.1	conserved unknown protein	n/a;n/a;n/a
comp12119_c0_seq1.p1	Ec-10_000130.1	Translation initiation factor 3, N-terminal	GO:0003743;GO:0006413
comp30758_c0_seq7.p1	Ec-10_000140.1	Armadillo-type fold	GO:0005488
comp29833_c0_seq2.p1	Ec-10_000150.1	Ion transport domain	GO:0005216;GO:0006811;GO:0016020;GO:0055085
comp30304_c0_seq3.p1	Ec-10_000160.1	expressed unknown protein	n/a;n/a;n/a
comp31379_c0_seq2.p1	Ec-10_000170.1	conserved unknown protein	n/a;n/a;n/a
comp32835_c0_seq4.p1	Ec-10_000180.1	Protein of unknown function DUF962	n/a;n/a;n/a
comp21472_c0_seq1.p1	Ec-10_000190.1	Membrane-associated, eicosanoid/glutathione metabolism (MAPEG) protein	n/a;n/a;n/a
comp11909_c0_seq1.p1	Ec-10_000200.1	hypothetical protein	NA
comp12232_c0_seq1.p1	Ec-10_000210.1	Carbohydrate-binding WSC	n/a;n/a;n/a
comp27145_c1_seq3.p1	Ec-10_000230.1	SWAP/Surp	GO:0003723;GO:0006396
comp34748_c0_seq1.p1	Ec-10_000250.2	EF-hand domain pair	GO:0005509
comp26595_c0_seq1.p1	Ec-10_000260.1	cupin superfamily protein	NA
comp27458_c0_seq3.p1	Ec-10_000270.1	Phosphatidylinositol 3-/4-kinase, catalytic domain	GO:0016773
comp28509_c0_seq3.p1	Ec-10_000340.2	FG-GAP repeat	n/a;n/a;n/a
comp31586_c0_seq3.p1	Ec-10_000380.1	DOMON domain	GO:0004500;GO:0006548
comp11948_c0_seq1.p1	Ec-10_000420.1	Ribosomal protein L4 domain	GO:0003735;GO:0005840;GO:0006412
comp12830_c0_seq1.p1	Ec-10_000480.1	expressed unknown protein	n/a;n/a;n/a
comp104878_c0_seq1.p1	Ec-10_000500.1	expressed unknown protein	n/a;n/a;n/a
comp33598_c0_seq1.p1	Ec-10_000510.1	Biopterin transport-related protein BT1	GO:0016020;GO:0006810;GO:0016021
comp17845_c0_seq1.p1	Ec-10_000520.1	NAD(P)-binding domain	GO:0003824;GO:0005488;GO:0008152
comp31635_c0_seq4.p1	Ec-10_000530.2	Myosin head, motor domain	GO:0003774;GO:0005524;GO:0016459
comp25823_c0_seq1.p1	Ec-10_000540.1	Pleckstrin homology domain	NA
comp30540_c0_seq3.p1	Ec-10_000550.1	Heat shock protein 90	GO:0005524
comp34644_c0_seq1.p1	Ec-10_000560.1	Brix domain	n/a;n/a;n/a
comp26775_c0_seq1.p1	Ec-10_000590.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp30466_c0_seq1.p1	Ec-10_000630.5	expressed unknown protein	n/a;n/a;n/a
comp58890_c0_seq1.p1	Ec-10_000650.1	hypothetical protein	n/a;n/a;n/a
comp33939_c0_seq1.p1	Ec-10_000670.1	conserved unknown protein	n/a;n/a;n/a
comp20458_c0_seq1.p1	Ec-10_000680.1	carboxy-terminal peptidase	GO:0008236;GO:0006508
comp26944_c1_seq1.p1	Ec-10_000710.1	AAA+ ATPase domain	n/a;n/a;n/a
comp24793_c0_seq1.p1	Ec-10_000720.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168
comp25058_c0_seq3.p1	Ec-10_000730.1	K Homology domain, type 1	GO:0003723
comp12020_c0_seq1.p1	Ec-10_000740.1	HhH-GPD domain	GO:0006284
comp32920_c1_seq10.p1	Ec-10_000750.1	expressed unknown protein	GO:0003735;GO:0005622;GO:0005840;GO:0006412
comp19533_c0_seq1.p1	Ec-10_000770.1	Sulfotransferase	GO:0008146;GO:0016021
comp27021_c0_seq1.p1	Ec-10_000780.1	Glutaminyl-tRNA Synthetase	GO:0005524;GO:0004819;GO:0005737;GO:0006425;GO:0006418;GO:0000166;GO:0006412;GO:0004812
comp33051_c0_seq3.p1	Ec-10_000790.1	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0006511;GO:0036459
comp32747_c0_seq19.p1	Ec-10_000800.1	Chromosome segregation protein	GO:0016020;GO:0007165;GO:0006935;GO:0004871
comp31622_c0_seq1.p1	Ec-10_000830.1	expressed unknown protein	n/a;n/a;n/a
comp30545_c4_seq1.p1	Ec-10_000870.1	Dynein light chain, type 1/2	GO:0005875;GO:0007017
comp33987_c0_seq1.p1	Ec-10_000880.1	Ketose-bisphosphate aldolase, class-II	GO:0005975;GO:0008270;GO:0016832
comp28030_c0_seq1.p1	Ec-10_000890.1	Histidine phosphatase superfamily, clade-1	n/a;n/a;n/a
comp30833_c2_seq4.p1	Ec-10_000920.1	Alpha/Beta hydrolase fold	GO:0004091
comp33024_c1_seq3.p1	Ec-10_000960.1	2-oxoglutarate dehydrogenase, E2 component	n/a;n/a;n/a
comp22731_c0_seq1.p1	Ec-10_000970.1	ADP-ATP translocase	GO:0005471;GO:0005524;GO:0006810;GO:0016021
comp34876_c0_seq1.p1	Ec-10_000980.1	Small nuclear ribonucleoprotein-associated protein B	NA
comp21116_c0_seq1.p1	Ec-10_000990.1	NOT2/NOT3/NOT5	GO:0005634;GO:0006355
comp14536_c0_seq1.p1	Ec-10_001020.1	expressed unknown protein	n/a;n/a;n/a
comp15769_c0_seq1.p1	Ec-10_001030.1	DNA polymerase family X lyase domain	GO:0003677;GO:0003824
comp32468_c3_seq16.p1	Ec-10_001040.1	expressed unknown protein	GO:0006810;GO:0030288;GO:0005215
comp24338_c1_seq1.p1	Ec-10_001070.1	BOP1, N-terminal domain	GO:0006364;GO:0042254
comp21521_c0_seq2.p1	Ec-10_001100.1	arginase	GO:0046872
comp29922_c0_seq1.p1	Ec-10_001120.1	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	GO:0005524;GO:0006468;GO:0005509;GO:0004672
comp29922_c0_seq1.p2	Ec-10_001130.2	Rad51 DNA recombinase 2	NA
comp30246_c0_seq2.p1	Ec-10_001140.1	Gaa1-like, GPI transamidase component	GO:0042765;GO:0016021
comp12206_c0_seq1.p1	Ec-10_001150.1	RNA 3'-terminal phosphate cyclase domain	GO:0003824
comp32504_c1_seq29.p1	Ec-10_001160.1	Thioredoxin-like fold	GO:0045454;n/a
comp32504_c1_seq5.p1	Ec-10_001170.1	expressed unknown protein	n/a;n/a;n/a
comp20459_c0_seq1.p1	Ec-10_001180.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a
comp15189_c0_seq1.p1	Ec-10_001190.1	Ribosomal protein S3, C-terminal	GO:0005840;GO:0015935;GO:0006412;GO:0003735
comp27427_c0_seq3.p2	Ec-10_001200.1	expressed unknown protein	n/a;n/a;n/a
comp27427_c0_seq3.p1	Ec-10_001210.1	Amine oxidase domain protein	GO:0006118;GO:0009055;GO:0016491;GO:0055114
comp20654_c0_seq1.p1	Ec-10_001220.1	NUDIX hydrolase domain-like	GO:0016787
comp28452_c0_seq5.p2	Ec-10_001230.1	Rab11B, RAB family GTPase	GO:0016020;GO:0007165;GO:0006184;GO:0007264;GO:0005525;GO:0015031
comp28452_c0_seq5.p1	Ec-10_001240.1	expressed unknown protein	n/a;n/a;n/a
comp28452_c0_seq1.p1	Ec-10_001250.1	expressed unknown protein	n/a;n/a;n/a
comp47799_c0_seq1.p1	Ec-10_001260.1	Kinesin motor domain	GO:0003777;GO:0005524;GO:0007018;GO:0008017
comp11838_c0_seq1.p1	Ec-10_001270.1	conserved unknown protein	GO:0007186;GO:0001584;GO:0016021
comp28673_c0_seq3.p1	Ec-10_001280.1	Delta14-sterol reductase	GO:0016627;GO:0016020;GO:0016628;GO:0003824;GO:0003674;GO:0050613;GO:0016491
comp28673_c0_seq3.p2	Ec-10_001290.1	Mitogen-activated protein kinase	GO:0016772
comp12123_c0_seq1.p1	Ec-10_001300.1	Ran binding domain	GO:0046907
comp26739_c0_seq2.p1	Ec-10_001310.1	Mitogen-activated protein kinase	GO:0005524;GO:0006468;GO:0004672
comp34498_c0_seq1.p1	Ec-10_001320.1	NAD(P)-binding domain	GO:0003824;GO:0005488;GO:0008152;n/a
comp34369_c0_seq1.p1	Ec-10_001330.1	eukaryotic elongation factor-1 B gamma	n/a;n/a;n/a
comp26313_c0_seq5.p1	Ec-10_001340.1	EF-hand domain pair	GO:0005509
comp33680_c0_seq1.p1	Ec-10_001350.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468
comp20904_c0_seq1.p1	Ec-10_001370.1	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplast precursor	GO:0005524
comp29137_c0_seq2.p1	Ec-10_001400.1	Domain of unknown function DUF1336	n/a;n/a;n/a
comp29137_c0_seq2.p2	Ec-10_001410.1	Serine/threonine protein kinase	GO:0005524;GO:0006468;GO:0004672
comp26278_c0_seq2.p1	Ec-10_001420.1	Fatty acid desaturase	GO:0006629
comp30791_c0_seq4.p1	Ec-10_001430.1	Predicted unusual protein kinase	GO:0016772
comp30791_c0_seq3.p1	Ec-10_001440.1	DNA polymerase, palm domain	GO:0003677;GO:0006260;GO:0006139;GO:0003676;GO:0003887;GO:0000166
comp29297_c0_seq1.p1	Ec-10_001450.1	expressed unknown protein	n/a;n/a;n/a
comp26772_c0_seq2.p1	Ec-10_001480.1	2-succinylbenzoate--CoA ligase-like	GO:0008152;GO:0003824
comp34327_c0_seq1.p1	Ec-10_001490.1	Hypothetical protein	n/a;n/a;n/a
comp32648_c4_seq1.p1	Ec-10_001500.1	Arginyl-tRNA protein transferase	GO:0016598;GO:0042176;GO:0004057
comp69429_c0_seq1.p2	Ec-10_001510.1	possible vacuolar protein. Armadillo/beta-catenin-like repeats	GO:0005488
comp24213_c1_seq2.p1	Ec-10_001520.1	Domain of unknown function DUF814	n/a;n/a;n/a
comp21016_c0_seq1.p1	Ec-10_001530.1	Tetratricopeptide-like helical domain	GO:0005515
comp21016_c0_seq2.p1	Ec-10_001540.1	Protein of unknown function DUF819	GO:0031177
comp26820_c0_seq5.p1	Ec-10_001550.1	Plastid lipid-associated protein/fibrillin conserved domain	GO:0005198
comp24858_c0_seq1.p1	Ec-10_001560.1	conserved unknown protein	GO:0016021
comp27104_c0_seq2.p1	Ec-10_001570.1	Proteasome component (PCI) domain	GO:0005737;GO:0003743;GO:0005515;GO:0005852
comp32062_c3_seq1.p1	Ec-10_001600.1	expressed unknown protein	n/a;n/a;n/a
comp31777_c0_seq3.p1	Ec-10_001610.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0031072
comp30111_c1_seq1.p1	Ec-10_001650.1	Galactosyl transferase	GO:0016758;GO:0016757;GO:0005794;GO:0016021
comp29897_c0_seq1.p1	Ec-10_001660.1	Zinc finger, MYND-type	GO:0008270
comp24421_c0_seq2.p1	Ec-10_001670.1	conserved unknown protein	n/a;n/a;n/a
comp29866_c0_seq1.p1	Ec-10_001680.1	BTB/POZ	GO:0005515
comp19974_c0_seq1.p1	Ec-10_001700.3	Mannosyl-oligosaccharide 1,2-alpha-mannosidase, family GH47	GO:0004571;GO:0005509;GO:0016020
comp27104_c0_seq2.p2	Ec-10_001710.2	Vacuolar protein sorting-associate protein Vta1/Callose synthase, N-terminal domain	n/a;n/a;n/a
comp27435_c0_seq2.p1	Ec-10_001810.1	D-isomer specific 2-hydroxyacid dehydrogenase	GO:0003824;GO:0005488;GO:0008152
comp11722_c0_seq1.p1	Ec-10_001820.2	expressed unknown protein	n/a;n/a;n/a
comp32845_c0_seq5.p1	Ec-10_001830.1	Hypothetical leucine rich repeat protein	GO:0005515;GO:0005509
comp24497_c0_seq2.p1	Ec-10_001840.1	P-type ATPase, subfamily IV	GO:0000287;GO:0004012;GO:0005524;GO:0015914;GO:0016021
comp28566_c0_seq2.p1	Ec-10_001880.1	Hypothetical protein	n/a;n/a;n/a
comp33099_c0_seq13.p1	Ec-10_001890.1	possible NAD/NADP octopine/nopaline dehydrogenase	GO:0003824;GO:0005488;GO:0008152
comp28276_c0_seq1.p1	Ec-10_001920.1	Armadillo-like helical	NA
comp34392_c0_seq1.p1	Ec-10_001940.1	60S ribosomal protein L28	GO:0005840;GO:0006412;GO:0005622;GO:0003735
comp25736_c0_seq2.p1	Ec-10_001950.1	Cupin 2, conserved barrel	n/a;n/a;n/a
comp31043_c0_seq6.p1	Ec-10_001970.1	Protein of unknown function DUF2358	n/a;n/a;n/a
comp32344_c0_seq8.p1	Ec-10_001980.1	Histone deacetylase domain protein	NA
comp26476_c0_seq2.p1	Ec-10_001990.1	WD40-repeat-containing domain	GO:0005515;GO:0008380
comp25568_c1_seq1.p1	Ec-10_002060.1	RNA polymerase II-associated protein 1, C-terminal	GO:0008152;GO:0003824;GO:0030170
comp32612_c0_seq2.p1	Ec-10_002070.1	Actin family	GO:0005515
comp25392_c0_seq2.p1	Ec-10_002110.1	EXS conserved domain	GO:0016021
comp26791_c0_seq1.p1	Ec-10_002120.1	Hypothetical protein	n/a;n/a;n/a
comp28012_c0_seq2.p1	Ec-10_002130.1	conserved unknown protein	GO:0001584;GO:0007186;GO:0016021
comp30480_c0_seq6.p1	Ec-10_002140.1	WD40/YVTN repeat-like-containing domain	GO:0005515
comp19760_c1_seq3.p1	Ec-10_002140.2	WD40/YVTN repeat-like-containing domain	GO:0005515
comp45943_c0_seq1.p1	Ec-10_002150.1	WD40 repeat	GO:0005515
comp32991_c1_seq1.p1	Ec-10_002170.1	CHROMODOMAIN HELICASE DNA BINDING	GO:0003677;GO:0005524;GO:0004386;GO:0003676
comp33133_c8_seq1.p1	Ec-10_002180.1	Cupin-like domain protein	n/a;n/a;n/a
comp12771_c0_seq2.p1	Ec-10_002190.1	6-pyruvoyl tetrahydropterin synthase/QueD family protein	n/a;n/a;n/a
comp11984_c0_seq1.p1	Ec-10_002210.1	DnaJ domain	GO:0004871;GO:0005622;GO:0007275
comp20596_c0_seq1.p1	Ec-10_002220.1	expressed unknown protein	n/a;n/a;n/a
comp19392_c0_seq1.p1	Ec-10_002230.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0006875;n/a
comp29661_c0_seq1.p1	Ec-10_002240.1	TLDc domain	GO:0005097;GO:0005622;GO:0032313
comp12856_c0_seq1.p1	Ec-10_002250.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	GO:0016020;GO:0016192;GO:0006886
comp9811_c0_seq1.p1	Ec-10_002260.2	hypothetical protein	NA
comp26614_c0_seq2.p1	Ec-10_002270.1	expressed unknown protein	n/a;n/a;n/a
comp25754_c1_seq1.p1	Ec-10_002280.1	conserved unknown protein	n/a;n/a;n/a
comp31748_c0_seq9.p1	Ec-10_002320.1	WW domain	GO:0005515
comp29507_c0_seq1.p1	Ec-10_002370.1	Tyrosyl-DNA phosphodiesterase C-terminal domain	n/a;n/a;n/a
comp32029_c3_seq9.p1	Ec-10_002390.1	Zinc finger, RING/FYVE/PHD-type	GO:0003700;GO:0005634;GO:0006355
comp29266_c0_seq2.p1	Ec-10_002430.1	sirohydrochlorin ferrochelatase, putative chloroplast precursor	GO:0009236;GO:0016852
comp24491_c0_seq1.p1	Ec-10_002440.1	hypothetical protein	n/a;n/a;n/a
comp27625_c0_seq5.p1	Ec-10_002450.1	Pyridoxal 5'-phosphate synthase	GO:0008152;GO:0003824;GO:0042823
comp30324_c0_seq1.p1	Ec-10_002460.1	Nucleotide-binding alpha-beta plait domain	GO:0000166
comp31741_c0_seq3.p1	Ec-10_002470.4	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a
comp30960_c0_seq4.p1	Ec-10_002480.1	Fimbrin	GO:0005515
comp31116_c0_seq3.p1	Ec-10_002530.1	Cellulose synthase (UDP-forming), family GT2	NA
comp27314_c0_seq2.p1	Ec-10_002540.3	Hypothetical protein	n/a;n/a;n/a
comp20337_c0_seq3.p1	Ec-10_002550.1	expressed unknown protein	n/a;n/a;n/a
comp20688_c0_seq1.p1	Ec-10_002560.1	Mpv17/PMP22	GO:0016021
comp58624_c0_seq1.p2	Ec-10_002570.1	Kelch-type beta propeller	GO:0005515
comp25075_c0_seq1.p1	Ec-10_002610.1	RNA-induced silencing complex, nuclease component Tudor-SN	GO:0016442;GO:0031047
comp34236_c0_seq1.p1	Ec-10_002620.1	30s ribosomal protein S13, C-terminal	GO:0005840;GO:0003723;GO:0005622;GO:0006412;GO:0003735
comp30511_c0_seq1.p1	Ec-10_002640.2	hypothetical protein	n/a;n/a;n/a
comp20103_c0_seq1.p1	Ec-10_002650.1	Protein of unknown function DUF177	n/a;n/a;n/a
comp21091_c0_seq2.p2	Ec-10_002670.1	conserved unknown protein	n/a;n/a;n/a
comp20024_c0_seq1.p1	Ec-10_002680.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468
comp58498_c0_seq1.p1	Ec-10_002700.1	conserved unknown protein	n/a;n/a;n/a
comp24747_c0_seq2.p1	Ec-10_002710.1	ADF-H/Gelsolin-like domain	GO:0005515;GO:0006886;GO:0006888;GO:0030127
comp32082_c0_seq1.p1	Ec-10_002720.1	F-box domain	GO:0005515
comp12089_c0_seq1.p1	Ec-10_002740.1	Hypothetical protein	n/a;n/a;n/a
comp30726_c0_seq2.p1	Ec-10_002750.1	Nucleophile aminohydrolases, N-terminal	GO:0051603;GO:0004298;GO:0005839;GO:0006511
comp32798_c0_seq6.p1	Ec-10_002760.1	ENTH/VHS	n/a;n/a;n/a
comp31372_c0_seq9.p2	Ec-10_002770.1	putative carbonic anhydrase	GO:0008415;GO:0016740
comp27565_c0_seq1.p1	Ec-10_002780.1	conserved unknown protein	n/a;n/a;n/a
comp30598_c0_seq5.p1	Ec-10_002790.1	hypothetical protein	n/a;n/a;n/a
comp24986_c0_seq2.p1	Ec-10_002840.1	Alpha/beta hydrolase fold-3	GO:0008152;GO:0016787
comp9472_c0_seq2.p1	Ec-10_002850.1	Hypothetical leucine rich repeat protein	NA
comp30888_c0_seq5.p1	Ec-10_002870.1	Oligosaccharyl transferase complex, subunit OST3/OST6	NA
comp30888_c0_seq6.p2	Ec-10_002880.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777
comp11916_c0_seq1.p1	Ec-10_002890.1	SR RNA splicing protein	GO:0003676;GO:0000166
comp20153_c0_seq2.p1	Ec-10_002900.1	Ribosomal protein L14b/L23e	GO:0003735;GO:0005840;GO:0006412
comp12056_c0_seq1.p1	Ec-10_002940.1	Protein phosphatase 4 core regulatory subunit R2	n/a;n/a;n/a
comp21584_c0_seq1.p1	Ec-10_002950.1	Riboflavin kinase domain, bacterial/eukaryotic	GO:0009231;GO:0008531
comp29353_c0_seq2.p1	Ec-10_002970.1	MutS protein homolog 1B MutS-like ATPases involved in mismatch repair, family 1	n/a;n/a;n/a
comp26006_c0_seq1.p1	Ec-10_002980.1	LIP1, Ras superfamily GTPase	GO:0005525;GO:0007264
comp11689_c0_seq1.p1	Ec-10_003020.1	Farnesyl pyrophosphate synthase	GO:0008299
comp12085_c0_seq1.p1	Ec-10_003030.1	Cytochrome c/c1 haem-lyase	GO:0004408;GO:0005739
comp29429_c1_seq2.p1	Ec-10_003040.1	Plus-3 domain, subgroup	GO:0005634;GO:0003677;GO:0016593;GO:0006352;GO:0016570;GO:0006368
comp29688_c1_seq1.p1	Ec-10_003110.1	Methyltransferase type 11	GO:0008152;GO:0008168
comp32920_c2_seq1.p1	Ec-10_003130.1	Ankyrin repeats, transient-receptor-potential calcium channel	GO:0005515
comp28147_c0_seq2.p1	Ec-10_003150.1	conserved unknown protein	n/a;n/a;n/a
comp29051_c1_seq3.p1	Ec-10_003170.1	transportin 1 isoform 2	GO:0005488
comp27390_c0_seq1.p1	Ec-10_003190.1	hypothetical protein	NA
comp24219_c0_seq1.p1	Ec-10_003200.1	Ubiquitin-conjugating enzyme E2	GO:0019787;GO:0043687;GO:0051246
comp14095_c0_seq1.p1	Ec-10_003220.1	EF-hand domain pair	GO:0005509
comp27423_c0_seq3.p1	Ec-10_003230.1	Peptidase C19, ubiquitin-specific peptidase, DUSP domain	GO:0004843
comp29985_c0_seq1.p1	Ec-10_003250.1	hypothetical protein	n/a;n/a;n/a
comp12291_c0_seq1.p1	Ec-10_003260.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a
comp20871_c0_seq1.p1	Ec-10_003270.1	Phosphoribosylaminoimidazole carboxylase PurE domain	GO:0006189
comp12776_c0_seq1.p1	Ec-10_003290.1	Early transcription elongation factor of RNA pol II, NGN section	n/a;n/a;n/a
comp19367_c0_seq1.p2	Ec-10_003300.1	expressed unknown protein	n/a;n/a;n/a
comp27315_c0_seq2.p1	Ec-10_003310.1	Glycerol-3-phosphate dehydrogenase	GO:0016491;GO:0055114
comp21171_c0_seq1.p1	Ec-10_003320.1	T-complex protein, epsilon subunit	GO:0005524;GO:0044267
comp30864_c0_seq3.p1	Ec-10_003330.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp30434_c0_seq1.p1	Ec-10_003340.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp25448_c0_seq2.p1	Ec-10_003350.1	Zinc finger, U1-type	GO:0005634;GO:0003676;GO:0008270
comp32615_c1_seq31.p1	Ec-10_003370.5	hypothetical protein	n/a;n/a;n/a
comp32615_c1_seq22.p1	Ec-10_003390.3	expressed unknown protein	GO:0005215;GO:0006810;GO:0016020;GO:0055085
comp27670_c0_seq1.p1	Ec-10_003470.1	Bifunctional glycosyltransferase, family GT74 / family GT2	NA
comp31038_c0_seq4.p1	Ec-10_003510.1	P38 Map Kinase family member (pmk-1)	GO:0004672;GO:0005524;GO:0006468
comp28762_c0_seq5.p1	Ec-10_003520.2	conserved unknown protein	n/a;n/a;n/a
comp32811_c0_seq16.p1	Ec-10_003530.2	Nascent polypeptide-associated complex subunit alpha	n/a;n/a;n/a
comp24846_c0_seq1.p1	Ec-10_003550.1	hypothetical protein	n/a;n/a;n/a
comp26713_c0_seq1.p1	Ec-10_003560.1	Plastid lipid-associated protein/fibrillin conserved domain	GO:0005198
comp20723_c0_seq1.p1	Ec-10_003570.1	conserved unknown protein	n/a;n/a;n/a
comp29396_c0_seq2.p1	Ec-10_003590.1	Domain of unknown function DUF625	n/a;n/a;n/a
comp12128_c0_seq1.p1	Ec-10_003600.1	Ribosomal RNA large subunit methyltransferase RlmN/Cfr	GO:0005737;GO:0006364;GO:0008173
comp12561_c0_seq1.p1	Ec-10_003620.1	hypothetical protein	n/a;n/a;n/a
comp29223_c0_seq1.p1	Ec-10_003630.1	Armadillo-type fold	GO:0005488
comp12659_c0_seq1.p1	Ec-10_003650.1	Methyltransferase type 11	GO:0008152;GO:0008168
comp31619_c0_seq10.p1	Ec-10_003670.1	hypothetical protein	n/a;n/a;n/a
comp31241_c0_seq7.p1	Ec-10_003680.1	KIF-1 binding protein	n/a;n/a;n/a
comp29143_c0_seq1.p3	Ec-10_003710.1	Tim17 homolog, mitochondrial inner membrane protein of TIM23 complex	GO:0005743;GO:0008565;GO:0015031

comp33498_c0_seq1.p1	Ec-10_003730.1	Carbohydrate kinase	GO:0005975;GO:0016773	PTHR10196:SF57: ; PTHR10196: ; G3DSA:3.30.420.40: ; IPR018485: Carbohydrate kinase, FGGY, C-terminal; IPR018484: Carbohydrate kinase, FGGY, N-terminal; SSF53067:	NA
comp29143_c0_seq1.p1	Ec-10_003740.1	conserved unknown protein	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32411_c1_seq13.p1	Ec-10_003770.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0016887	PTHR19211: ; IPR003593: AAA+ ATPase domain; IPR003439: ABC transporter-like; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; PF12848: ABC transporter; IPR017871: ABC transporter, conserved site	NA
comp27566_c0_seq3.p1	Ec-10_003810.1	Methylmalonate Semialdehyde Dehydrogenase	GO:0016620;GO:0008152;GO:0055114;GO:0004491;GO:0016491	IPR016161: Aldehyde/histidinol dehydrogenase; IPR015590: Aldehyde dehydrogenase domain; IPR016162: Aldehyde dehydrogenase N-terminal domain; IPR016160: Aldehyde dehydrogenase, cysteine active site; IPR010061: Methylmalonate-semialdehyde dehydrogenase; PTHR11699: ; IPR016163: Aldehyde dehydrogenase, C-terminal	KOG2449
comp34222_c0_seq1.p1	Ec-10_003900.1	Ribosomal protein L18e/L15P	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR021131: Ribosomal protein L18e/L15P; IPR030878: Ribosomal protein L15; PTHR11721: ; G3DSA:3.100.10.10: ; IPR001196: Ribosomal protein L15, conserved site	NA
comp20192_c0_seq1.p1	Ec-10_003910.1	Putative tyrosine phosphatase	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR007482: Protein-tyrosine phosphatase-like, PTPLA; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3187
comp34320_c0_seq1.p1	Ec-10_003920.1	ATP-dependent Clp protease, proteolytic subunit	GO:0004252;GO:0006508;GO:0008462	IPR029045: ClpP/crotonase-like domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR018215: ClpP, active site; IPR001907: ATP-dependent Clp protease proteolytic subunit; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023562: Clp protease proteolytic subunit /Translocation-enhancing protein TepA	KOG0840
comp12351_c0_seq1.p2	Ec-10_003970.1	er lumen protein retaining receptor 1	GO:0006621;GO:0046923;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000133: ER lumen protein retaining receptor; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28917_c0_seq4.p1	Ec-10_003980.1	Sterile alpha motif, type 1	GO:0005515	IPR013761: Sterile alpha motif/pointed domain; IPR001841: Zinc finger, RING-type; IPR021129: Sterile alpha motif, type 1; IPR009030: Insulin-like growth factor binding protein, N-terminal; IPR004087: K Homology domain; IPR004088: K Homology domain, type 1; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR001202: WW domain; PF13920: Zinc finger, C3HC4 type (RING finger); Coil: ; G3DSA:2.20.70.10:	NA
comp32797_c1_seq19.p1	Ec-10_003990.1	Complex 1 LYR protein	n/a;n/a;n/a	IPR008011: Complex 1 LYR protein; IPR026868: LYR motif-containing protein 2	NA
comp25328_c0_seq1.p1	Ec-10_004000.2	Rab8C, RAB family GTPase	GO:0005524;GO:0006355;GO:0007264;GO:0005622;GO:0005525;GO:0008134;GO:0015031	PTHR24073:SF380: ; IPR002041: Ran GTPase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; IPR003579: Small GTPase superfamily, Rab type; IPR020849: Small GTPase superfamily, Ras type; PS51419: small GTPase Rab1 family profile.; PR00449: Transforming protein P21 ras signature; Coil: ; PTHR24073:	NA
comp26322_c0_seq1.p1	Ec-10_004010.1	Sulfotransferase	GO:0001733;GO:0005794;GO:0009058;GO:0016021	IPR009729: Galactose-3-O-sulfotransferase; PTHR14647:SF60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp33743_c0_seq1.p1	Ec-10_004040.1	AAA family ATPase	GO:0004252;GO:0006508;GO:0004289	IPR003959: ATPase, AAA-type, core; IPR003593: AAA+ ATPase domain; IPR003960: ATPase, AAA-type, conserved site; G3DSA:1.10.8.60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; PTHR23077:	NA
comp29859_c1_seq2.p1	Ec-10_004060.1	Domain of unknown function DUF1683, C-terminal	n/a;n/a;n/a	PTHR14374: ; IPR012880: Domain of unknown function DUF1683, C-terminal; IPR021773: Foie gras liver health family 1	NA
comp34493_c0_seq1.p1	Ec-10_004070.1	Hippocampus abundant transcript 1 protein (Putative tetracycline transporter-like protein)	n/a;GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24003: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001958: Tetracycline resistance protein, TetA/multidrug resistance protein MdtG; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31179_c1_seq2.p1	Ec-10_004080.1	Protein of unknown function DUF2306, membrane	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR018750: Protein of unknown function DUF2306, membrane; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34622_c0_seq1.p1	Ec-10_004130.1	SKI-interacting protein, SKIP	GO:0000398;GO:0005681	IPR017862: SKI-interacting protein, SKIP; IPR004015: SKI-interacting protein SKIP, SNW domain; Coil:	NA
comp29146_c0_seq1.p1	Ec-10_004150.2	Small Conductance Mechanosensitive Ion channel	GO:0016020;GO:0055085	IPR018247: EF-Hand 1, calcium-binding site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; PTHR31618:SF1: ; G3DSA:2.30.30.60: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR31618: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006685: Mechanosensitive ion channel MscS; IPR010920: LSM domain	KOG4629
comp34178_c0_seq1.p1	Ec-10_004180.1	Cysteinyl-tRNA Synthetase	GO:0005524;GO:0006418;GO:0000166;GO:0004812	IPR015803: Cysteine-tRNA ligase; SIGNAL_PEPTIDE: Signal peptide region; IPR024909: Cysteinyl-tRNA synthetase/mycothiol ligase; IPR015273: Cysteinyl-tRNA synthetase, class Ia, DALR; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR009080: Aminoacyl-tRNA synthetase, class 1a, anticodon-binding; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; SSF52374: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.120.640: ; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2007
comp26045_c0_seq1.p1	Ec-10_004190.2	beta(1,4)-N-acetylglucosaminyltransferase	n/a;n/a;n/a	PTHR12154:SF4: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; G3DSA:3.40.50.2000: ; IPR013969: Oligosaccharide biosynthesis protein Alg14-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG3339
comp20138_c0_seq1.p1	Ec-10_004220.1	Coatomer protein complex, gamma sub-unit	GO:0016192;GO:0006886;GO:0030117;GO:0005515;GO:0006461	IPR011989: Armadillo-like helical; IPR017109: Adaptor protein complex AP-4, epsilon subunit; IPR028269: AP-4 complex subunit epsilon-1, C-terminal; IPR016024: Armadillo-type fold; PTHR22780: ; IPR002553: Clathrin/coatomer adaptor, adaptin-like, N-terminal	KOG1062
comp31700_c0_seq7.p1	Ec-10_004250.1	C2H2 zinc finger protein	GO:0006352;GO:0006355;GO:0008270	IPR000812: Transcription factor TFIIB; PTHR11618:SF22: ; IPR007087: Zinc finger, C2H2; SSF57783: ; G3DSA:2.20.25.10:	NA
comp22896_c0_seq1.p1	Ec-10_004270.1	Atlastin, dynamin-related GTPase	GO:0005525;GO:0003924	G3DSA:1.20.1000.10: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003191: Guanylate-binding protein, C-terminal; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR015894: Guanylate-binding protein, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10751: ; IPR030386: GB1/RHD3-type guanine nucleotide-binding (G) domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34055_c0_seq1.p1	Ec-10_004300.1	Alpha-1,2-mannosyltransferase, family GT22	GO:0006506;GO:0031227;GO:0016757	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005599: GPI mannosyltransferase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24341_c0_seq1.p1	Ec-10_004310.1	conserved unknown protein	GO:0006118;GO:0009055;GO:0016491	PF13450: NAD(P)-binding Rossmann-like domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR10668: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.50.50.60: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF51905:	NA
comp33138_c0_seq5.p1	Ec-10_004320.1	ApaG domain	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR14289: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007474: ApaG domain; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26575_c0_seq4.p1	Ec-10_004330.1	Beta-lactamase-like	GO:0016787	PTHR12553: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF12706: Beta-lactamase superfamily domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:3.60.15.10: ; SSF56281: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31953_c0_seq3.p1	Ec-10_004340.1	Armadillo-like helical	n/a;GO:0008565;GO:0005488;GO:0006886	IPR001494: Importin-beta, N-terminal domain; IPR014877: CRM1 C-terminal domain; IPR011989: Armadillo-like helical; PTHR12596: ; IPR016024: Armadillo-type fold	NA
comp19602_c0_seq1.p2	Ec-10_004380.1	RNA polymerase Rpb7, N-terminal	GO:0003899;GO:0006351	IPR012340: Nucleic acid-binding, OB-fold; IPR003029: S1 domain; PTHR12709: ; IPR005576: RNA polymerase Rpb7, N-terminal	NA
comp26836_c0_seq1.p1	Ec-10_004390.3	Nucleosome assembly protein (NAP)	GO:0005634;GO:0006334	SSF143113: ; PTHR11875:SF49: ; IPR002164: Nucleosome assembly protein (NAP)	NA
comp33720_c0_seq1.p1	Ec-10_004400.1	WD40 repeat	GO:0005515	IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; IPR006594: LIS1 homology motif; IPR020472: G-protein beta WD-40 repeat; PTHR22848:	NA
comp25994_c0_seq2.p1	Ec-10_004410.1	elongation factor P	GO:0003746;GO:0006414	IPR013852: Translation elongation factor P/YeiP, conserved site; IPR011768: Translation elongation factor P; IPR012340: Nucleic acid-binding, OB-fold; IPR013185: Translation elongation factor, KOW-like; IPR014722: Ribosomal protein L2 domain 2; IPR015365: Elongation factor P, C-terminal; IPR008991: Translation protein SH3-like domain; IPR001059: Translation elongation factor P/YeiP, central; PTHR30053:	NA
comp19638_c0_seq2.p1	Ec-10_004420.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp21643_c0_seq3.p1	Ec-10_004440.1	carnitine/choline acetyltransferase	GO:0016746	IPR000542: Acyltransferase ChoActase/COT/CPT; SSF52777:	KOG3719
comp32734_c0_seq19.p1	Ec-10_004450.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32851_c1_seq22.p1	Ec-10_004460.1	DNA binding domain, putative	GO:0003684;GO:0005634;GO:0006289	IPR009061: Putative DNA-binding domain; IPR022656: XPA C- terminal; PTHR10142:SF0: ; IPR000465: XPA	NA
comp32390_c0_seq24.p1	Ec-10_004480.1	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase, family GT41	GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; IPR029489: O-GlcNAc transferase, C-terminal; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; PTHR23083: ; IPR019734: Tetratricopeptide repeat	NA
comp19588_c0_seq1.p1	Ec-10_004530.1	Zinc finger, RING-type	GO:0005515;GO:0008270	IPR017907: Zinc finger, RING-type, conserved site; IPR001841: Zinc finger, RING-type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF13923: Zinc finger, C3HC4 type (RING finger); PTHR22894: ; IPR010652: Protein of unknown function DUF1232; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31117_c4_seq1.p1	Ec-10_004540.1	Suppressor of white apricot N-terminal domain	n/a;n/a;n/a	IPR019147: Suppressor of white apricot N-terminal domain; Coil: ; PTHR13161:	NA
comp26893_c0_seq4.p1	Ec-10_004560.4	Notch domain	GO:0016020;GO:0030154	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000800: Notch domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21459_c0_seq1.p1	Ec-10_004590.1	Ribosomal protein L11, bacterial-type	GO:0005840;GO:0006412;GO:0003735	PD001367: RIBOSOMAL RIBONUCLEOPROTEIN L11 RRNA-BINDING RNA-BINDING METHYLATION 50S L11 BACTERIAL CHLOROPLAST; IPR020783: Ribosomal protein L11, C-terminal; IPR006519: Ribosomal protein L11, bacterial-type; IPR020784: Ribosomal protein L11, N-terminal; IPR000911: Ribosomal protein L11/L12	NA
comp32527_c0_seq66.p1	Ec-10_004600.1	Ankyrin Repeat Transient Receptor Potential Channel	NA	IPR029877: Transient receptor potential-gamma protein; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR002153: Transient receptor potential channel, canonical; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005821: Ion transport domain; IPR020683: Ankyrin repeat-containing domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3614
comp25867_c3_seq2.p1	Ec-10_004650.1	putative anion:sodium symporter	GO:0016020	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR002657: Bile acid:sodium symporter/arsenical resistance protein Acr3; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11734_c0_seq1.p1	Ec-10_004660.1	CRAL-TRIO domain	n/a;n/a;n/a	PTHR10174: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011074: CRAL/TRIO, N-terminal domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001251: CRAL-TRIO domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27284_c1_seq1.p1	Ec-10_004730.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp27284_c1_seq2.p1	Ec-10_004740.1	TatD family	GO:0016888	IPR018228: Deoxyribonuclease, TatD-related, conserved site; IPR001130: TatD family; SSF51556: ; G3DSA:3.20.20.140:	NA
comp32187_c0_seq14.p1	Ec-10_004770.1	RNA polymerase 1-4 RNA polymerase I large subunit	GO:0003677;GO:0006351;GO:0003899;GO:0006350	IPR006592: RNA polymerase, N-terminal; SSF64484: ; IPR000722: RNA polymerase, alpha subunit; IPR007080: RNA polymerase Rpb1, domain 1; IPR007066: RNA polymerase Rpb1, domain 3; PTHR19376: ; IPR015699: DNA-directed RNA pol I, largest subunit; IPR007083: RNA polymerase Rpb1, domain 4; G3DSA:2.40.40.20: ; IPR007081: RNA polymerase Rpb1, domain 5; G3DSA:3.30.1490.180:	KOG0262
comp27975_c0_seq1.p1	Ec-10_004800.1	SH2 domain containing protein	GO:0003700;GO:0004871;GO:0005634;GO:0006355;GO:0007165;GO:0007242	IPR024983: CHAT domain; IPR000980: SH2 domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp12399_c0_seq1.p2	Ec-10_004830.1	Chaperonin Cpn10	GO:0005737;GO:0006457	IPR020818: Chaperonin Cpn10; IPR011032: GroES (chaperonin 10)-like	NA
comp20419_c0_seq2.p1	Ec-10_004860.1	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain	GO:0051287;GO:0055114	IPR000595: Cyclic nucleotide-binding domain; SSF51735: ; IPR006140: D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain; IPR006139: D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain; IPR018490: Cyclic nucleotide-binding-like; SSF52283: ; IPR016040: NAD(P)-binding domain; PTHR10996: ; IPR014710: RmlC-like jelly roll fold	NA
comp31134_c0_seq2.p2	Ec-10_004870.1	PDCD5-related protein	GO:0003677	IPR002836: PDCD5-related protein	NA
comp31134_c0_seq2.p1	Ec-10_004880.1	Duplicated hybrid motif	n/a;n/a;n/a	IPR011055: Duplicated hybrid motif; G3DSA:2.70.70.10: ; IPR016047: Peptidase M23	NA
comp27553_c0_seq1.p1	Ec-10_004890.2	conserved unknown protein	NA	NA	NA
comp11743_c0_seq1.p1	Ec-10_004940.1	Domain of unknown function DUF1279	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR009688: Domain of unknown function DUF1279; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24889_c0_seq1.p1	Ec-10_004950.1	U3 snoRNP-associated protein Utp7	GO:0005515	IPR012952: BING4, C-terminal domain; PD023243: REPEAT WD VACUOLE CHROMOSOME WD-REPEAT READING FRAME OPEN MEMBRANE AUTOPHAGY; IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; PTHR14085:	NA
comp28735_c1_seq1.p1	Ec-10_004960.1	Patatin/Phospholipase A2-related	GO:0006629	PTHR12406: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016035: Acyl transferase/acyl hydrolase/lysophospholipase; IPR002641: Patatin/Phospholipase A2-related; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25775_c0_seq1.p1	Ec-10_004970.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp24199_c0_seq2.p1	Ec-10_004980.1	fructose-1,6-bisphosphate aldolase	GO:0004332;GO:0006096	IPR029769: Fructose-bisphosphate aldolase class-I, eukaryotic-type; IPR013785: Aldolase-type TIM barrel; SIGNAL_PEPTIDE: Signal peptide region; IPR029768: Fructose-bisphosphate aldolase class-I active site; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SSF51569: ; Coil: ; IPR000741: Fructose-bisphosphate aldolase, class-I; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31901_c0_seq4.p1	Ec-10_004990.2	Ankyrin repeat-containing domain	n/a;n/a;n/a	IPR020683: Ankyrin repeat-containing domain; PF13857: Ankyrin repeats (many copies); PTHR24193: ; IPR002110: Ankyrin repeat	NA
comp31960_c0_seq5.p1	Ec-10_005030.1	Phosphoacetylglucosamine mutase	GO:0004610;GO:0016868;GO:0005975	IPR005843: Alpha-D-phosphohexomutase, C-terminal; IPR005846: Alpha-D-phosphohexomutase, alpha/beta/alpha domain III; IPR016657: Phosphoacetylglucosamine mutase; IPR005845: Alpha-D-phosphohexomutase, alpha/beta/alpha domain II; IPR016055: Alpha-D-phosphohexomutase, alpha/beta/alpha I/II/III; PTHR22573: ; IPR005844: Alpha-D-phosphohexomutase, alpha/beta/alpha domain I	NA
comp32480_c0_seq24.p1	Ec-10_005070.2	DNA polymerase	GO:0003676	SSF56672: ; IPR006133: DNA-directed DNA polymerase, family B, exonuclease domain; PTHR10670:SF0: ; IPR006134: DNA-directed DNA polymerase, family B, multifunctional domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013697: DNA polymerase epsilon, catalytic subunit A, C-terminal; IPR012337: Ribonuclease H-like domain; Coil: ; IPR006172: DNA-directed DNA polymerase, family B; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10670:	NA
comp33157_c1_seq27.p1	Ec-10_005080.1	Rab11A, RAB family GTPase	GO:0016020;GO:0007165;GO:0007264;GO:0005525;GO:0015031	IPR002041: Ran GTPase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR005225: Small GTP-binding protein domain; IPR001806: Small GTPase superfamily; IPR003579: Small GTPase superfamily, Rab type; IPR020849: Small GTPase superfamily, Ras type; PS51419: small GTPase Rab1 family profile.; PTHR24073:	NA
comp20336_c0_seq1.p1	Ec-10_005100.2	CTLH, C-terminal LisH motif	NA	NA	NA
comp26889_c0_seq2.p1	Ec-10_005110.1	SPRY domain	GO:0005515	IPR001870: B30.2/SPRY domain; PTHR12864: ; IPR013320: Concanavalin A-like lectin/glucanase domain; IPR003877: SPRY domain	NA
comp11863_c0_seq1.p1	Ec-10_005120.1	Conserved unknown protein	NA	NA	NA
comp33919_c0_seq1.p1	Ec-10_005130.1	SAP domain	GO:0003676	IPR003034: SAP domain; PTHR21594: ; SSF68906:	NA
comp30691_c0_seq1.p1	Ec-10_005150.1	expressed unknown protein	NA	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011057: Mss4-like; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30691_c0_seq1.p2	Ec-10_005160.1	Major facilitator superfamily	GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24003: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001958: Tetracycline resistance protein, TetA/multidrug resistance protein MdtG; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31269_c0_seq4.p1	Ec-10_005170.1	MPN/PAD-1 domain-containing protein	GO:0005515	IPR015063: USP8 dimerisation domain; IPR000555: JAB1/MPN/MOV34 metalloenzyme domain; PTHR12947: ; G3DSA:3.40.140.10: ; SSF102712: ; Coil:	NA
comp25270_c0_seq3.p1	Ec-10_005190.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR002885: Pentatricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; PTHR24015:	NA
comp31497_c1_seq9.p1	Ec-10_005200.1	conserved unknown protein	GO:0005622;GO:0003676	IPR022159: Tuftelin interacting protein, N-terminal domain; IPR022783: GC-rich sequence DNA-binding factor domain; PTHR23329: ; SIGNAL_PEPTIDE: Signal peptide region; IPR000467: G-patch domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF101447: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2184
comp11360_c0_seq1.p1	Ec-10_005240.1	rRNA small subunit methyltransferase G	GO:0006364;GO:0005737;GO:0008649	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR003034: SAP domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR003682: rRNA small subunit methyltransferase G; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR31760:	NA
comp12948_c0_seq1.p1	Ec-10_005250.1	Zinc finger, HIT-type	n/a;n/a;n/a	IPR007529: Zinc finger, HIT-type; PTHR15555: ; SSF144232:	NA
comp26665_c0_seq2.p1	Ec-10_005260.1	Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase, family GH85	GO:0033925;GO:0005737	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR005201: Glycoside hydrolase, family 85; PTHR13246: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2331
comp24938_c0_seq1.p1	Ec-10_005270.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	IPR001678: SAM-dependent methyltransferase RsmB/NOP2-type; PTHR22807: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR023267: RNA (C5-cytosine) methyltransferase; Coil:	NA
comp30546_c0_seq3.p1	Ec-10_005300.1	Similarity to ribonuclease D (RNase D)	GO:0002161	PTHR13620: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR007214: YbaK/aminoacyl-tRNA synthetase-associated domain; IPR002562: 3'-5' exonuclease domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR012337: Ribonuclease H-like domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29349_c0_seq8.p3	Ec-10_005320.1	SR RNA splicing protein	GO:0003676;GO:0000166	NA	NA
comp33909_c0_seq1.p1	Ec-10_005330.1	TH1 protein	GO:0045892;GO:0005634;GO:0005515	IPR001202: WW domain; IPR006942: TH1 protein; Coil: ; G3DSA:2.20.70.10:	NA
comp29349_c0_seq13.p1	Ec-10_005340.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp11859_c0_seq1.p1	Ec-10_005350.1	E2F-associated phosphoprotein	n/a;n/a;n/a	IPR019370: E2F-associated phosphoprotein; PTHR15967:	NA
comp26799_c0_seq1.p2	Ec-10_005360.1	Ribosome-binding factor A	GO:0006364	IPR023799: Ribosome-binding factor A domain; IPR015946: K homology domain-like, alpha/beta; IPR000238: Ribosome-binding factor A	NA
comp26799_c0_seq1.p1	Ec-10_005370.1	Rrp6 is a component of the exosome 3'->5' exoribonuclease complex, a complex that degrades mRNAs.	GO:0005622;GO:0006139;GO:0003676;GO:0008408	IPR012588: Exosome-associated factor Rrp6, N-terminal; IPR010997: HRDC-like; IPR012337: Ribonuclease H-like domain; PTHR12124: ; IPR002562: 3'-5' exonuclease domain; IPR002121: HRDC domain	NA
comp26176_c0_seq1.p1	Ec-10_005390.1	Domain of unknown function DUF1995	GO:0005524;GO:0006139;GO:0019205	IPR018962: Domain of unknown function DUF1995	NA
comp21002_c0_seq1.p1	Ec-10_005400.1	GTR1, Ras superfamily GTPase	GO:0005634;GO:0005737;GO:0005525	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR006762: Gtr1/RagA G protein	NA
comp24430_c0_seq1.p1	Ec-10_005410.3	Histidine phosphatase superfamily, clade-1	GO:0006096;GO:0016868	G3DSA:2.30.30.330: ; SSF54001: ; Coil: ; IPR001683: Phox homologous domain	NA
comp28885_c0_seq10.p1	Ec-10_005430.1	conserved unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF144064: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21538_c0_seq1.p1	Ec-10_005470.1	Small-subunit processome, Utp14	GO:0006364;GO:0032040	IPR006709: Small-subunit processome, Utp14; Coil:	NA
comp28570_c0_seq4.p1	Ec-10_005490.1	Quinoprotein alcohol dehydrogenase-like superfamily	n/a;n/a;n/a	PF13360: PQQ-like domain; G3DSA:3.40.50.980: ; IPR018391: Pyrrolo-quinoline quinone beta-propeller repeat; IPR000873: AMP-dependent synthetase/ligase; G3DSA:2.30.38.10: ; IPR027295: Quinoprotein alcohol dehydrogenase-like domain; PTHR24096: ; G3DSA:3.30.300.30: ; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily; PF13570: PQQ-like domain; SSF56801:	NA
comp12497_c0_seq1.p1	Ec-10_005530.1	Winged helix-turn-helix DNA-binding domain	n/a;n/a;n/a	IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; IPR016689: ESCRT-2 complex, Snf8; IPR007286: EAP30	NA
comp22205_c0_seq1.p1	Ec-10_005540.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp27992_c0_seq2.p1	Ec-10_005550.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp23362_c0_seq1.p1	Ec-10_005560.1	Carboxypeptidase	GO:0005515	IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR003961: Fibronectin type III; IPR000742: Epidermal growth factor-like domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013032: EGF-like, conserved site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001563: Peptidase S10, serine carboxypeptidase; IPR018202: Peptidase S10, serine carboxypeptidase, active site; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1282
comp31377_c1_seq3.p1	Ec-10_005570.1	Protein kinase-like domain	GO:0016772	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR020636: Calcium/calmodulin-dependent/calcium-dependent protein kinase; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site	NA
comp32333_c3_seq31.p1	Ec-10_005590.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp26492_c0_seq2.p1	Ec-10_005610.1	Chloride channel protein EriC	GO:0016020;GO:0055085;GO:0006821;GO:0030554;GO:0005247	IPR014743: Chloride channel, core; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000644: CBS domain; SSF54631: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001807: Chloride channel, voltage gated; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.10.580.10: ; PTHR11689: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30231_c0_seq1.p1	Ec-10_005630.1	CRAL-TRIO domain	n/a;n/a;n/a	PTHR10174: ; IPR001251: CRAL-TRIO domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32177_c6_seq5.p1	Ec-10_005640.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0005634;GO:0000981;GO:0006355;GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001138: Zn(2)-C6 fungal-type DNA-binding domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp13091_c0_seq1.p1	Ec-10_005650.1	Tetratricopeptide TPR1	GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat	NA
comp28355_c0_seq1.p1	Ec-10_005670.1	SAP domain	GO:0003676	IPR003034: SAP domain; Coil: ; SSF68906:	NA
comp30879_c0_seq2.p2	Ec-10_005680.1	Protein arginine N-methyltransferase	GO:0008168;GO:0006479;GO:0005737	NA	NA
comp30879_c0_seq2.p1	Ec-10_005690.1	Armadillo-like helical	GO:0005488	IPR026829: Monensin-resistant homologue 2; IPR011989: Armadillo-like helical; PF12783: Guanine nucleotide exchange factor in Golgi transport N-terminal; IPR016024: Armadillo-type fold; Coil: ; PTHR10663:	NA
comp31418_c1_seq4.p1	Ec-10_005710.1	expressed unknown protein	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp27405_c0_seq1.p1	Ec-10_005720.1	Cupin-like domain protein	n/a;n/a;n/a	NA	NA
comp26403_c0_seq3.p1	Ec-10_005740.1	NAD(P)H-Nitrate reductase	GO:0030151;GO:0055114;GO:0016491	IPR018506: Cytochrome b5, heme-binding site; IPR017927: Ferredoxin reductase-type FAD-binding domain; PTHR19370: ; IPR008333: Oxidoreductase, FAD-binding domain; IPR014756: Immunoglobulin E-set; G3DSA:2.40.30.10: ; IPR001433: Oxidoreductase FAD/NAD(P)-binding; IPR008335: Eukaryotic molybdopterin oxidoreductase; IPR001709: Flavoprotein pyridine nucleotide cytochrome reductase; IPR012137: Nitrate reductase NADH dependent; IPR001199: Cytochrome b5-like heme/steroid binding domain; IPR001834: NADH:cytochrome b5 reductase (CBR); IPR000572: Oxidoreductase, molybdopterin-binding domain; SSF52343: ; G3DSA:3.40.50.80: ; IPR017938: Riboflavin synthase-like beta-barrel; IPR005066: Moybdenum cofactor oxidoreductase, dimerisation	NA
comp29118_c0_seq3.p1	Ec-10_005780.1	Conserved protein of Unknown function, DUF493 family	n/a;n/a;n/a	IPR027471: YbeD-like domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR007454: Uncharacterised protein family UPF0250; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32526_c0_seq5.p1	Ec-10_005790.1	Rab3 GTPase-activating protein, non-catalytic subunit, distant homolog	n/a;n/a;n/a	IPR029257: Rab3GAP regulatory subunit, C-terminal; IPR032839: Rab3-GAP regulatory subunit, N-terminal; IPR026059: Rab3-GAP regulatory subunit	NA
comp29118_c0_seq4.p1	Ec-10_005800.1	BIG1, ArfGEF protein of the BIG/GBF family	NA	IPR011989: Armadillo-like helical; IPR000904: Sec7 domain; IPR000462: CDP-alcohol phosphatidyltransferase; G3DSA:1.10.220.20: ; PTHR10663: ; IPR023394: Sec7 domain, alpha orthogonal bundle; PF12783: Guanine nucleotide exchange factor in Golgi transport N-terminal; Coil: ; IPR016024: Armadillo-type fold; IPR015403: Domain of unknown function DUF1981, Sec7 associated	NA
comp29965_c0_seq2.p1	Ec-10_005870.1	Inositol monophosphatase	GO:0046854	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:3.30.540.10: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000760: Inositol monophosphatase; SSF56655: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:3.40.190.80: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30856_c0_seq1.p1	Ec-10_005900.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp29293_c0_seq3.p2	Ec-10_005940.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp29293_c0_seq3.p3	Ec-10_005950.1	Peptidase S54, rhomboid domain	GO:0004252;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; PTHR22790: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF144091: ; IPR022764: Peptidase S54, rhomboid domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29293_c0_seq3.p1	Ec-10_005960.2	Chaperone	GO:0006457;GO:0005524;GO:0051082	IPR017998: Chaperone tailless complex polypeptide 1 (TCP-1); IPR027410: TCP-1-like chaperonin intermediate domain; IPR027409: GroEL-like apical domain; IPR002194: Chaperonin TCP-1, conserved site; IPR002423: Chaperonin Cpn60/TCP-1 family; SSF54849: ; IPR027413: GroEL-like equatorial domain; PTHR11353: ; SSF48592: ; IPR012715: T-complex protein 1, alpha subunit	NA
comp24189_c0_seq1.p1	Ec-10_005970.1	START-like domain	NA	SSF55961: ; IPR002913: START domain; IPR023393: START-like domain	NA
comp31528_c1_seq4.p1	Ec-10_005990.1	DNA photolyase, class 2	GO:0003904;GO:0006281	IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; G3DSA:1.25.40.80: ; IPR006050: DNA photolyase, N-terminal; G3DSA:1.10.579.10: ; IPR005101: DNA photolyase, FAD-binding/Cryptochrome, C-terminal; IPR008148: DNA photolyase, class 2	NA
comp31528_c1_seq4.p2	Ec-10_006030.1	Pyridoxamine 5'-phosphate oxidase-like, FMN-binding domain	GO:0004733;GO:0055114;GO:0010181	IPR019576: Pyridoxine 5'-phosphate oxidase, dimerisation, C-terminal; IPR000659: Pyridoxamine 5'-phosphate oxidase; IPR012349: FMN-binding split barrel; IPR011576: Pyridoxamine 5'-phosphate oxidase-like, FMN-binding domain; IPR019740: Pyridoxamine 5'-phosphate oxidase, conserved site; SignalP-TM:	NA
comp31528_c0_seq2.p1	Ec-10_006050.2	Armadillo-like helical	GO:0005488	IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold	NA
comp31627_c2_seq1.p1	Ec-10_006070.1	carboxylase	GO:0016874	PTHR22855: ; IPR011762: Acetyl-coenzyme A carboxyltransferase, N-terminal; IPR000022: Carboxyl transferase; IPR029045: ClpP/crotonase-like domain; IPR011763: Acetyl-coenzyme A carboxyltransferase, C-terminal	KOG0540
comp11582_c0_seq1.p1	Ec-10_006080.1	hypothetical protein	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25038_c0_seq1.p2	Ec-10_006090.1	Uncharacterised protein family, transmembrane-17	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR019184: Uncharacterised protein family, transmembrane-17; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR13531: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28769_c0_seq1.p1	Ec-10_006110.1	Carbamoyl-phosphate synthase	GO:0005524;GO:0003824;GO:0004088;GO:0006541;GO:0006207	IPR005481: Carbamoyl-phosphate synthase, large subunit, N-terminal; IPR029062: Class I glutamine amidotransferase-like; IPR016185: Pre-ATP-grasp domain; IPR011761: ATP-grasp fold; IPR006275: Carbamoyl-phosphate synthase, large subunit; IPR005483: Carbamoyl-phosphate synthase large subunit, CPSase domain; PR00099: Carbamoyl-phosphate synthase protein GATase domain signature; IPR005479: Carbamoyl-phosphate synthetase large subunit-like, ATP-binding domain; PTHR11405: ; SSF56059: ; PR00096: Glutamine amidotransferase superfamily signature; IPR013815: ATP-grasp fold, subdomain 1; IPR011607: Methylglyoxal synthase-like domain; IPR005480: Carbamoyl-phosphate synthetase, large subunit oligomerisation domain; IPR002474: Carbamoyl-phosphate synthase, small subunit N-terminal domain; IPR013816: ATP-grasp fold, subdomain 2; IPR017926: Glutamine amidotransferase; IPR006274: Carbamoyl-phosphate synthase, small subunit	KOG0370
comp32704_c0_seq7.p2	Ec-10_006120.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29202_c0_seq2.p1	Ec-10_006130.1	Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain	GO:0055114;GO:0045454;GO:0016491	IPR012999: Pyridine nucleotide-disulphide oxidoreductase, class I, active site; PR00368: FAD-dependent pyridine nucleotide reductase signature; IPR004099: Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain; PTHR22912: ; PR00411: Pyridine nucleotide disulphide reductase class-I signature; IPR016156: FAD/NAD-linked reductase, dimerisation domain; IPR001327: Pyridine nucleotide-disulphide oxidoreductase, NAD-binding domain; G3DSA:3.50.50.60: ; PIRSF000350: ; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	NA
comp45297_c0_seq1.p1	Ec-10_006150.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp29202_c0_seq2.p2	Ec-10_006150.2	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31040_c1_seq1.p3	Ec-10_006160.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31040_c1_seq1.p1	Ec-10_006180.1	RNA polymerase sigma-70 like domain	GO:0003677;GO:0006355;GO:0016987;GO:0003700;GO:0006352	NA	NA
comp31040_c2_seq2.p1	Ec-10_006190.1	DUF1253 domain protein	n/a;GO:0005634	IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR010678: Digestive organ expansion factor, predicted	NA
comp34624_c0_seq1.p1	Ec-10_006200.1	malate dehydrogenase	GO:0016616;GO:0003824;GO:0055114;GO:0005975	SSF51735: ; IPR001236: Lactate/malate dehydrogenase, N-terminal; SignalP-TM: ; IPR022383: Lactate/malate dehydrogenase, C-terminal; IPR010097: Malate dehydrogenase, type 1; IPR016040: NAD(P)-binding domain; IPR001557: L-lactate/malate dehydrogenase; IPR001252: Malate dehydrogenase, active site; IPR015955: Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal	KOG1494
comp31118_c0_seq1.p1	Ec-10_006220.1	Armadillo-like helical	GO:0005488	IPR001313: Pumilio RNA-binding repeat; IPR011989: Armadillo-like helical; PTHR13102: ; IPR016024: Armadillo-type fold	NA
comp31118_c0_seq1.p2	Ec-10_006230.1	Mitochondrial biogenesis protein AIM24	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002838: Mitochondrial biogenesis protein AIM24; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR016031: Tryptophan RNA-binding attenuator protein-like domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26897_c0_seq1.p2	Ec-10_006240.1	Obtusifoliol 14alpha-Demethylase	GO:0020037;GO:0005506;GO:0055114;GO:0016705	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001128: Cytochrome P450; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002403: Cytochrome P450, E-class, group IV; IPR017972: Cytochrome P450, conserved site; PTHR24286: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0684
comp26897_c0_seq1.p1	Ec-10_006250.1	ERCC4 domain containing protein	GO:0003677;GO:0004518;GO:0006259	PTHR13451: ; IPR006166: ERCC4 domain; IPR027421: DNA polymerase family X lyase domain; IPR011335: Restriction endonuclease type II-like; IPR020819: DNA repair nuclease, XPF-type/Helicase; IPR010996: DNA polymerase beta-like, N-terminal domain	KOG2379
comp12537_c0_seq3.p1	Ec-10_006260.1	conserved unknown protein	GO:0008152;GO:0016740;n/a	NA	NA
comp31068_c0_seq3.p1	Ec-10_006290.1	Ankyrin repeat-containing domain	GO:0005515	SIGNAL_PEPTIDE: Signal peptide region; PF13637: Ankyrin repeats (many copies); PF13857: Ankyrin repeats (many copies); SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR24123: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR020683: Ankyrin repeat-containing domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp123935_c0_seq1.p1	Ec-10_006310.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp29231_c0_seq1.p1	Ec-10_006340.1	GTB1; RNA binding / hydrolase, acting on ester bonds, also similar to transcription elongation facto	GO:0003723	PF14635: Helix-hairpin-helix motif; IPR003029: Ribosomal protein S1, RNA-binding domain; IPR028088: Helix-turn-helix DNA-binding domain of Spt6; IPR006641: YqgF/RNase H-like domain; IPR027999: Death-like domain of Spt6; IPR017072: Transcription elongation factor Spt6; IPR023097: Tex RuvX-like domain; IPR012340: Nucleic acid-binding, OB-fold; SSF158832: ; IPR023323: Tex-like domain; IPR028083: Spt6 acidic, N-terminal domain; IPR000980: SH2 domain; IPR022967: RNA-binding domain, S1; IPR012337: Ribonuclease H-like domain; Coil: ; IPR010994: RuvA domain 2-like; PTHR10145: ; IPR028231: Transcription elongation factor Spt6, YqgF domain	NA
comp34171_c0_seq1.p1	Ec-10_006360.1	similar to 2-oxoisovalerate dehydrogenase alpha subunit, mitochondrial precursor	GO:0008152;GO:0016624	IPR001017: Dehydrogenase, E1 component; IPR029061: Thiamin diphosphate-binding fold; PTHR11516: ; SignalP-TM:	NA
comp30235_c0_seq2.p1	Ec-10_006370.2	WD40 repeat	GO:0005515	PTHR22850: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp13864_c0_seq1.p1	Ec-10_006400.1	conserved unknown protein	n/a;n/a;n/a	PTHR31027: ; Coil:	NA
comp32456_c0_seq3.p1	Ec-10_006420.3	hypothetical protein	NA	NA	NA
comp32658_c0_seq5.p1	Ec-11_000020.1	Ammonium transporter AmtB-like domain	GO:0008519;GO:0015696;GO:0016020	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001905: Ammonium transporter; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR002229: Blood group Rhesus C/E/D polypeptide; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR024041: Ammonium transporter AmtB-like domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR029020: Ammonium/urea transporter	NA
comp32245_c0_seq13.p1	Ec-11_000030.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	IPR001841: Zinc finger, RING-type; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PTHR27001: ; IPR001245: Serine-threonine/tyrosine-protein kinase catalytic domain; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; SSF57850: ; IPR000719: Protein kinase domain; IPR020683: Ankyrin repeat-containing domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; PF13920: Zinc finger, C3HC4 type (RING finger); G3DSA:1.10.510.10: ; Coil: ; IPR002110: Ankyrin repeat	NA
comp58344_c0_seq1.p1	Ec-11_000040.1	EF-hand domain pair	GO:0003676;GO:0004519;GO:0016787;GO:0046872	IPR011992: EF-hand domain pair; SSF47473: ; Coil:	NA
comp32436_c1_seq5.p1	Ec-11_000100.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13414: TPR repeat; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; IPR023566: Peptidyl-prolyl cis-trans isomerase, FKBP-type; IPR019734: Tetratricopeptide repeat	NA
comp26772_c0_seq2.p2	Ec-11_000120.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31761_c0_seq5.p1	Ec-11_000130.1	THO complex, subunitTHOC2, C-terminal	n/a;n/a;n/a	IPR021418: THO complex, subunitTHOC2, C-terminal; Coil: ; PTHR21597: ; IPR021726: THO complex, subunitTHOC2, N-terminal	NA
comp26781_c1_seq2.p1	Ec-11_000140.1	3-hydroxyisobutyrate dehydrogenase	GO:0051287	IPR006115: 6-phosphogluconate dehydrogenase, NADP-binding; IPR013328: 6-phosphogluconate dehydrogenase, domain 2; SSF51735: ; IPR008927: 6-phosphogluconate dehydrogenase C-terminal domain-like; PTHR22981: ; IPR016040: NAD(P)-binding domain; IPR029154: 3-hydroxyisobutyrate dehydrogenase, NAD-binding domain	KOG0409
comp30656_c0_seq2.p1	Ec-11_000190.1	RmlC-like jelly roll fold	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR000595: Cyclic nucleotide-binding domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018490: Cyclic nucleotide-binding-like; IPR014710: RmlC-like jelly roll fold; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34013_c0_seq1.p1	Ec-11_000210.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31095_c1_seq17.p1	Ec-11_000220.1	Similar to RNA Polymerase II CTD phosphatase Fcp1, putative	GO:0005622	PTHR23081: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023214: HAD-like domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004274: NLI interacting factor; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR001357: BRCT domain	NA
comp35302_c0_seq1.p1	Ec-11_000240.1	Ankyrin repeat-containing domain	GO:0005515;n/a	PTHR24148: ; IPR020683: Ankyrin repeat-containing domain; PF13857: Ankyrin repeats (many copies); Coil: ; IPR002110: Ankyrin repeat	NA
comp28980_c1_seq3.p1	Ec-11_000280.1	50S ribosomal protein L4	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR013005: 50S ribosomal protein uL4; IPR023574: Ribosomal protein L4 domain; IPR002136: Ribosomal protein L4/L1e	NA
comp33993_c0_seq1.p1	Ec-11_000360.1	SDH3, succinate dehydrogenase subunit 3	GO:0006099;GO:0045281;GO:0000104	PTHR10978: ; IPR000701: Succinate dehydrogenase/Fumarate reductase, transmembrane subunit; SSF81343: ; G3DSA:1.20.1300.10: ; IPR014314: Succinate dehydrogenase, cytochrome b556 subunit; SignalP-TM:	KOG0449
comp20087_c0_seq1.p1	Ec-11_000370.1	SAM-dependent methyltransferases	GO:0008152;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR10108: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013216: Methyltransferase type 11	KOG1269
comp27521_c0_seq2.p1	Ec-11_000390.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32951_c0_seq4.p1	Ec-08_004870.1	Mannuronan C-5-epimerase	n/a;n/a;n/a	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; IPR012334: Pectin lyase fold; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR011050: Pectin lyase fold/virulence factor; IPR022441: Parallel beta-helix repeat-2; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007742: Periplasmic copper-binding protein NosD, beta helix domain; IPR006626: Parallel beta-helix repeat; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33069_c0_seq10.p1	Ec-11_000420.1	PHM/PNGase F domain	GO:0003824	IPR000945: Dopamine beta-hydroxylase-related; IPR005018: DOMON domain; IPR008977: PHM/PNGase F domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR000323: Copper type II, ascorbate-dependent monooxygenase, N-terminal; IPR024548: Copper type II ascorbate-dependent monooxygenase, C-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR014784: Copper type II, ascorbate-dependent monooxygenase-like, C-terminal; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33069_c0_seq18.p1	Ec-11_000420.2	PHM/PNGase F domain	GO:0003824	IPR005018: DOMON domain; IPR000945: Dopamine beta-hydroxylase-related; IPR008977: PHM/PNGase F domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR000323: Copper type II, ascorbate-dependent monooxygenase, N-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR028464: DBH-like monooxygenase protein 2; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp11228_c0_seq2.p1	Ec-11_000440.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30086_c0_seq3.p1	Ec-11_000450.1	DNA polymerase epsilon subunit B, N-terminal	GO:0005634;GO:0003677;GO:0006260;GO:0003887	IPR016266: DNA polymerase epsilon, subunit B; PTHR12708: ; IPR007185: DNA polymerase alpha/epsilon, subunit B; IPR024639: DNA polymerase epsilon subunit B, N-terminal	NA
comp30478_c4_seq1.p1	Ec-11_000460.1	asparagine-rich protein	n/a;n/a;n/a	SSF50729: ; G3DSA:3.30.200.20: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; IPR001849: Pleckstrin homology domain; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; IPR011993: Pleckstrin homology-like domain; G3DSA:1.10.510.10: ; IPR020636: Calcium/calmodulin-dependent/calcium-dependent protein kinase	NA
comp30478_c0_seq1.p1	Ec-11_000490.1	Beta-grasp domain	n/a;n/a;n/a	IPR001041: 2Fe-2S ferredoxin-type domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012675: Beta-grasp domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006058: 2Fe-2S ferredoxin, iron-sulphur binding site; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31123_c0_seq1.p2	Ec-11_000500.1	Zinc finger, CW-type	GO:0008270	PTHR23336: ; Coil: ; SignalP-TM: ; IPR011124: Zinc finger, CW-type	NA
comp32764_c5_seq6.p2	Ec-11_000530.1	Vesicle transport protein, Got1/SFT2-like	GO:0016192	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR007305: Vesicle transport protein, Got1/SFT2-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR21493: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25451_c0_seq2.p1	Ec-11_000540.1	conserved unknown protein	GO:0008152;GO:0016758;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF53756: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:3.40.50.2000: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28143_c0_seq1.p1	Ec-11_000550.1	ATP-dependent RNA helicase, mitochondrial, putative	GO:0005524;GO:0007275;GO:0005576;GO:0004386;GO:0005179;GO:0003676	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR022192: Mitochondrial degradasome RNA helicase subunit, C-terminal domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR12131: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001650: Helicase, C-terminal; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	NA
comp20767_c0_seq1.p1	Ec-11_000580.1	Protein of unknown function DUF1295	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001104: 3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR32251: ; SignalP-noTM: ; IPR010721: Protein of unknown function DUF1295; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32660_c0_seq6.p1	Ec-11_000600.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR30509: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006726: Para-hydroxybenzoic acid efflux pump subunit AaeB/fusaric acid resistance protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33636_c0_seq1.p1	Ec-11_000610.1	Glycosyltransferase AER61, uncharacterised	GO:0016757	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR007657: Glycosyltransferase AER61, uncharacterised; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28990_c0_seq1.p1	Ec-11_000620.1	Peptidase S54, rhomboid	GO:0004252;GO:0006508;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR022764: Peptidase S54, rhomboid domain; IPR002610: Peptidase S54, rhomboid; SSF144091: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25634_c0_seq1.p1	Ec-11_000630.1	Basic-leucine zipper domain	GO:0003700;GO:0006355;GO:0043565	IPR004827: Basic-leucine zipper domain; SSF57959: ; G3DSA:1.20.5.170: ; Coil:	NA
comp28778_c0_seq1.p1	Ec-11_000650.4	Amine oxidase	GO:0016491;GO:0055114	IPR002937: Amine oxidase; PTHR10742:SF306: ; PTHR10742: ; IPR023753: FAD/NAD(P)-binding domain	NA
comp32133_c2_seq6.p1	Ec-11_000680.1	Las1-like	n/a;n/a;n/a	IPR007174: Las1-like	NA
comp32124_c1_seq5.p1	Ec-11_000710.1	RABSH2	GO:0005515;GO:0007264;GO:0005622;GO:0005525	NA	NA
comp32124_c4_seq2.p1	Ec-11_000710.2	RABSH2, a protein conserved in some stramenopiles (also in oomycetes), characterised by a combinatio	GO:0005515;GO:0005525;GO:0005622;GO:0007264	IPR000980: SH2 domain	NA
comp31497_c2_seq7.p1	Ec-11_000730.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31497_c2_seq7.p2	Ec-11_000740.1	UAA transporter	GO:0055085	SSF103481: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013657: UAA transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10778: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32124_c0_seq2.p1	Ec-11_000770.1	hypothetical protein	GO:0004765;GO:0005524	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp33213_c0_seq3.p1	Ec-11_000780.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32014_c0_seq2.p1	Ec-11_000820.1	Zinc finger, RING-type	GO:0005515;GO:0008270	IPR017907: Zinc finger, RING-type, conserved site; SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; Coil:	NA
comp30438_c0_seq4.p1	Ec-11_000830.1	aspartate kinase/homoserine dehydrogenase	GO:0008652;GO:0055114;GO:0050661;GO:0004072;GO:0016491	IPR001048: Aspartate/glutamate/uridylate kinase; SSF51735: ; PTHR21499: ; IPR001342: Homoserine dehydrogenase, catalytic; IPR002912: ACT domain; SSF55021: ; SSF53347: ; IPR005106: Aspartate/homoserine dehydrogenase, NAD-binding; IPR018042: Aspartate kinase, conserved site; G3DSA:3.30.360.10: ; IPR016040: NAD(P)-binding domain; IPR001341: Aspartate kinase	KOG0456
comp19411_c0_seq2.p1	Ec-11_000840.2	SGF29 tudor-like domain	n/a;n/a;n/a	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR010750: SGF29 tudor-like domain; IPR001766: Fork head domain; PTHR21539:SF0: ; PTHR21539: ; SignalP-TM:	NA
comp13017_c0_seq1.p1	Ec-11_000890.1	Transmembrane protein 65	n/a;GO:0005515	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR019537: Transmembrane protein 65; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029016: GAF domain-like; PTHR21706: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR003018: GAF domain	KOG4619
comp31394_c0_seq6.p1	Ec-11_000920.1	Phenylalanyl-tRNA synthetase, B3/B4	n/a;n/a;n/a	IPR012796: Lysidine-tRNA(Ile) synthetase, C-terminal; IPR020825: Phenylalanyl-tRNA synthetase, B3/B4; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011063: tRNA(Ile)-lysidine/2-thiocytidine synthase; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; IPR012795: tRNA(Ile)-lysidine synthase, N-terminal; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR012094: tRNA(Ile)-lysidine synthase; PTHR11807: ; SSF52402: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29300_c0_seq2.p1	Ec-11_000930.2	Ankyrin repeat-containing domain	n/a;n/a;n/a	IPR020683: Ankyrin repeat-containing domain; PTHR24193: ; IPR002110: Ankyrin repeat	NA
comp32245_c0_seq4.p1	Ec-11_000940.2	Nrap protein	n/a;n/a;n/a	IPR005554: Nrap protein	NA
comp20923_c0_seq1.p1	Ec-11_000955.1	Hypothetical leucine rich repeat calmodulin binding protein	NA	SSF52047: ; IPR006553: Leucine-rich repeat, cysteine-containing subtype; IPR032675: Leucine-rich repeat domain, L domain-like; Coil: ; PTHR24006: ; IPR000048: IQ motif, EF-hand binding site	NA
comp29979_c0_seq6.p1	Ec-11_000960.1	Phosphoglycerate dehydrogenase, incomplete	GO:0051287;GO:0055114	SSF51735: ; IPR006140: D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain; SIGNAL_PEPTIDE: Signal peptide region; IPR029753: D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain conserved site; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR006139: D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SSF52283: ; PTHR10996: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0068
comp34175_c0_seq1.p1	Ec-11_000970.1	Single hybrid motif	n/a;n/a;n/a	PTHR23151: ; G3DSA:2.40.50.100: ; IPR011053: Single hybrid motif; IPR000089: Biotin/lipoyl attachment; SignalP-TM:	NA
comp21489_c0_seq3.p1	Ec-11_000980.2	Arf1, ARF family GTPase	n/a;n/a;n/a	IPR024156: Small GTPase superfamily, ARF type; PTHR11711: ; IPR005225: Small GTP-binding protein domain; IPR003579: Small GTPase superfamily, Rab type; PTHR11711:SF181: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR006689: Small GTPase superfamily, ARF/SAR type; SM00178: Sar1p-like members of the Ras-family of small GTPases	NA
comp32667_c0_seq20.p1	Ec-11_000990.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp24829_c0_seq1.p1	Ec-11_001000.1	expressed unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32302_c1_seq15.p1	Ec-11_001010.1	ASCH domain	n/a;n/a;n/a	IPR007374: ASCH domain; IPR015947: PUA-like domain; PTHR12963: ; G3DSA:2.30.130.30:	NA
comp29166_c0_seq1.p1	Ec-11_001020.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp21391_c0_seq1.p1	Ec-11_001030.1	Isopentenyl-diphosphate delta-isomerase type 1 fused to squalene synthase; probably two separate ORFs	GO:0008299;GO:0004452;GO:0009058;GO:0016740	PTHR11626: ; IPR008949: Isoprenoid synthase domain; IPR006449: Farnesyl-diphosphate farnesyltransferase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR019845: Squalene/phytoene synthase, conserved site; IPR015797: NUDIX hydrolase domain-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002060: Squalene/phytoene synthase; IPR011876: Isopentenyl-diphosphate delta-isomerase, type 1; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000086: NUDIX hydrolase domain	KOG0142
comp33701_c0_seq1.p1	Ec-11_001050.1	NOP56 subunit of the C/D ribonucleoprotein complex	n/a;n/a;n/a	NA	NA
comp27912_c0_seq4.p1	Ec-11_001070.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp30173_c0_seq1.p1	Ec-11_001130.1	similar to ELMO domain-containing protein 1	GO:0005856;GO:0006909	IPR006816: Engulfment/cell motility, ELMO; PTHR12771:	NA
comp30173_c1_seq2.p1	Ec-11_001140.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp29477_c0_seq1.p2	Ec-11_001150.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	IPR020683: Ankyrin repeat-containing domain; IPR002110: Ankyrin repeat	NA
comp29477_c0_seq1.p1	Ec-11_001160.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824	PTHR12320: ; IPR001932: PPM-type phosphatase domain	NA
comp26576_c0_seq3.p1	Ec-11_001170.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24015: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002885: Pentatricopeptide repeat; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26159_c0_seq4.p1	Ec-11_001190.1	Protein kinase-like domain	GO:0016772	IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24362: ; IPR011009: Protein kinase-like domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33198_c0_seq6.p4	Ec-11_001210.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32530_c0_seq50.p3	Ec-11_001230.1	Alpha/Beta hydrolase fold	GO:0003824;GO:0004806;GO:0006629	IPR002921: Fungal lipase-like domain; IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR21493: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32520_c2_seq11.p1	Ec-11_001240.1	AATF leucine zipper-containing domain	GO:0005634	IPR012617: Apoptosis-antagonizing transcription factor, C-terminal; Coil: ; IPR025160: AATF leucine zipper-containing domain; PTHR15565: ; SignalP-TM:	NA
comp33045_c1_seq9.p1	Ec-11_001250.1	eukaryotic peptide chain release factor 1	GO:0005737;GO:0006415;GO:0016149	IPR005141: eRF1 domain 2; IPR029064: 50S ribosomal protein L30e-like; SSF53137: ; G3DSA:3.30.420.60: ; IPR005142: eRF1 domain 3; IPR005140: eRF1 domain 1/Pelota-like; IPR004403: Peptide chain release factor eRF1/aRF1; IPR024049: Peptide Chain Release Factor eRF1/aRF1, N-terminal	NA
comp20502_c0_seq2.p1	Ec-11_001260.1	Transporter-associated domain	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR005170: Transporter-associated domain; IPR000644: CBS domain; PTHR22777: ; SSF54631: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR016166: FAD-binding, type 2; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.10.580.10: ; IPR002550: Domain of unknown function DUF21; IPR016169: CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25914_c0_seq2.p2	Ec-11_001270.2	Hypothetical leucine rich repeat protein	GO:0005515	NA	NA
comp31898_c0_seq3.p1	Ec-11_001290.1	Zinc finger, TAZ-type	GO:0003712;GO:0004402;GO:0005634;GO:0006355;GO:0008270	PTHR13808: ; IPR000197: Zinc finger, TAZ-type; PTHR13808:SF1:	NA
comp69793_c0_seq1.p1	Ec-11_001300.2	Protein phosphatase 2C (PP2C)-like domain	GO:0003824	IPR000222: PPM-type phosphatase, divalent cation binding; IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C family; Coil:	NA
comp11812_c0_seq1.p1	Ec-11_001320.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	PF13489: Methyltransferase domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR10108: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21103_c0_seq1.p1	Ec-11_001330.1	conserved unknown protein	GO:0003677;GO:0006260;GO:0005664	IPR020529: Origin recognition complex, subunit 6, metazoa/plant; PTHR13394:	NA
comp31801_c0_seq18.p1	Ec-11_001340.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; PTHR21530: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp24344_c0_seq1.p1	Ec-11_001350.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp24628_c0_seq3.p1	Ec-11_001360.1	SUN domain	n/a;n/a;n/a	IPR012919: SUN domain; PTHR12911: ; Coil:	NA
comp32261_c1_seq12.p1	Ec-11_001390.1	Hypothetical leucine rich repeat protein	GO:0005515	SIGNAL_PEPTIDE: Signal peptide region; IPR001611: Leucine-rich repeat; IPR032675: Leucine-rich repeat domain, L domain-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SM00364: Leucine-rich repeats, bacterial type; SignalP-noTM: ; IPR003591: Leucine-rich repeat, typical subtype; PTHR24373: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp50311_c0_seq1.p1	Ec-11_001420.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp43169_c0_seq1.p1	Ec-11_001420.2	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20287_c0_seq1.p1	Ec-11_001430.1	Galactose-3-O-sulfotransferase	GO:0001733;GO:0005794;GO:0009058;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009729: Galactose-3-O-sulfotransferase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30408_c0_seq4.p2	Ec-11_001450.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009724: Protein of unknown function DUF1301, TMEM70; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-noTM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	NA
comp28549_c0_seq1.p1	Ec-11_001460.1	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	GO:0016020;GO:0008444;GO:0008654;GO:0016021;GO:0016780	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR000462: CDP-alcohol phosphatidyltransferase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14269: ; IPR004570: CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1617
comp24414_c0_seq1.p1	Ec-11_001480.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp22103_c0_seq3.p1	Ec-11_001540.1	Histidine phosphatase superfamily, clade-1	GO:0003824;GO:0008152	IPR013078: Histidine phosphatase superfamily, clade-1; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001345: Phosphoglycerate/bisphosphoglycerate mutase, active site; PTHR23029: ; IPR029033: Histidine phosphatase superfamily; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp26960_c0_seq2.p1	Ec-11_001580.1	Heat shock protein DnaJ, cysteine-rich domain	GO:0031072;GO:0051082	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR001305: Heat shock protein DnaJ, cysteine-rich domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp20341_c0_seq1.p1	Ec-11_001590.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31988_c0_seq2.p1	Ec-11_001610.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp24939_c0_seq1.p1	Ec-11_001620.1	WD40 repeat	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; Coil: ; PTHR15574:	NA
comp32995_c0_seq5.p1	Ec-11_001630.1	Formylglycine-generating sulphatase enzyme domain	n/a;n/a;n/a	IPR005532: Sulfatase-modifying factor enzyme; PF12847: Methyltransferase domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR016187: C-type lectin fold; IPR024775: DinB-like domain; PTHR23150: ; IPR027577: 5-histidylcysteine sulfoxide synthase	NA
comp33584_c0_seq1.p1	Ec-11_001640.1	JAB1/MPN/MOV34 metalloenzyme domain	GO:0005515	IPR000555: JAB1/MPN/MOV34 metalloenzyme domain; G3DSA:3.40.140.10: ; SSF102712: ; IPR024969: Rpn11/EIF3F C-terminal domain; PTHR10410: ; Coil:	NA
comp32690_c0_seq4.p1	Ec-11_001670.1	putative GPI-anchor transamidase	GO:0003923;GO:0016255;GO:0006508;GO:0042765;GO:0004197	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001096: Peptidase C13, legumain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR028361: GPI-anchor transamidase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR12000: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1349
comp32310_c0_seq1.p1	Ec-11_001710.2	Hypothetical protein	n/a;n/a;n/a	IPR011010: DNA breaking-rejoining enzyme, catalytic core; IPR013762: Integrase-like, catalytic domain	NA
comp21598_c0_seq1.p1	Ec-11_001730.2	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	n/a;n/a;n/a	SSF109993: ; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	NA
comp28065_c0_seq2.p1	Ec-11_001760.1	Calcineurin-like phosphoesterase domain, apaH type	GO:0016787	PTHR12849: ; IPR029052: Metallo-dependent phosphatase-like; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; IPR007708: Lariat debranching enzyme, C-terminal	NA
comp20295_c0_seq1.p1	Ec-11_001770.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp34300_c0_seq1.p1	Ec-11_001780.1	conserved unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25764_c0_seq3.p1	Ec-11_001820.1	Actin-related protein 10	GO:0005515	IPR027127: Actin-related protein 10; G3DSA:3.30.420.40: ; IPR004000: Actin family; SSF53067:	NA
comp32623_c3_seq1.p1	Ec-11_001830.2	histone deacetylase of possible bacterial origin with ankyrin repeats at the N-terminus	NA	IPR006447: Myb domain, plants; IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; IPR020683: Ankyrin repeat-containing domain; IPR023801: Histone deacetylase domain; PTHR10625:SF130: ; Coil: ; SSF52768: ; IPR000286: Histone deacetylase superfamily; IPR002110: Ankyrin repeat; IPR017930: Myb domain	NA
comp31710_c0_seq2.p1	Ec-11_001840.2	Glycerate 3-kinase	NA	PTHR10285:SF78: ; PTHR10285: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp70849_c0_seq1.p1	Ec-11_001850.1	Hypothetical leucine rich repeat protein	NA	G3DSA:3.80.10.10: ; PTHR24106: ; SSF52047: ; Coil: ; PF13516: Leucine Rich repeat; IPR003590: Leucine-rich repeat, ribonuclease inhibitor subtype	NA
comp31710_c0_seq4.p1	Ec-11_001850.3	Hypothetical leucine rich repeat protein	NA	PTHR24106: ; SSF52047: ; IPR032675: Leucine-rich repeat domain, L domain-like; Coil: ; IPR003590: Leucine-rich repeat, ribonuclease inhibitor subtype	NA
comp29916_c0_seq1.p1	Ec-11_001870.1	conserved unknown protein	n/a;n/a;n/a	SSF63748: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; G3DSA:2.30.30.270: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp24203_c0_seq1.p2	Ec-11_001880.1	similar to Stromal cell-derived factor 2 precursor (SDF-2)	GO:0016020	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; G3DSA:2.80.10.50: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027005: Glycosyltransferase 39-like; SignalP-noTM: ; IPR016093: MIR motif; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24203_c0_seq1.p5	Ec-11_001900.1	Dimerization-anchoring domain of cAMP-dependent protein kinase, regulatory subunit	n/a;n/a;n/a	IPR003117: Dimerisation-anchoring domain of cAMP-dependent protein kinase, regulatory subunit	NA
comp22247_c0_seq1.p1	Ec-11_001920.1	flagellar associated protein	n/a;n/a;n/a	IPR025252: Domain of unknown function DUF4200; PTHR21683: ; Coil:	NA
comp32245_c0_seq27.p1	Ec-11_001930.1	TrmE, organellal GTPase involved in tRNA modification	GO:0005525	SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SSF116878: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005225: Small GTP-binding protein domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11649: ; IPR018948: GTP-binding protein TrmE, N-terminal; IPR025867: tRNA modification GTPase MnmE C-terminal domain; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR027266: GTP-binding protein TrmE/Glycine cleavage system T protein, domain 1; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR004520: tRNA modification GTPase MnmE; IPR006073: GTP binding domain; SignalP-noTM: ; IPR027368: tRNA modification GTPase MnmE domain 2; Coil:	NA
comp21217_c0_seq2.p1	Ec-11_001960.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27346_c0_seq1.p1	Ec-11_001970.1	Protein of unknown function DUF408	n/a;n/a;n/a	IPR007308: Protein of unknown function DUF408; Coil:	NA
comp29447_c0_seq3.p1	Ec-11_001980.1	SPX, N-terminal	GO:0006508;GO:0008236;GO:0016020;GO:0016021	IPR004331: SPX domain; PTHR10783:	NA
comp27689_c0_seq1.p1	Ec-11_001990.1	conserved unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27068_c0_seq3.p1	Ec-11_002010.1	Zinc finger, RING/FYVE/PHD-type	GO:0005515;GO:0008270	IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; Coil:	NA
comp33652_c0_seq1.p1	Ec-11_002020.1	Magnesium-dependent phosphatase-1, eukaryotic/archaeal type	GO:0016791	IPR010036: Magnesium-dependent phosphatase-1, eukaryotic/archaeal type; IPR024734: Magnesium-dependent phosphatase-1, eukaryotic type; IPR023214: HAD-like domain	NA
comp32243_c2_seq13.p2	Ec-11_002030.1	RNA binding protein	GO:0003723;GO:0000178	IPR012340: Nucleic acid-binding, OB-fold; IPR004088: K Homology domain, type 1; SSF110324: ; IPR026699: Exosome complex RNA-binding protein 1/RRP40/RRP4	NA
comp32314_c0_seq5.p1	Ec-11_002040.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008168	NA	NA
comp31453_c0_seq12.p1	Ec-11_002050.1	Ankyrin repeat	GO:0005515	IPR020683: Ankyrin repeat-containing domain; Coil: ; IPR002110: Ankyrin repeat; PTHR24188:	NA

comp11691_c0_seq1.p1	Ec-11_002070.1	Adenylosuccinate lyase	GO:0003824	IPR008948: L-Aspartase-like; SIGNAL_PEPTIDE: Signal peptide region; IPR022761: Fumarate lyase, N-terminal; IPR004769: Adenylosuccinate lyase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; G3DSA:1.20.200.10: ; IPR019468: Adenylosuccinate lyase C-terminal; IPR000362: Fumarate lyase family; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR024083: Fumarase/histidase, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020557: Fumarate lyase, conserved site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2700
comp24727_c0_seq1.p1	Ec-11_002190.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20363_c0_seq1.p1	Ec-11_002210.1	Voltage dependent anion channel	GO:0055085;GO:0005741	PTHR11743: ; IPR023614: Porin domain; IPR027246: Eukaryotic porin/Tom40	NA
comp24502_c0_seq2.p1	Ec-11_002240.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp28113_c0_seq2.p1	Ec-11_002250.1	Sybindin-like protein	GO:0006810;GO:0005801;GO:0006888	IPR007233: Sybindin-like protein; IPR011012: Longin-like domain; G3DSA:3.30.450.70:	NA
comp34868_c0_seq1.p1	Ec-11_002290.1	Oxidoreductase FAD/NAD(P)-binding	GO:0016491;GO:0055114	PTHR19370: ; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:2.40.30.10: ; SignalP-TM: ; SSF52343: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001433: Oxidoreductase FAD/NAD(P)-binding; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.40.50.80: ; SignalP-noTM: ; IPR017938: Riboflavin synthase-like beta-barrel; PTHR19370:SF123: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24538_c0_seq2.p1	Ec-11_002300.1	IBR domain protein	GO:0003676;GO:0005622;GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017907: Zinc finger, RING-type, conserved site; SSF57850: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1814
comp20670_c0_seq2.p1	Ec-11_002310.1	Adenylosuccinate synthetase	GO:0006164;GO:0005525;GO:0004019	G3DSA:3.90.170.10: ; IPR018220: Adenylosuccinate synthase, active site; IPR001114: Adenylosuccinate synthetase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:1.10.300.10: ; G3DSA:3.40.440.10:	NA
comp12813_c0_seq2.p1	Ec-11_002360.1	Asparaginase	GO:0006520	IPR027474: L-asparaginase, N-terminal; IPR027473: L-asparaginase, C-terminal domain; PTHR11707: ; IPR006034: Asparaginase/glutaminase; PIRSF500176:	KOG0503
comp34261_c0_seq1.p1	Ec-11_002370.1	FeS cluster biogenesis	GO:0051536;GO:0016226;GO:0005198	PTHR10072: ; IPR017870: FeS cluster insertion, C-terminal, conserved site; IPR000361: FeS cluster biogenesis; IPR016092: FeS cluster insertion protein	NA
comp31121_c1_seq2.p1	Ec-11_002380.1	Dynein light chain-related	n/a;n/a;n/a	IPR016561: Dynein light chain, roadblock-type; G3DSA:3.30.450.30: ; PTHR10779: ; IPR004942: Dynein light chain-related; SSF103196:	NA
comp26711_c0_seq2.p1	Ec-11_002390.1	putative Sec61/secY	NA	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023201: SecY subunit domain; IPR030659: SecY conserved site; IPR002208: SecY/SEC61-alpha family; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR019561: Translocon Sec61/SecY, plug domain	NA
comp29991_c0_seq5.p1	Ec-11_002440.3	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR38149: ; SIGNAL_PEPTIDE: Signal peptide region; IPR019195: ABC transporter, ATPase, putative; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32544_c0_seq5.p1	Ec-11_002450.1	aldehyde dehydrogenase	GO:0016620;GO:0008152;GO:0055114;GO:0004030;GO:0006081;GO:0016491	IPR016161: Aldehyde/histidinol dehydrogenase; IPR015590: Aldehyde dehydrogenase domain; IPR016162: Aldehyde dehydrogenase N-terminal domain; IPR012394: Aldehyde dehydrogenase NAD(P)-dependent; PTHR11699: ; Coil: ; IPR016163: Aldehyde dehydrogenase, C-terminal	KOG2456
comp29420_c0_seq1.p1	Ec-11_002460.1	Threonine aldolase	GO:0006520;GO:0003824;GO:0004793;GO:0030170	IPR015424: Pyridoxal phosphate-dependent transferase; PTHR10289: ; IPR001597: Aromatic amino acid beta-eliminating lyase/threonine aldolase; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2	KOG1368
comp12646_c0_seq1.p1	Ec-11_002480.1	6-phosphofructo-2-kinase and histidine phosphatase domain-containing protein	GO:0005524;GO:0006000;GO:0003873	IPR013078: Histidine phosphatase superfamily, clade-1; IPR001345: Phosphoglycerate/bisphosphoglycerate mutase, active site; IPR029033: Histidine phosphatase superfamily; IPR003094: Fructose-2,6-bisphosphatase; IPR014756: Immunoglobulin E-set; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR013079: 6-phosphofructo-2-kinase	NA
comp14980_c0_seq1.p1	Ec-11_002490.1	conserved unknown protein	n/a;n/a;n/a	SSF117916:	NA
comp29431_c0_seq2.p1	Ec-11_002500.1	AMP-dependent synthetase/ligase	GO:0008152;GO:0003824	G3DSA:3.40.50.980: ; PTHR24096: ; IPR000873: AMP-dependent synthetase/ligase; SSF56801:	NA
comp11852_c0_seq1.p1	Ec-11_002520.1	Protein of unknown function DUF159	n/a;n/a;n/a	IPR003738: Protein of unknown function DUF159	NA
comp30468_c0_seq1.p1	Ec-11_002530.1	alpha,alpha-trehalose-phosphate synthase	n/a;n/a;n/a	NA	NA
comp31836_c0_seq4.p1	Ec-11_002540.3	Trehalose 6-phosphate synthase, family GT20 / Trehalose 6-phosphate phosphatase	GO:0003824;GO:0005992	SSF53756: ; IPR001830: Glycosyl transferase, family 20; Coil: ; PTHR10788:SF6: ; PTHR10788: ; IPR023214: HAD-like domain; IPR003337: Trehalose-phosphatase; G3DSA:3.40.50.2000:	KOG1050
comp34377_c0_seq1.p1	Ec-11_002560.1	Chromosome transmission fidelity protein 8	n/a;n/a;n/a	IPR018607: Chromosome transmission fidelity protein 8	NA
comp31560_c0_seq3.p1	Ec-11_002580.1	Prolyl 4-hydroxylase, alpha subunit	GO:0005506;GO:0055114;GO:0031418;GO:0016705	IPR006620: Prolyl 4-hydroxylase, alpha subunit; PTHR10869:	NA
comp33170_c0_seq1.p1	Ec-11_002590.1	Glutathione S-transferase	GO:0015035	IPR001853: DSBA-like thioredoxin domain; PTHR13887: ; IPR014440: HCCA isomerase/glutathione S-transferase kappa; IPR012336: Thioredoxin-like fold	none
comp33148_c0_seq9.p1	Ec-11_002600.1	Helicase superfamily 1/2, ATP-binding domain	GO:0003677;GO:0005524;GO:0004386;GO:0003676	IPR017907: Zinc finger, RING-type, conserved site; IPR001841: Zinc finger, RING-type; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR000330: SNF2-related; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR014001: Helicase superfamily 1/2, ATP-binding domain; PTHR10799: ; IPR001650: Helicase, C-terminal	NA
comp32812_c1_seq5.p1	Ec-11_002610.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp12476_c0_seq1.p1	Ec-11_002620.2	Single-stranded nucleic acid binding R3H	GO:0003676	IPR001374: R3H domain	NA
comp27246_c0_seq2.p1	Ec-11_002660.1	DEAD box helicase	GO:0003676;GO:0005524	SSF54928: ; IPR014014: RNA helicase, DEAD-box type, Q motif; IPR011545: DEAD/DEAH box helicase domain; IPR012562: GUCT; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001650: Helicase, C-terminal; PTHR24031:	KOG0331
comp33071_c0_seq8.p9	Ec-11_002670.1	Uncharacterised protein family UPF0434/Trm112	n/a;n/a;n/a	IPR005651: Uncharacterised protein family UPF0434/Trm112; SSF158997: ; PTHR12773: ; G3DSA:2.20.25.10:	NA
comp31702_c0_seq1.p1	Ec-11_002680.1	Nucleotide-diphospho-sugar transferases	GO:0004197;GO:0006508	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002495: Glycosyl transferase, family 8; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR029044: Nucleotide-diphospho-sugar transferases; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12330_c0_seq1.p1	Ec-11_002710.1	Putative fluoride ion transporter CrcB	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003691: Putative fluoride ion transporter CrcB; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33071_c0_seq8.p1	Ec-11_002720.1	Peptidase S16, lon N-terminal	GO:0004176;GO:0006508	IPR003111: Peptidase S16, lon N-terminal; IPR015947: PUA-like domain; Coil:	NA
comp31426_c1_seq11.p1	Ec-11_002740.1	Heat shock protein 40 like protein	GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; IPR001623: DnaJ domain; PF13414: TPR repeat; PTHR24077: ; Coil: ; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat	NA

comp19515_c0_seq1.p1	Ec-12_000330.1	Plastid lipid-associated protein/fibrillin conserved domain	n/a;n/a;n/a	IPR006843: Plastid lipid-associated protein/fibrillin conserved domain	NA
comp26686_c0_seq1.p1	Ec-12_000350.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR006342: Methyltransferase FkbM	NA
comp33109_c0_seq1.p1	Ec-12_000360.1	Mannuronan C-5-epimerase	NA	IPR011050: Pectin lyase fold/virulence factor; PF13229: Right handed beta helix region; IPR012334: Pectin lyase fold; IPR006626: Parallel beta-helix repeat	NA
comp34583_c0_seq1.p1	Ec-12_000370.1	Domain of unknown function DUF3598	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; IPR012674: Calycin; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011038: Calycin-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR022017: Domain of unknown function DUF3598; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp23788_c0_seq2.p2	Ec-12_000450.1	hypothetical protein	n/a;n/a;n/a	G3DSA:3.40.50.80:	NA
comp27151_c0_seq1.p1	Ec-12_000460.1	Domain of unknown function DUF4140	n/a;n/a;n/a	PTHR31005: ; IPR025554: Domain of unknown function DUF4140; IPR011935: Conserved hypothetical protein CHP02231; Coil:	NA
comp20237_c0_seq1.p1	Ec-12_000500.1	Rubredoxin-type fold	GO:0006118;GO:0009055;GO:0046872	SSF57802: ; IPR024935: Rubredoxin domain; IPR024934: Rubredoxin-like domain; IPR004039: Rubredoxin-type fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32617_c2_seq1.p1	Ec-12_000510.1	Amidohydrolase 2	GO:0008152;GO:0003824	PTHR21240: ; SSF51556: ; G3DSA:3.20.20.140: ; IPR006992: Amidohydrolase 2	NA
comp33739_c0_seq1.p1	Ec-12_000520.1	LETM1-like	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR011685: LETM1-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30723_c0_seq1.p1	Ec-12_000530.1	structural maintenance of chromosomes 1 protein	GO:0005515;GO:0005524;GO:0005694;GO:0051276	IPR028468: Structural maintenance of chromosomes protein 1; IPR010935: SMCs flexible hinge; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR003395: RecF/RecN/SMC, N-terminal; PTHR18937: ; IPR024704: Structural maintenance of chromosomes protein	NA
comp13849_c0_seq1.p1	Ec-12_000540.1	Cytochrome b5-like heme/steroid binding domain	GO:0020037	IPR020683: Ankyrin repeat-containing domain; IPR001199: Cytochrome b5-like heme/steroid binding domain; IPR002110: Ankyrin repeat	NA
comp32568_c0_seq2.p1	Ec-12_000570.1	Protein of unknown function DUF4498	n/a;n/a;n/a	IPR029416: Protein of unknown function DUF4498	NA
comp32383_c0_seq6.p1	Ec-12_000580.1	SET and Chromo-like domain protein	GO:0016817;GO:0005515;GO:0008270	NA	NA
comp29260_c0_seq3.p1	Ec-12_000590.1	CCT domain	GO:0005515	PTHR31717: ; IPR010402: CCT domain	NA
comp12207_c0_seq1.p1	Ec-12_000600.1	rab GDP dissociation inhibitor protein	GO:0005093;GO:0015031	PTHR11787: ; G3DSA:3.30.519.10: ; IPR016040: NAD(P)-binding domain; G3DSA:1.10.405.10: ; IPR000806: Rab GDI protein; IPR018203: GDP dissociation inhibitor; SSF51905:	KOG1439
comp26852_c0_seq1.p1	Ec-12_000610.1	Ribonuclease H-like domain	GO:0003676	IPR004649: Ribonuclease H2, subunit A; IPR024567: Ribonuclease HII/HIII domain; IPR001352: Ribonuclease HII/HIII; IPR012337: Ribonuclease H-like domain; IPR023160: Ribonuclease HII, helix-loop-helix cap domain	NA
comp32431_c0_seq12.p2	Ec-12_000620.1	Sec11 homolog, catalytic subunit of the Signal Peptidase Complex	GO:0016020;GO:0008236;GO:0006508;GO:0016021	IPR019759: Peptidase S24/S26A/S26B; IPR001733: Peptidase S26B; IPR015927: Peptidase S24/S26A/S26B/S26C; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR019756: Peptidase S26A, signal peptidase I, serine active site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR028360: Peptidase S24/S26, beta-ribbon domain	NA
comp21294_c0_seq2.p1	Ec-12_000630.1	Tetratricopeptide-like helical domain	GO:0005515	IPR002885: Pentatricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; PTHR24015:	NA
comp31842_c0_seq1.p1	Ec-12_000640.1	beta-ketoacyl synthase	GO:0003824;GO:0008152	IPR014031: Beta-ketoacyl synthase, C-terminal; SIGNAL_PEPTIDE: Signal peptide region; IPR017568: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PTHR11712: ; IPR014030: Beta-ketoacyl synthase, N-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR016038: Thiolase-like, subgroup; IPR018201: Beta-ketoacyl synthase, active site; IPR016039: Thiolase-like; IPR020841: Polyketide synthase, beta-ketoacyl synthase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1394
comp31842_c0_seq1.p2	Ec-12_000650.1	beta-ketoacyl synthase	GO:0008152;GO:0003824;GO:0004315;GO:0006633	SIGNAL_PEPTIDE: Signal peptide region; IPR013751: 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR016038: Thiolase-like, subgroup; IPR004655: 3-oxoacyl-[acyl-carrier-protein] synthase 3; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR016039: Thiolase-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013747: 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III C-terminal; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	no relat
comp21316_c0_seq1.p1	Ec-12_000670.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp21963_c0_seq2.p1	Ec-12_000680.1	Hypothetical protein	n/a;n/a;n/a	IPR029488: Hemingway/KIAA1430	NA
comp30558_c0_seq3.p2	Ec-12_000720.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp28553_c0_seq2.p1	Ec-12_000740.1	Aminotransferase	GO:0003824;GO:0009058;GO:0030170	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR015424: Pyridoxal phosphate-dependent transferase; IPR004839: Aminotransferase, class I/classII; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027619: Putative C-S lyase; SignalP-noTM: ; PTHR11751: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	NA
comp32333_c0_seq1.p1	Ec-12_000750.1	Hypothetical protein	n/a;n/a;n/a	IPR008984: SMAD/FHA domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000253: Forkhead-associated (FHA) domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29978_c0_seq5.p3	Ec-12_000770.1	Cysteine alpha-hairpin motif superfamily	n/a;n/a;n/a	PTHR13523: ; IPR009069: Cysteine alpha-hairpin motif superfamily	NA
comp29978_c0_seq5.p1	Ec-12_000780.1	NAD(P)-binding domain	GO:0008152;GO:0016491	PTHR24322: ; SIGNAL_PEPTIDE: Signal peptide region; PTHR24322:SF540: ; IPR002347: Glucose/ribitol dehydrogenase; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002198: Short-chain dehydrogenase/reductase SDR; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25217_c0_seq1.p1	Ec-12_000800.2	Sec23/Sec24, helical domain	GO:0006886;GO:0006888;GO:0030127	SSF81995: ; IPR006900: Sec23/Sec24, helical domain; IPR012990: Sec23/Sec24 beta-sandwich; PTHR13803: ; IPR006896: Sec23/Sec24, trunk domain; IPR029006: ADF-H/Gelsolin-like domain; IPR006895: Zinc finger, Sec23/Sec24-type; PTHR13803:SF4: ; IPR007123: Gelsolin-like domain; IPR002035: von Willebrand factor, type A	NA
comp29879_c0_seq3.p3	Ec-12_000830.1	Cilia/flagella-associated protein 20	n/a;n/a;n/a	IPR007714: Cilia/flagella-associated protein 20/WDR90/C3orf67	NA
comp29879_c0_seq3.p1	Ec-12_000840.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp32699_c0_seq24.p1	Ec-12_000850.2	Histidinol-phosphate transaminase	GO:0003824;GO:0030170	IPR005861: Histidinol-phosphate aminotransferase family; PTHR11751:SF424: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR004839: Aminotransferase, class I/classII; IPR015424: Pyridoxal phosphate-dependent transferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11751: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR001917: Aminotransferase, class-II, pyridoxal-phosphate binding site; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2	KOG0633
comp31901_c0_seq16.p1	Ec-12_000870.2	1,3-beta-glucan synthase, family GT48	GO:0000148;GO:0003843;GO:0006075;GO:0016020	PTHR12741: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003440: Glycosyl transferase, family 48; IPR026899: 1,3-beta-glucan synthase subunit FKS1-like, domain-1; PTHR12741:SF7: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp88670_c0_seq1.p1	Ec-12_000900.2	Ankyrin repeat-containing domain	n/a;n/a;n/a	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR001752: Kinesin motor domain; IPR002110: Ankyrin repeat	NA
comp48454_c0_seq1.p1	Ec-12_000910.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005509	IPR018247: EF-Hand 1, calcium-binding site; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR19871: ; SSF47473: ; IPR003593: AAA+ ATPase domain; Coil:	NA
comp34097_c0_seq1.p1	Ec-12_000920.1	RNA recognition motif domain	GO:0003676;GO:0000166	SSF54928: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; Coil: ; PTHR23139:	NA
comp33850_c0_seq1.p1	Ec-12_000930.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp12055_c0_seq1.p1	Ec-12_000940.1	RME1L1, RME1-like GTPase/ATPase without a C-terminal EH domain	GO:0003924;GO:0005525	IPR030381: Dynamin-type guanine nucleotide-binding (G) domain; IPR022812: Dynamin superfamily; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR11216: ; PF00350: Dynamin family	NA
comp24764_c0_seq1.p1	Ec-12_000950.1	Pyruvate kinase	GO:0000287;GO:0004743;GO:0006096;GO:0030955	IPR015806: Pyruvate kinase, beta-barrel insert domain; IPR015795: Pyruvate kinase, C-terminal; IPR018209: Pyruvate kinase, active site; IPR015813: Pyruvate/Phosphoenolpyruvate kinase-like domain; IPR011037: Pyruvate kinase-like, insert domain; IPR015794: Pyruvate kinase, alpha/beta; IPR001697: Pyruvate kinase; IPR015793: Pyruvate kinase, barrel	KOG2323
comp76826_c0_seq1.p1	Ec-12_000960.1	Major facilitator superfamily domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020846: Major facilitator superfamily domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:1.20.1250.20: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA

comp22087_c0_seq1.p1	Ec-12_004730.1	dynein intermediate chain family	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR12442:	NA
comp24256_c0_seq1.p1	Ec-12_004740.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp25150_c0_seq3.p2	Ec-12_004750.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; Coil: ; SSF68906: ; PTHR22763:	NA
comp18481_c0_seq2.p1	Ec-12_004760.1	p28, 28 kDa light chain of axonemal inner dynein arms	NA	Coil: ; PTHR13183: ; IPR019347: Axonemal dynein light chain	KOG4001
comp11808_c0_seq1.p1	Ec-12_004820.1	similarity to sodium/hydrogen exchanger and potassium exchanger	GO:0006813	SSF51735: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR16254: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006153: Cation/H+ exchanger; IPR016040: NAD(P)-binding domain; IPR003148: Regulator of K+ conductance, N-terminal; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29607_c0_seq3.p5	Ec-12_004830.1	conserved unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29607_c0_seq3.p1	Ec-12_004840.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PF13659: Methyltransferase domain	NA
comp31346_c0_seq5.p1	Ec-12_004850.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp29076_c0_seq3.p1	Ec-12_004860.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	PTHR24055: ; IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; PTHR24055:SF164: ; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	NA
comp19590_c0_seq1.p1	Ec-12_004870.1	hemolysin-type calcium-binding region	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33105_c1_seq8.p1	Ec-12_004880.1	Signal peptidase I (SPase I) (Leader peptidase I)	GO:0008236;GO:0009003;GO:0016021	IPR019759: Peptidase S24/S26A/S26B; SIGNAL_PEPTIDE: Signal peptide region; IPR015927: Peptidase S24/S26A/S26B/S26C; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR019757: Peptidase S26A, signal peptidase I, lysine active site; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR019758: Peptidase S26A, signal peptidase I, conserved site; IPR000223: Peptidase S26A, signal peptidase I; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR028360: Peptidase S24/S26, beta-ribbon domain; IPR019756: Peptidase S26A, signal peptidase I, serine active site	NA
comp25170_c0_seq2.p1	Ec-12_004890.1	uroporphyrinogen synthase, putative chloroplast precursor	GO:0033014;GO:0004852	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR003754: Tetrapyrrole biosynthesis, uroporphyrinogen III synthase; G3DSA:3.40.50.10090: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp34032_c0_seq1.p1	Ec-12_004900.1	Rab50, RAB family GTPase	GO:0007264;GO:0005525;GO:0015031	IPR002041: Ran GTPase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; IPR003579: Small GTPase superfamily, Rab type; PS51419: small GTPase Rab1 family profile.; IPR020849: Small GTPase superfamily, Ras type; PTHR24073:	NA
comp30136_c0_seq3.p1	Ec-12_004910.1	Small-subunit processome, Utp12	GO:0006364;GO:0032040	PTHR19853: ; IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR007148: Small-subunit processome, Utp12; IPR020472: G-protein beta WD-40 repeat; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; Coil:	NA
comp11298_c0_seq1.p1	Ec-12_004930.1	Major facilitator superfamily	GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24003: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004331: SPX, N-terminal; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32625_c1_seq12.p1	Ec-12_004940.1	conserved unknown protein	GO:0016021;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PF03083: Sugar efflux transporter for intercellular exchange; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10791: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31728_c0_seq6.p1	Ec-12_004950.1	Isopenicillin N synthase-like	n/a;n/a;n/a	IPR027443: Isopenicillin N synthase-like; SSF51197: ; PTHR10209:	NA
comp30145_c0_seq7.p1	Ec-12_004980.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270	IPR001594: Zinc finger, DHHC-type, palmitoyltransferase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22883: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR22883:SF43: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp13061_c0_seq1.p1	Ec-12_005000.1	Oxidoreductase-like, N-terminal	n/a;n/a;n/a	IPR019180: Oxidoreductase-like, N-terminal	NA
comp20837_c0_seq1.p1	Ec-12_005020.1	Arginine/Asparagine/Proline hydroxylase	GO:0018193	IPR007803: Arginine/Asparagine/Proline hydroxylase; SSF51197: ; IPR027443: Isopenicillin N synthase-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR12366: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20837_c0_seq1.p1	Ec-12_005030.1	Mediator complex, subunit Med21	NA	NA	NA
comp32082_c1_seq1.p1	Ec-12_005050.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32082_c1_seq2.p1	Ec-12_005060.1	Pyrimidine 5'-nucleotidase, eukaryotic	GO:0000287;GO:0005737;GO:0008253	IPR006434: Pyrimidine 5'-nucleotidase, eukaryotic; IPR023214: HAD-like domain	NA
comp24051_c0_seq7.p1	Ec-12_005070.1	Valine--tRNA ligase	GO:0004832;GO:0005524;GO:0006438;GO:0005737;GO:0006418;GO:0000166;GO:0006412;GO:0004812	IPR002303: Valine-tRNA ligase; IPR010978: tRNA-binding arm; IPR001412: Aminoacyl-tRNA synthetase, class I, conserved site; IPR019499: Valyl-tRNA synthetase, tRNA-binding arm; PTHR11946: ; IPR009080: Aminoacyl-tRNA synthetase, class 1a, anticodon-binding; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; SSF52374: ; IPR009008: Valyl/Leucyl/Isoleucyl-tRNA synthetase, editing domain; IPR013155: Methionyl/Valyl/Leucyl/Isoleucyl-tRNA synthetase, anticodon-binding; IPR002300: Aminoacyl-tRNA synthetase, class Ia; Coil:	KOG0432
comp35144_c0_seq1.p2	Ec-12_005080.1	Zinc finger, CCCH-type	GO:0046872	IPR000571: Zinc finger, CCCH-type; SSF90229:	NA
comp20292_c0_seq1.p1	Ec-12_005090.2	Zinc finger, PHD-type	GO:0005515;GO:0008270	PTHR13793:SF87: ; IPR019786: Zinc finger, PHD-type, conserved site; IPR001965: Zinc finger, PHD-type; PF13831: PHD-finger; PF13832: PHD-zinc-finger like domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR13793: ; Coil: ; IPR011011: Zinc finger, FYVE/PHD-type; IPR019787: Zinc finger, PHD-finger	NA
comp25368_c0_seq4.p1	Ec-12_005100.1	peptidyl-prolyl cis-trans isomerase, FKBP-type	GO:0006457	SSF54534: ; G3DSA:3.10.50.40: ; IPR023566: Peptidyl-prolyl cis-trans isomerase, FKBP-type; IPR001179: Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	KOG0544
comp34072_c0_seq1.p1	Ec-12_005110.1	adenylate kinase	GO:0005524;GO:0006139;GO:0004017;GO:0019205;GO:0016776	IPR007862: Adenylate kinase, active site lid domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR006259: Adenylate kinase subfamily; IPR000850: Adenylate kinase/UMP-CMP kinase; PF00406: Adenylate kinase	NA
comp26382_c0_seq1.p1	Ec-12_005120.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp11960_c0_seq1.p1	Ec-12_005130.1	Transmembrane protein TauE like	GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PTHR14255: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002781: Transmembrane protein TauE like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31711_c0_seq1.p1	Ec-12_005140.1	Progesterone-induced-blocking factor 1	n/a;n/a;n/a	IPR026205: Progesterone-induced-blocking factor 1; Coil:	NA
comp13025_c0_seq2.p1	Ec-12_005150.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp29214_c0_seq1.p1	Ec-12_005160.1	Phox homologous domain	GO:0035091	Coil: ; IPR001683: Phox homologous domain; SignalP-TM:	NA
comp21129_c0_seq1.p1	Ec-12_005170.1	Ionotropic glutamate receptor	GO:0004970;GO:0016020	PF00497: Bacterial extracellular solute-binding proteins, family 3; PTHR18966: ; G3DSA:1.10.287.70: ; IPR028082: Periplasmic binding protein-like I; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; [illegible] G3DSA:3.40.190.10: ; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SignalP-noTM: ; IPR001320: Ionotropic glutamate receptor; [illegible] bound protein predicted to be embedded in the membrane.	NA
comp19428_c0_seq1.p1	Ec-12_005180.1	AAA ATPase	GO:0004176;GO:0004252;GO:0006508;n/a	IPR003959: ATPase, AAA-type, core; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; PTHR23078: ; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.10.8.60: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0741
comp33099_c0_seq12.p1	Ec-12_005190.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp14549_c0_seq1.p1	Ec-12_005200.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PTHR10098: ; IPR011990: Tetratricopeptide-like helical domain; PF13374: Tetratricopeptide repeat; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat	NA
comp31863_c1_seq1.p1	Ec-12_005210.2	Formylglycine-dependent sulfatase	GO:0008152;GO:0008484	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000917: Sulfatase, N-terminal; G3DSA:3.30.1120.10: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR017849: Alkaline phosphatase-like, alpha/beta/alpha; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10342: ; IPR024607: Sulfatase, conserved site; IPR017850: Alkaline-phosphatase-like, core domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3867
comp29909_c0_seq2.p1	Ec-12_005220.1	Glycosyltransferase, GlcNAc	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR021067: Glycosyltransferase, GlcNAc; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	NA
comp34517_c0_seq1.p1	Ec-12_005240.1	NAD(P)-binding domain	GO:0003824;GO:0005488;GO:0008152	SSF51735: ; IPR016040: NAD(P)-binding domain; PTHR15020: ; PF13460: NADH(P)-binding	NA
comp28644_c0_seq1.p1	Ec-12_005250.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp30678_c0_seq3.p1	Ec-12_005260.1	Kelch-type beta propeller	GO:0005515	SSF117281: ; IPR015915: Kelch-type beta propeller	NA
comp37770_c0_seq1.p1	Ec-12_005270.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA

comp21413_c0_seq1.p1	Ec-12_008630.1	DNA recombination and repair protein RecA, C-terminal	GO:0003677;GO:0005524;GO:0006259;GO:0008094	NA
comp12022_c0_seq1.p1	Ec-12_008660.1	Trimeric LpxA-like	n/a;n/a;n/a	NA
comp27081_c0_seq2.p1	Ec-12_008680.1	FNIP	n/a;n/a;n/a	NA
comp32779_c0_seq2.p1	Ec-12_008690.1	glutamate-1-semialdehyde 2,1-aminomutase, putative chloroplast precursor	GO:0003824;GO:0030170	NA
comp32617_c2_seq15.p1	Ec-12_008700.1	ABC transporter-like	GO:0005524;GO:0016887	NA
comp26586_c0_seq1.p1	Ec-12_008710.1	conserved unknown protein	n/a;n/a;n/a	NA
comp24208_c0_seq1.p1	Ec-12_008720.1	long chain acyl-coA synthetase	GO:0008152;GO:0003824	KOG1256
comp32231_c0_seq10.p1	Ec-12_008750.1	plastidic ATP/ADP transporter	GO:0006810;GO:0005524;GO:0005471;GO:0016021	NA
comp24374_c1_seq2.p1	Ec-12_008760.1	Tha4/Hcf106 protein	n/a;GO:0008565;GO:0015031	NA
comp26803_c0_seq2.p1	Ec-12_008770.1	Light harvesting complex protein	GO:0009765;GO:0016020	NA
comp30392_c0_seq1.p1	Ec-12_008780.1	expressed unknown protein	n/a;n/a;n/a	NA
comp30934_c0_seq7.p1	Ec-12_008810.2	hypothetical protein	n/a;n/a;n/a	NA
comp27377_c0_seq1.p1	Ec-12_008840.1	Electron transfer flavoprotein, alpha/beta-subunit, N-terminal	GO:0009055;n/a	NA
comp25204_c0_seq2.p1	Ec-12_008850.1	GTP diphosphokinase	n/a;n/a;n/a	NA
comp30392_c0_seq1.p2	Ec-12_008860.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	NA
comp32754_c1_seq9.p1	Ec-12_008870.1	n/a	GO:0008017	NA
comp32754_c1_seq10.p1	Ec-12_008890.1	phosphatidic acid phosphatase	GO:0003824;GO:0016020	KOG3030
comp20460_c0_seq1.p1	Ec-12_008900.1	Putaive LSm10 protein	NA	NA
comp22723_c0_seq2.p1	Ec-12_008910.2	Phosphatidic acid phosphatase type 2/haloperoxidase	GO:0003824;GO:0016020	NA
comp20816_c0_seq1.p1	Ec-12_008920.1	Tetraspanin/Peripherin	GO:0016021	NA
comp64366_c0_seq1.p1	Ec-12_008950.1	Ankyrin repeat-containing domain	n/a;GO:0005515	NA
comp25679_c1_seq1.p1	Ec-12_008970.1	hypothetical protein	n/a;n/a;n/a	NA
comp31069_c1_seq6.p1	Ec-12_008980.1	oxidoreductase	GO:0016614;GO:0055114	no relat
comp20708_c0_seq3.p1	Ec-12_008990.1	conserved unknown protein	n/a;n/a;n/a	NA
comp27451_c1_seq7.p1	Ec-12_009070.1	Protein-tyrosine phosphatase-like	GO:0003676;GO:0005622;GO:0008270	NA
comp43873_c0_seq1.p1	Ec-12_009080.1	SAP domain	n/a;n/a;n/a	NA
comp21583_c0_seq1.p1	Ec-12_009090.1	Hypothetical leucine rich repeat protein	NA	NA
comp12887_c0_seq1.p1	Ec-12_009100.1	ABC transporter ATP-binding protein	GO:0016020;GO:0005524;GO:0008236;GO:0006508;GO:0016887	KOG0927
comp20456_c0_seq2.p1	Ec-12_009110.1	Protein of unknown function DUF92, TMEM19	GO:0016021	NA
comp20676_c0_seq1.p1	Ec-12_009140.1	Hypothetical protein	n/a;n/a;n/a	NA
comp21407_c0_seq1.p1	Ec-12_009150.1	Organic solute transporter subunit alpha/Transmembrane protein 184	n/a;n/a;n/a	NA
comp11932_c0_seq1.p1	Ec-13_000020.1	hypothetical protein	n/a;n/a;n/a	NA
comp30999_c0_seq4.p2	Ec-13_000105.1	hypothetical protein	NA	NA
comp32937_c0_seq5.p1	Ec-13_000130.1	Hypothetical protein	n/a;n/a;n/a	NA
comp26405_c0_seq2.p1	Ec-13_000140.1	expressed unknown protein	n/a;n/a;n/a	NA
comp28834_c0_seq1.p1	Ec-13_000230.1	Cytochrome B561-related	NA	NA
comp11704_c0_seq1.p1	Ec-13_000260.1	Vacuolar protein sorting protein 26 related	n/a;n/a;n/a	NA
comp29121_c0_seq2.p1	Ec-13_000290.2	Origin recognition complex, subunit 3	GO:0003677;GO:0005664;GO:0006260	NA
comp30174_c0_seq2.p1	Ec-13_000300.1	Protein of unknown function DUF583	n/a;n/a;n/a	NA
comp32699_c0_seq12.p1	Ec-13_000320.1	Transmembrane protein TauE like	GO:0016021	NA
comp32933_c1_seq3.p1	Ec-13_000340.1	Glutathione S-transferase	n/a;n/a;n/a	KOG1695
comp32017_c0_seq3.p1	Ec-13_000350.1	expressed unknown protein	n/a;n/a;n/a	NA
comp20055_c0_seq1.p1	Ec-13_000360.1	CMGC family protein kinase	GO:0006468;GO:0004674;GO:0004672	NA
comp29752_c0_seq3.p1	Ec-13_000370.1	Hypothetical protein	n/a;n/a;n/a	NA
comp31592_c0_seq8.p1	Ec-13_000430.2	Sulfotransferase	GO:0008146;GO:0016021	NA
comp27993_c0_seq2.p1	Ec-13_000440.1	Zinc finger, HIT-type	n/a;n/a;n/a	NA
comp26909_c0_seq2.p1	Ec-13_000460.2	expressed unknown protein	n/a;n/a;n/a	NA
comp95731_c0_seq1.p1	Ec-13_000490.1	hypothetical protein	n/a;n/a;n/a	NA
comp34434_c0_seq1.p1	Ec-13_000510.1	eukaryotic translation initiation factor 2B beta subunit	GO:0044237	NA
comp34326_c0_seq1.p1	Ec-13_000640.1	GrpE nucleotide exchange factor	GO:0006457;GO:0051087;GO:0042803;GO:0000774	NA
comp24038_c0_seq2.p1	Ec-13_000660.2	Ankyrin repeat-containing domain	n/a;n/a;n/a	NA
comp19449_c0_seq2.p1	Ec-13_000710.2	Cullin repeat-like-containing domain	n/a;n/a;n/a	NA
comp20202_c0_seq1.p1	Ec-13_000720.1	GTP binding domain	GO:0005525	NA
comp31027_c0_seq1.p1	Ec-13_000730.1	Restriction endonuclease type II-like	GO:0003677;GO:0005515;GO:0006259;GO:0004518	NA
comp11844_c0_seq1.p1	Ec-13_000740.1	expressed unknown protein	n/a;n/a;n/a	NA
comp31430_c0_seq5.p1	Ec-13_000750.1	Thioredoxin domain	GO:0045454	NA
comp30256_c0_seq6.p1	Ec-13_000830.1	EsV-1-7 domain protein	NA	NA
comp32939_c0_seq1.p1	Ec-13_000840.1	putative transcription antitermination protein	GO:0032968;GO:0006355;GO:0003711	NA
comp34561_c0_seq1.p1	Ec-13_000850.1	Sas10/Utp3/C1D	n/a;n/a;n/a	NA
comp26707_c0_seq1.p1	Ec-13_000950.1	RNA-binding S4	GO:0003723	NA
comp27845_c0_seq1.p1	Ec-13_000960.1	Haemerythrin/HHE cation-binding motif	n/a;n/a;n/a	NA
comp30423_c0_seq7.p1	Ec-13_000970.1	Transmembrane amino acid transporter	NA	NA
comp23803_c0_seq1.p1	Ec-13_001020.1	Ctr copper transporter	GO:0005375;GO:0035434;GO:0016021	NA
comp13568_c0_seq2.p1	Ec-13_001070.1	NMD3	n/a;n/a;n/a	NA
comp33065_c0_seq22.p1	Ec-13_001120.3	hypothetical protein	GO:0006355;GO:0043565;GO:0003700	NA
comp30898_c0_seq3.p1	Ec-13_001240.1	Phosphatidylinositol-4-phosphate 5-kinase, core	GO:0016307;GO:0046488	NA
comp32484_c3_seq12.p1	Ec-13_001310.1	Peptidyl-prolyl cis-trans isomerase, PpiC-type	GO:0016853	NA
comp26932_c0_seq4.p1	Ec-13_001350.2	HAD-superfamily hydrolase	NA	NA
comp32849_c0_seq10.p1	Ec-13_001370.1	Phosphate transporter	GO:0016020;GO:0006817;GO:0005315	NA
comp30925_c0_seq2.p1	Ec-13_001390.1	cAMP/cGMP-dependent protein kinase	GO:0001932;GO:0004672;GO:0005509;GO:0005524;GO:0005952;GO:0006468;GO:0008603	KOG0032
comp32858_c2_seq3.p1	Ec-13_001400.1	Voltage-dependent anion channel	GO:0055085;GO:0016021	NA
comp31893_c1_seq4.p1	Ec-13_001410.1	WD40/YVTN repeat-like-containing domain	GO:0005515	NA
comp30156_c0_seq3.p1	Ec-13_001420.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0006470	NA
comp30532_c0_seq7.p1	Ec-13_001430.1	conserved unknown protein	n/a;n/a;n/a	NA
comp32840_c3_seq3.p1	Ec-13_001430.2	conserved unknown protein	n/a;n/a;n/a	NA
comp31090_c0_seq3.p1	Ec-13_001530.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	NA
comp27893_c0_seq1.p1	Ec-13_001590.2	Mad3/BUB1 homology region 1	n/a;n/a;n/a	NA
comp32165_c0_seq10.p1	Ec-13_001600.1	hypothetical protein	n/a;n/a;n/a	NA
comp32165_c0_seq1.p1	Ec-13_001620.1	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a	NA
comp31580_c0_seq1.p1	Ec-13_001630.2	Ankyrin repeat-containing domain	n/a;n/a;n/a	NA
comp30448_c0_seq7.p1	Ec-13_001650.1	Galactose-binding domain-like	GO:0005975;n/a	NA
comp10096_c0_seq1.p1	Ec-13_001750.1	High mobility group domain protein	GO:0005634;GO:0003677;GO:0005515;GO:0006355	NA
comp32703_c0_seq24.p1	Ec-13_001800.1	Nucleotide-diphospho-sugar transferase domain protein	NA	NA
comp11983_c0_seq1.p1	Ec-13_001810.1	MEMO-like domain protein	NA	NA
comp29177_c0_seq1.p1	Ec-13_001910.1	STE20-like serine/threonine kinase	GO:0016772	KOG0582
comp25968_c0_seq1.p2	Ec-13_001930.1	Putative thioesterase/thiol ester dehydrase-isomerase	NA	NA
comp12255_c0_seq1.p1	Ec-13_001950.1	Homoaconitate hydratase	GO:0008152	KOG0454
comp12829_c0_seq1.p1	Ec-13_001980.1	Ubiquitin C-terminal hydrolase	GO:0005622;GO:0004221;GO:0006511;GO:0008242	NA
comp29203_c0_seq4.p1	Ec-13_002060.1	Protein phosphatase 2C	GO:0004722;GO:0006470	NA
comp12170_c0_seq1.p1	Ec-13_002070.1	RING-type Zinc finger domain protein	GO:0005515;GO:0008270	NA
comp26149_c0_seq2.p2	Ec-13_002090.2	Conserved hypothetical protein	NA	NA
comp32873_c1_seq31.p1	Ec-13_002100.1	PBipA, plastid GTPase BipA/TypA	NA	NA
comp19414_c0_seq1.p1	Ec-13_002110.1	SANT: 'SWI3, ADA2, N-CoR and TFIIIB' DNA-binding domains	NA	NA
comp31508_c0_seq1.p2	Ec-13_002120.1	Chromosome segregation ATPases	GO:0005515;GO:0000042	NA
comp26138_c0_seq1.p1	Ec-13_002140.1	Cation/H+ exchanger, CPA1 family	GO:0006812;GO:0006814;GO:0006885;GO:0015299;GO:0015385;GO:0016021;GO:0055085	NA
comp13127_c0_seq1.p1	Ec-13_002160.1	Threonine synthase	GO:0004795;GO:0006520;GO:0006566;GO:0030170	KOG2616
comp26149_c0_seq2.p1	Ec-13_002170.1	PFfh, plastid Ffh subunit of the signal recognition particle	GO:0006614;GO:0005525	NA
comp28054_c0_seq2.p1	Ec-13_002180.1	hypothetical protein	n/a;n/a;n/a	NA
comp34378_c0_seq1.p1	Ec-13_002220.1	Nucleic acid-binding, OB-fold	GO:0003676;GO:0004386;n/a	NA
comp11963_c0_seq1.p1	Ec-13_002270.1	n/a	n/a;n/a;n/a	NA
comp21491_c0_seq1.p1	Ec-13_002280.1	Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase	GO:0008428;GO:0051252	NA
comp17885_c0_seq1.p1	Ec-13_002290.1	Calreticulin	GO:0005509;GO:0005783;GO:0006457;GO:0051082	KOG0674
comp11809_c0_seq1.p1	Ec-13_002300.1	Proteasome, subunit alpha/beta	GO:0051603;GO:0004298;GO:0005839	NA
comp32546_c0_seq1.p1	Ec-13_002340.1	hypothetical protein	n/a;n/a;n/a	NA
comp32243_c1_seq2.p1	Ec-13_002360.1	Glutathione S-transferase	GO:0005515;n/a	KOG1695
comp32323_c0_seq10.p1	Ec-13_002392.1	hypothetical protein	NA	NA
comp21443_c0_seq1.p1	Ec-13_002400.1	Cytochrome cd1-nitrite reductase-like, haem d1 domain	n/a;GO:0005515	NA
comp19857_c0_seq2.p1	Ec-13_002450.1	hypothetical protein	GO:0016021;GO:0055085;n/a	NA
comp19497_c0_seq1.p1	Ec-13_002480.1	hypothetical protein	n/a;n/a;n/a	NA
comp27027_c0_seq2.p1	Ec-13_002530.1	aspartate kinase	GO:0008652;GO:0004072	KOG0456
comp32489_c0_seq37.p1	Ec-13_002540.1	Metallo-dependent phosphatase-like	n/a;n/a;n/a	NA
comp20840_c0_seq3.p1	Ec-13_002620.1	WD40/YVTN repeat-like-containing domain	GO:0005515	NA
comp34385_c0_seq1.p1	Ec-13_002630.1	S-adenosyl-L-methionine-dependent methyltransferase, MraW, recognition domain	GO:0008168	NA
comp28081_c0_seq2.p1	Ec-13_002650.1	Pectin lyase fold	n/a;n/a;n/a	NA
comp33079_c2_seq14.p2	Ec-13_002660.1	HECT	GO:0004842	NA
comp32176_c1_seq13.p1	Ec-13_002700.1	expressed unknown protein	n/a;n/a;n/a	NA
comp24093_c0_seq3.p1	Ec-13_002710.1	GMP synthase (glutamine-hydrolyzing)	GO:0003922;GO:0005524;GO:0006164;GO:0006177	KOG1622
comp30257_c1_seq1.p1	Ec-13_002760.1	Origin recognition complex, subunit 5	GO:0005634;GO:0006260;GO:0000808	NA
comp30257_c1_seq1.p2	Ec-13_002770.1	Ribosomal protein L24	GO:0005840;GO:0005622;GO:0006412;GO:0003735	NA
comp23132_c0_seq3.p1	Ec-13_002780.3	hypothetical protein	GO:0006520;GO:0016491;GO:0055114	NA
comp30657_c0_seq5.p1	Ec-13_002810.1	inosine triphosphate pyrophosphatase, putative	NA	NA
comp18489_c0_seq1.p1	Ec-13_002830.1	Ribosomal protein L24e-related	GO:0005840;GO:0005622;GO:0042254;GO:0006412;GO:0003735	NA
comp33079_c2_seq16.p1	Ec-13_002850.1	Armadillo-type fold	GO:0005488	NA
comp28981_c1_seq1.p1	Ec-13_002890.2	Peptidase S8/S53 domain	GO:0004252;GO:0006508	NA
comp33147_c0_seq6.p1	Ec-13_002900.1	fibronectin type III domain-containing protein	n/a;n/a;n/a	NA
comp49455_c0_seq1.p1	Ec-13_002910.1	Profilin	GO:0003779;GO:0030036;GO:0015629;GO:0007010	NA
comp12816_c0_seq1.p1	Ec-13_002920.1	Actin-related protein 2/3 complex subunit 3	GO:0030833;GO:0005856;GO:0005885;GO:0034314	NA
comp34562_c0_seq1.p1	Ec-13_002930.1	expressed unknown protein	n/a;n/a;n/a	NA
comp32562_c0_seq2.p1	Ec-13_002940.1	ATP-grasp fold, subdomain 2	GO:0005524	NA
comp32145_c1_seq3.p1	Ec-13_002960.1	Nitrogen permease regulator 2	GO:0005351;GO:0009401;n/a	NA
comp11751_c0_seq2.p1	Ec-13_002970.1	Putative ubiquitin-conjugating enzyme E2	GO:0043687;GO:0019787;GO:0016881;GO:0051246	NA
comp11380_c0_seq2.p1	Ec-13_003090.1	hypothetical protein	n/a;n/a;n/a	NA
comp29540_c0_seq1.p1	Ec-13_003480.1	expressed unknown protein	n/a;n/a;n/a	NA
comp31336_c0_seq7.p1	Ec-13_003520.1	Acyl-CoA-binding protein, ACBP	GO:0000062	NA
comp26900_c0_seq2.p1	Ec-13_003780.1	Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase	n/a;n/a;n/a	NA
comp32145_c3_seq8.p1	Ec-13_003820.1	hypothetical protein	n/a;n/a;n/a	NA
comp33124_c0_seq6.p1	Ec-13_003840.1	Endo-1,3-beta-glucanase, family GH81	GO:0033903;GO:0052861;GO:0016998;GO:0052862	KOG2254
comp31037_c0_seq5.p1	Ec-13_003850.1	expressed unknown protein	n/a;n/a;n/a	NA
comp28351_c0_seq2.p1	Ec-13_003860.1	RWD domain	GO:0005515	NA
comp11732_c0_seq1.p1	Ec-13_003870.1	Domain of unknown function DUF3351	n/a;n/a;n/a	NA
comp11426_c0_seq1.p1	Ec-13_003910.4	conserved unknown protein	n/a;n/a;n/a	NA
comp34987_c0_seq1.p1	Ec-13_003920.1	Uncharacterised protein family Ycf19	GO:0016020	NA
comp20156_c0_seq2.p1	Ec-13_003930.1	Ribosomal protein S24/S35, mitochondrial, conserved domain	n/a;n/a;n/a	NA
comp32622_c0_seq41.p1	Ec-13_003970.1	FAR1 DNA binding domain	n/a;GO:0006355	NA
comp21403_c0_seq2.p1	Ec-13_004150.1	hypothetical protein	n/a;n/a;n/a	NA
comp30467_c0_seq2.p1	Ec-13_004200.1	Peptidase S8/S53 domain	GO:0004252;GO:0006508	NA
comp33236_c1_seq5.p1	Ec-13_004250.1	hypothetical protein	n/a;n/a;n/a	NA
comp29148_c0_seq4.p1	Ec-13_004270.1	hypothetical protein	n/a;n/a;n/a	NA
comp56020_c0_seq1.p1	Ec-13_004280.1	hypothetical protein	n/a;n/a;n/a	NA
comp26626_c0_seq1.p1	Ec-13_004520.1	Tetratricopeptide repeat containing protein	GO:0015969;GO:0005515	NA
comp12049_c0_seq1.p1	Ec-13_004550.1	hypothetical protein	NA	NA
comp25969_c0_seq1.p1	Ec-13_004570.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	NA
comp31342_c3_seq1.p1	Ec-13_004640.2	ENTH domain	n/a;n/a;n/a	NA
comp33943_c0_seq1.p1	Ec-13_004660.1	Ribosomal protein S9	GO:0005840;GO:0006412;GO:0003735	NA
comp29549_c1_seq1.p1	Ec-13_004690.1	Hypothetical protein	n/a;n/a;n/a	NA
comp31157_c0_seq2.p1	Ec-13_004700.1	Homeodomain-like	GO:0003677	NA
comp30889_c0_seq2.p1	Ec-14_000070.1	expressed unknown protein	n/a;n/a;n/a	NA
comp24653_c0_seq1.p1	Ec-14_000090.1	conserved unknown protein	n/a;n/a;n/a	NA
comp27782_c1_seq2.p2	Ec-14_000100.3	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270	NA
comp27012_c1_seq1.p1	Ec-14_000110.3	Mediator complex, subunit Med31	GO:0001104;GO:0006355;GO:0016592	NA
comp33871_c0_seq1.p1	Ec-14_000120.1	Beta2-adaptin/TBP, C-terminal domain	GO:0003677	NA
comp26538_c0_seq1.p1	Ec-14_000150.1	Histone deactylase domain protein	n/a;n/a;n/a	NA
comp30382_c0_seq3.p1	Ec-14_000160.1	Pseudouridine synthase, catalytic domain	GO:0003723;GO:0001522;GO:0016866;GO:0009451;GO:0009982	NA
comp30382_c0_seq4.p1	Ec-14_000170.1	Aldolase-type TIM barrel	GO:0003824	NA
comp29789_c0_seq1.p1	Ec-14_000180.1	C2 domain	GO:0005515	NA
comp35780_c0_seq1.p1	Ec-14_000220.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0005622;GO:0008152;GO:0016301;GO:0016310;GO:0016774	NA
comp29605_c0_seq4.p1	Ec-14_000220.2	S-adenosyl-L-methionine-dependent methyltransferase	GO:0005622;GO:0008152;GO:0016301;GO:0016310;GO:0016774	NA
comp27717_c0_seq2.p1	Ec-14_000230.1	Gamma-tubulin complex component protein	GO:0005815;GO:0000922;GO:0000226	NA
comp27395_c0_seq2.p1	Ec-14_000240.1	Glycosyltransferase, family GT8	GO:0016757;GO:0016758;GO:0016051	NA
comp30617_c0_seq1.p1	Ec-14_000250.1	WD40-repeat-containing domain	GO:0005515	NA
comp32279_c2_seq18.p1	Ec-14_000260.1	expressed unknown protein	n/a;n/a;n/a	NA
comp2301_c0_seq1.p1	Ec-14_000280.1	NSF attachment protein	GO:0006886;GO:0005515	NA
comp31688_c0_seq1.p1	Ec-14_000290.1	expressed unknown protein	n/a;n/a;n/a	NA
comp26612_c0_seq3.p1	Ec-14_000320.3	Proteasome component (PCI) domain	GO:0005515	NA
comp26612_c0_seq3.p3	Ec-14_000330.1	Replication factor A protein 3	GO:0003677;GO:0005634;GO:0006260;GO:0006281;GO:0006310	NA
comp20010_c0_seq3.p1	Ec-14_000340.1	conserved unknown protein	n/a;n/a;n/a	NA
comp18374_c0_seq2.p1	Ec-14_000350.1	Pectin lyase fold	n/a;n/a;n/a	NA
comp32917_c0_seq9.p1	Ec-14_000360.1	DNA-directed RNA polymerase I, subunit RPA34.5	n/a;n/a;n/a	NA
comp32917_c0_seq7.p1	Ec-14_000370.1	Protein of unknown function DUF393	n/a;n/a;n/a	NA
comp28252_c0_seq1.p1	Ec-14_000380.1	FKBP-type peptidyl-prolyl cis-trans isomerase 2	GO:0006457	KOG0544
comp27043_c0_seq1.p2	Ec-14_000400.1	HD domain	GO:0003824	NA
comp33243_c0_seq18.p1	Ec-14_000410.3	Zinc finger, RanBP2-type	GO:0008270	NA
comp16448_c0_seq1.p1	Ec-14_000420.1	ABC transporter, ATP-binding protein	GO:0005524;GO:0016887	NA
comp32934_c0_seq3.p1	Ec-14_000430.1	MCO is implicated in celullar iron transport playing also role in the copper resistance	n/a;n/a;n/a	KOG1263
comp32790_c0_seq9.p1	Ec-14_000450.2	expressed unknown protein	n/a;n/a;n/a	NA
comp30032_c0_seq2.p1	Ec-14_000490.1	WD40 repeat	GO:0005515	NA
comp30032_c0_seq2.p2	Ec-14_000495.1	hypothetical protein	GO:0005515	NA
comp12167_c0_seq1.p1	Ec-14_000500.1	Histidine triad (HIT) protein	GO:0003824	NA
comp12167_c0_seq1.p2	Ec-14_000510.1	expressed unknown protein	n/a;n/a;n/a	NA
comp34200_c0_seq1.p1	Ec-14_000520.1	CobW/HypB/UreG domain	n/a;n/a;n/a	NA
comp27043_c0_seq2.p1	Ec-14_000530.1	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	GO:0007186;GO:0005515;GO:0016021	NA
comp29165_c0_seq5.p1	Ec-14_000550.1	expressed unknown protein	n/a;n/a;n/a	NA
comp28862_c0_seq1.p1	Ec-14_000560.1	Calcineurin-like phosphoesterase domain, apaH type	GO:0016787	NA
comp31773_c0_seq3.p2	Ec-14_000570.1	Protein of unknown function DUF760	n/a;n/a;n/a	NA
comp11622_c0_seq1.p1	Ec-14_000580.1	Concanavalin A-like lectin/glucanase domain	n/a;GO:0005515	NA
comp30412_c0_seq2.p2	Ec-14_000590.1	expressed unknown protein	n/a;n/a;n/a	NA
comp30412_c0_seq2.p1	Ec-14_000600.1	3-phosphoinositide-dependent protein kinase (PDK1) Serine/threonine protein phosphatase 2A, regulato	GO:0004672;GO:0005524;GO:0006468	KOG0592
comp28090_c0_seq4.p1	Ec-14_000610.1	CTR-like protein kinase	GO:0006468;GO:0004672;GO:0016772	NA
comp20984_c0_seq2.p1	Ec-14_000620.1	DNA replication licensing factor Mcm3	GO:0005634;GO:0003677;GO:0005524;GO:0006270;GO:0042555;GO:0003678	NA
comp34296_c0_seq1.p1	Ec-14_000640.1	Heat shock protein 40 like protein	GO:0006457;GO:0031072;GO:0005515;GO:0051082	NA
comp31797_c0_seq3.p1	Ec-14_000680.1	Armadillo-type fold	GO:0005488	NA
comp12166_c0_seq1.p1	Ec-14_000690.1	protein phosphatase 2A regulatory subunit	n/a;GO:0005488	KOG0211
comp28319_c1_seq3.p1	Ec-14_000700.2	expressed unknown protein	n/a;n/a;n/a	NA
comp29603_c0_seq4.p1	Ec-14_000730.1	Immunoglobulin-like fold	n/a;n/a;n/a	NA
comp33216_c0_seq8.p1	Ec-14_000740.1	Tousled-like protein kinase	GO:0004672;GO:0005524;GO:0006468	KOG1151
comp33216_c0_seq8.p2	Ec-14_000750.1	Phox homologous domain	GO:0035091	NA
comp31076_c2_seq2.p1	Ec-14_000760.1	ING family	GO:0005634;GO:0016568	NA
comp31289_c0_seq4.p1	Ec-14_000770.1	conserved unknown protein	n/a;n/a;n/a	NA
comp24646_c0_seq3.p1	Ec-14_000780.1	Hypothetical leucine rich repeat protein	GO:0005515	NA
comp12657_c1_seq1.p1	Ec-14_000790.1	Glucosidase II beta subunit-like	GO:0005515	NA
comp20038_c0_seq2.p1	Ec-14_000800.1	Heat shock protein 40 like protein	GO:0031072	NA
comp29343_c0_seq1.p2	Ec-14_000810.1	NAD( ) synthase (glutamine-hydrolyzing)	GO:0006807;GO:0016810	KOG2303
comp29680_c0_seq2.p1	Ec-14_000820.1	Voltage Gated Calcium/Sodium Channel subunit alpha.	GO:0070588;GO:0005245;GO:0005891	KOG2301
comp19573_c0_seq1.p1	Ec-14_000830.1	Glutamate synthase (NADH/NADPH-dependent)	GO:0045181;GO:0051536;GO:0055114;GO:0006536;GO:0016491	KOG0399
comp31832_c0_seq18.p1	Ec-14_000840.1	Peptidase C69, dipeptidase A	GO:0006508;GO:0016805	NA
comp26963_c0_seq4.p1	Ec-14_000860.1	Dnm1, dynamin-related GTPase involved in mitochondrial division	GO:0005525	NA
comp24388_c0_seq3.p1	Ec-14_000870.1	UDP-glucosyltransferase, family GT1	GO:0008152;GO:0016758	KOG1192
comp30652_c0_seq4.p1	Ec-14_000880.1	Protein of unknown function DUF3493	n/a;n/a;n/a	NA
comp12189_c0_seq1.p1	Ec-14_000900.1	GBF1, ArfGEF protein of the BIG/GBF subfamily	GO:0005622;GO:0005086;GO:0032012	NA
comp33979_c0_seq1.p1	Ec-14_000910.1	Protein of unknown function DUF3119	n/a;n/a;n/a	NA
comp21260_c0_seq1.p1	Ec-14_000930.1	C2 domain	GO:0005515	NA
comp30652_c0_seq3.p1	Ec-14_000950.1	Pentatricopeptide repeat	NA	NA
comp31415_c0_seq2.p1	Ec-14_000980.1	HhH-GPD domain	GO:0006284	NA
comp32781_c0_seq2.p1	Ec-14_000990.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	NA
comp31755_c0_seq11.p1	Ec-14_001000.1	K Homology domain, type 1	GO:0003723	NA
comp26474_c0_seq1.p1	Ec-14_001010.1	Glycosyl transferase, family 1	GO:0009058	NA
comp91248_c0_seq1.p1	Ec-14_001020.2	hypothetical protein	n/a;n/a;n/a	NA
comp19868_c0_seq1.p2	Ec-14_001030.1	CAB/ELIP/HLIP superfamily of protein	n/a;n/a;n/a	NA
comp19868_c0_seq1.p1	Ec-14_001060.1	Dual specificity/tyrosine protein phosphatase, N-terminal	GO:0006470;GO:0008138	NA
comp20445_c0_seq1.p1	Ec-14_001070.1	ATPase, F0 complex, B chain/subunit B/MI25	GO:0015986;GO:0000276;GO:0015078	NA
comp13050_c0_seq1.p1	Ec-14_001080.1	GPI transamidase subunit PIG-U	GO:0006506;GO:0016021	NA
comp29963_c0_seq3.p1	Ec-14_001090.1	GPI-GlcNAc transferase complex, PIG-H component, conserved domain	GO:0017176	NA
comp33570_c0_seq1.p1	Ec-14_001100.1	Cathepsin L-like proteinase	GO:0006508;GO:0004197	KOG1543
comp34073_c0_seq1.p1	Ec-14_001120.1	PDZ domain	GO:0005515	NA
comp31717_c0_seq2.p1	Ec-14_001130.2	Alpha/Beta hydrolase fold	GO:0004252;GO:0004287;GO:0006508	NA
comp31959_c0_seq10.p1	Ec-14_001140.1	similar to Serine/threonine-protein kinase CTR1	GO:0004674;GO:0006468	NA
comp32851_c1_seq5.p1	Ec-14_001150.1	Thioredoxin-like fold	n/a;n/a;n/a	NA
comp29090_c0_seq2.p1	Ec-14_001160.1	Pentatricopeptide repeat	GO:0005576;GO:0006826;GO:0006879;GO:0008199	NA
comp29778_c0_seq3.p1	Ec-14_001220.1	EsV-1-164	n/a;n/a;n/a	NA
comp29890_c0_seq1.p1	Ec-14_001230.3	Tubulin	GO:0005874;GO:0007017	NA
comp31627_c0_seq1.p2	Ec-14_001240.1	DNA recombination and repair protein RecA	GO:0003677;GO:0006281;GO:0005524;GO:0009432;GO:0006259;GO:0003697;GO:0008094	KOG1433
comp30151_c0_seq4.p1	Ec-14_001250.1	Ankyrin repeat-containing domain	n/a;GO:0005515	NA
comp31627_c0_seq1.p1	Ec-14_001260.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	NA
comp31016_c0_seq2.p1	Ec-14_001290.1	Basic-leucine zipper domain	GO:0006355;GO:0043565;GO:0003700	NA
comp29045_c0_seq9.p1	Ec-14_001300.1	Tubby C-terminal-like domain	n/a;n/a;n/a	NA
comp28928_c0_seq3.p1	Ec-14_001310.3	RNA polymerase I, Rpa2 specific	GO:0003899;GO:0005634;GO:0006351	NA
comp32196_c0_seq17.p1	Ec-14_001330.1	NAD(P)-binding domain	GO:0008152;GO:0016491	NA
comp24959_c0_seq1.p1	Ec-14_001350.1	Pseudouridine synthase, catalytic domain	GO:0003723;GO:0009451;GO:0001522;GO:0009982	NA
comp28761_c0_seq1.p1	Ec-14_001370.1	Ferredoxin-dependent bilin reductase	GO:0010024;GO:0055114;GO:0050897;GO:0016636	NA
comp24118_c0_seq1.p1	Ec-14_001390.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	NA
comp31540_c0_seq11.p1	Ec-14_001410.1	conserved unknown protein	n/a;GO:0005515	NA
comp32167_c0_seq18.p1	Ec-14_001430.1	Uncharacterised protein family UPF0183	GO:0005097;GO:0005622;GO:0032313	NA
comp22679_c0_seq1.p1	Ec-14_001450.1	Zinc finger, CCCH-type	GO:0046872	NA
comp31871_c1_seq4.p1	Ec-14_001470.1	K Homology domain	GO:0003723;GO:0003676	NA
comp31871_c1_seq4.p2	Ec-14_001480.1	expressed unknown protein	n/a;n/a;n/a	NA
comp24754_c0_seq1.p1	Ec-14_001500.1	GOLD	GO:0006810;GO:0016021	NA
comp12489_c0_seq1.p1	Ec-14_001510.2	Putative subunit of the Anaphase Promoting Complex	GO:0005680	KOG1858
comp31706_c1_seq3.p1	Ec-14_001520.1	aldo/keto reductase family protein	GO:0016491;GO:0055114	NA
comp28928_c0_seq3.p2	Ec-14_001540.1	Pseudouridine synthase, catalytic domain	GO:0001522;GO:0003723;GO:0009451;GO:0009982	NA
comp32196_c0_seq32.p2	Ec-14_001550.1	expressed unknown protein	GO:0000166;GO:0004812;GO:0005524;GO:0005737;GO:0006412;GO:0006418;n/a	NA
comp12481_c0_seq2.p1	Ec-14_001570.1	CRAL-TRIO domain	n/a;n/a;n/a	NA
comp31279_c0_seq4.p1	Ec-14_001580.1	Rieske [2Fe-2S] iron-sulphur domain	GO:0016491;GO:0051537;GO:0055114	NA
comp34401_c0_seq1.p1	Ec-14_001590.1	Guanylate kinase (IC)	n/a;GO:0004385;GO:0006163	NA
comp24583_c0_seq1.p1	Ec-14_001600.1	Acyl-CoA dehydrogenase	GO:0033539;GO:0016627;GO:0055114;GO:0003995	no relat
comp43786_c0_seq1.p1	Ec-14_001610.1	conserved unknown protein	NA	NA
comp29740_c0_seq1.p1	Ec-14_001650.1	Isopenicillin N synthase-like	n/a;n/a;n/a	NA
comp30283_c0_seq4.p1	Ec-14_001660.1	Alpha/beta knot methyltransferases	n/a;GO:0008168	NA
comp30283_c0_seq4.p3	Ec-14_001670.1	Autophagy-related protein 12	GO:0005737;GO:0000045	NA
comp29706_c0_seq2.p1	Ec-14_001680.1	fructose-1,6-bisphosphate aldolase	GO:0004332;GO:0006096	KOG1557
comp31363_c0_seq3.p1	Ec-14_001690.1	BRCT domain	GO:0005622;n/a	NA
comp34620_c0_seq1.p1	Ec-14_001700.1	expressed unknown protein	n/a;n/a;n/a	NA
comp23691_c0_seq1.p1	Ec-14_001710.1	hypothetical protein	n/a;n/a;n/a	NA
comp32764_c5_seq28.p1	Ec-14_001720.1	Metacaspase	GO:0030693;GO:0006508;GO:0004197	KOG1546

comp11874_c0_seq1.p1	Ec-14_001730.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PF14629: Origin recognition complex (ORC) subunit 4 C-terminus; PTHR12087: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13191: AAA ATPase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33437_c0_seq1.p1	Ec-14_001770.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp20379_c0_seq1.p1	Ec-14_001800.1	Armadillo-like helical	GO:0005488	IPR022542: Domain of unknown function DUF3730; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold; PTHR16212:	NA
comp26663_c0_seq1.p1	Ec-14_001810.1	Myosin head, motor domain	GO:0005524;GO:0003774;GO:0005515;GO:0016459	SSF51735: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR016040: NAD(P)-binding domain; IPR001609: Myosin head, motor domain; Coil: ; PTHR13140: ; IPR000048: IQ motif, EF-hand binding site	NA
comp32704_c0_seq31.p1	Ec-14_001830.1	UPF0505 family	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR029707: UPF0505, invertebrates/plants; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029705: UPF0505 family; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32037_c0_seq2.p1	Ec-14_001840.1	tRNA endonuclease-like domain	GO:0004518;GO:0003676	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR21227: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR006677: tRNA intron endonuclease, catalytic domain-like; IPR006676: tRNA-splicing endonuclease; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011856: tRNA endonuclease-like domain; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32969_c0_seq2.p1	Ec-14_001850.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp30628_c0_seq3.p1	Ec-14_001860.1	Phosphatidylinositol 3-/4-kinase, catalytic domain	GO:0016773	IPR000403: Phosphatidylinositol 3-/4-kinase, catalytic domain; G3DSA:3.30.1010.10: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR011009: Protein kinase-like domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015433: Phosphatidylinositol Kinase; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR018936: Phosphatidylinositol 3/4-kinase, conserved site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26526_c0_seq3.p1	Ec-14_001870.1	ABC transporter type 1, transmembrane domain	GO:0005524;GO:0006810;GO:0016021;GO:0042626;GO:0055085	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR003439: ABC transporter-like; G3DSA:1.20.1560.10: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011527: ABC transporter type 1, transmembrane domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR017871: ABC transporter, conserved site; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; PTHR24221: ; SignalP-noTM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33564_c0_seq1.p1	Ec-14_001920.1	Alpha/beta hydrolase fold-1	n/a;n/a;n/a	IPR029058: Alpha/Beta hydrolase fold; IPR000073: Alpha/beta hydrolase fold-1	NA
comp32972_c0_seq16.p1	Ec-14_001930.1	Putative small multi-drug export	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009577: Putative small multi-drug export; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20749_c0_seq1.p1	Ec-14_001960.1	START domain	GO:0008289	SSF55961: ; IPR002913: START domain; IPR023393: START-like domain	NA
comp27122_c0_seq4.p1	Ec-14_001970.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30217_c0_seq1.p1	Ec-14_001980.1	SET domain and Rubisco LSMT substrate-binding domain protein	NA	NA	NA
comp30419_c0_seq1.p1	Ec-14_001990.2	Putative ubiquitin-protein ligase	GO:0008270;GO:0006512;GO:0004842	SSF57850: ; IPR011989: Armadillo-like helical; PTHR21725:SF1: ; PTHR21725: ; IPR000433: Zinc finger, ZZ-type; Coil: ; IPR003126: Zinc finger, UBR-type	NA
comp30419_c0_seq2.p1	Ec-14_002000.1	E3 ubiquitin ligase, UBR4	GO:0005506;GO:0006118;GO:0009055;GO:0020037	PTHR21725: ; Coil: ; IPR025704: E3 ubiquitin ligase, UBR4	NA
comp30221_c0_seq2.p1	Ec-14_002030.1	Metallopeptidase, catalytic domain	GO:0008237	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR024079: Metallopeptidase, catalytic domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; SSF55486: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11735_c0_seq1.p1	Ec-14_002040.1	Protein lojap/ribosomal silencing factor RsfS	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF81301: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004394: Protein Iojap/ribosomal silencing factor RsfS; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:3.30.460.10: ; IPR025656: Oligomerisation domain	NA
comp21574_c0_seq1.p1	Ec-14_002050.1	creatine kinase	GO:0003824;GO:0016301;GO:0016772	IPR000749: ATP:guanido phosphotransferase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR014746: Glutamine synthetase/guanido kinase, catalytic domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR022413: ATP:guanido phosphotransferase, N-terminal; SSF55931: ; IPR022415: ATP:guanido phosphotransferase active site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24962_c0_seq3.p1	Ec-14_002060.1	ADP-ribosylation factor-like 2-binding protein, domain	n/a;n/a;n/a	Coil: ; PTHR21532: ; IPR023379: ADP-ribosylation factor-like 2-binding protein, domain	NA
comp20872_c0_seq1.p1	Ec-14_002070.1	Fibronectin type III	GO:0005515	IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR003961: Fibronectin type III; IPR020472: G-protein beta WD-40 repeat; PTHR22847: ; IPR013783: Immunoglobulin-like fold; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; Coil:	NA
comp22150_c0_seq1.p1	Ec-14_002090.1	Nucleic acid-binding, OB-fold	GO:0003723	IPR012340: Nucleic acid-binding, OB-fold; IPR003029: Ribosomal protein S1, RNA-binding domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; PTHR10724: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR022967: RNA-binding domain, S1; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27413_c0_seq1.p1	Ec-14_002100.1	Hypothetical leucine rich repeat protein	NA	G3DSA:3.80.10.10: ; PTHR24106: ; SSF52047: ; PF13516: Leucine Rich repeat; IPR003590: Leucine-rich repeat, ribonuclease inhibitor subtype	NA
comp28561_c0_seq2.p1	Ec-14_002110.1	MSP domain	GO:0005198;GO:0005789	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR008962: PapD-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000535: MSP domain; IPR016763: Vesicle-associated membrane-protein-associated protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34000_c0_seq1.p1	Ec-14_002120.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020	PTHR24089: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25623_c0_seq1.p1	Ec-14_002130.1	Metal-dependent protein hydrolase	n/a;n/a;n/a	IPR003226: Metal-dependent protein hydrolase	NA
comp28594_c0_seq7.p1	Ec-14_002160.1	SUF system FeS cluster assembly, SufBD	GO:0016226	PTHR30508: ; SIGNAL_PEPTIDE: Signal peptide region; SSF101960: ; IPR000825: SUF system FeS cluster assembly, SufBD; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30050_c0_seq14.p1	Ec-14_002170.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13424: Tetratricopeptide repeat; IPR001440: Tetratricopeptide TPR1; PTHR19959: ; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat	NA
comp31634_c0_seq1.p1	Ec-14_002180.1	hypothetical protein	n/a;n/a;n/a	PF15236: Coiled-coil domain-containing protein 66; Coil:	NA
comp34816_c0_seq1.p1	Ec-14_002190.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29200_c0_seq8.p1	Ec-14_002200.1	hypothetical protein	n/a;n/a;n/a	IPR014002: Agenet domain, plant type; Coil:	NA
comp25264_c0_seq1.p1	Ec-14_002210.1	Heat Shock transcription factor	GO:0003700;GO:0005634;GO:0006355;GO:0043565	IPR011991: Winged helix-turn-helix DNA-binding domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR000232: Heat shock factor (HSF)-type, DNA-binding; PTHR10015:SF165: ; mobidb-lite: consensus disorder prediction; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR027725: Heat shock transcription factor family	NA
comp33842_c0_seq1.p1	Ec-14_002220.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29368_c0_seq5.p1	Ec-14_002230.1	Ankyrin repeat	GO:0005515	IPR020683: Ankyrin repeat-containing domain; Coil: ; IPR002110: Ankyrin repeat; PTHR24188:	NA
comp32764_c5_seq17.p1	Ec-14_002240.2	Thioredoxin-like fold	n/a;n/a;n/a	IPR005746: Thioredoxin; PTHR10438:SF227: ; IPR013766: Thioredoxin domain; IPR012336: Thioredoxin-like fold	NA
comp31760_c0_seq2.p1	Ec-14_002250.1	Sugar/inositol transporter	GO:0016020;GO:0055085;GO:0016021;GO:0022891;GO:0022857	IPR005829: Sugar transporter, conserved site; IPR005828: General substrate transporter; IPR003663: Sugar/inositol transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24063:	NA
comp27538_c0_seq1.p1	Ec-14_002260.1	Uncharacterised domain UPF0126	n/a;n/a;n/a	IPR005115: Uncharacterised domain UPF0126; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR30506: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29702_c0_seq3.p2	Ec-14_002270.2	4Fe-4S ferredoxin, iron-sulfur binding	GO:0016491;GO:0051536;GO:0055114	IPR021039: Iron-sulphur binding protein LdpA, C-terminal; G3DSA:3.30.70.20: ; IPR017900: 4Fe-4S ferredoxin, iron-sulphur binding, conserved site; IPR017896: 4Fe-4S ferredoxin-type, iron-sulphur binding domain; PTHR19248:SF20: ; SSF54862: ; IPR013283: ABC transporter ABCE	NA
comp29348_c0_seq1.p1	Ec-14_002280.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR008984: SMAD/FHA domain; IPR020683: Ankyrin repeat-containing domain; IPR000467: G-patch domain; IPR000253: Forkhead-associated (FHA) domain; PTHR13948: ; IPR002110: Ankyrin repeat	NA
comp31958_c0_seq7.p1	Ec-14_002300.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0000981;GO:0005634;GO:0006355;GO:0008270	IPR001138: Zn(2)-C6 fungal-type DNA-binding domain	NA
comp26304_c0_seq3.p1	Ec-14_002310.1	M16 family peptidase	GO:0003824;GO:0046872	IPR007863: Peptidase M16, C-terminal domain; SIGNAL_PEPTIDE: Signal peptide region; IPR011765: Peptidase M16, N-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011249: Metalloenzyme, LuxS/M16 peptidase-like; IPR011237: Peptidase M16 domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11851: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp16308_c0_seq2.p1	Ec-14_002320.1	Rab-GTPase-TBC domain	GO:0005097;GO:0032313	G3DSA:1.10.8.270: ; IPR000195: Rab-GTPase-TBC domain; PTHR22957:	NA
comp16308_c0_seq2.p2	Ec-14_002340.1	Golgi apparatus membrane protein TVP15	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013714: Golgi apparatus membrane protein TVP15; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31256_c0_seq4.p1	Ec-14_002360.1	RNA polymerase II-binding domain	n/a;n/a;n/a	IPR006903: RNA polymerase II-binding domain; IPR006569: CID domain; PTHR15921: ; IPR008942: ENTH/VHS	NA
comp21125_c0_seq3.p1	Ec-14_002380.1	Amino acid transporter, transmembrane	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013057: Amino acid transporter, transmembrane domain; PTHR22950: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27589_c0_seq3.p1	Ec-14_002390.1	Inosine/uridine-preferring nucleoside hydrolase domain	n/a;n/a;n/a	IPR001910: Inosine/uridine-preferring nucleoside hydrolase domain; SignalP-noTM: ; IPR023186: Inosine/uridine-preferring nucleoside hydrolase; PTHR12304:SF10: ; SignalP-TM:	NA
comp30549_c0_seq2.p1	Ec-14_002400.1	Sodium/sulphate symporter	GO:0016020;GO:0055085;GO:0006814;GO:0005215	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR10283: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004331: SPX, N-terminal; IPR001898: Sodium/sulphate symporter; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29702_c0_seq3.p1	Ec-14_002410.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp21614_c0_seq1.p1	Ec-14_002420.1	Cupin-like domain protein	n/a;n/a;n/a	IPR003347: JmjC domain; G3DSA:2.60.120.650: ; SSF51197: ; PTHR12461:SF56: ; mobidb-lite: consensus disorder prediction; PTHR12461: ; PF13621: Cupin-like domain; Coil:	NA
comp34988_c0_seq1.p1	Ec-14_002430.1	AP2/ERF domain	GO:0003700;GO:0006355	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR016177: DNA-binding domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR001471: AP2/ERF domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp19479_c0_seq1.p1	Ec-14_002440.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31640_c0_seq1.p1	Ec-14_002450.1	Peptidase M14, carboxypeptidase A	GO:0004181;GO:0006508;GO:0008270	PTHR12756: ; IPR000834: Peptidase M14, carboxypeptidase A; SSF53187: ; G3DSA:3.40.630.10: ; PTHR12756:SF12:	NA
comp28552_c0_seq4.p1	Ec-14_002460.1	carboxylase	GO:0009055;GO:0006118;GO:0016874;GO:0005507	IPR011762: Acetyl-coenzyme A carboxyltransferase, N-terminal; IPR013785: Aldolase-type TIM barrel; IPR029045: ClpP/crotonase-like domain; IPR000022: Carboxyl transferase; IPR000089: Biotin/lipoyl attachment; IPR000891: Pyruvate carboxyltransferase; IPR003379: Carboxylase, conserved domain; SSF51569: ; IPR001095: Acetyl-CoA carboxylase, alpha subunit; IPR011053: Single hybrid motif; PTHR18866: ; SSF89000: ; G3DSA:2.40.50.100: ; IPR001882: Biotin-binding site; IPR009057: Homeodomain-like; G3DSA:3.10.600.10: ; IPR011763: Acetyl-coenzyme A carboxyltransferase, C-terminal	NA
comp20204_c0_seq2.p1	Ec-14_002470.1	Hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11315_c0_seq1.p1	Ec-14_002500.1	conserved unknown protein	n/a;n/a;n/a	PTHR35213: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29935_c0_seq3.p1	Ec-14_002510.1	EIF3C (EUKARYOTIC TRANSLATION INITIATION FACTOR 3 subunit c)	GO:0031369;GO:0006413;GO:0003743;GO:0005852	IPR000717: Proteasome component (PCI) domain; IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; PTHR13937: ; IPR027516: Eukaryotic translation initiation factor 3 subunit C; Coil: ; IPR008905: Eukaryotic translation initiation factor 3 subunit C, N-terminal domain	NA
comp30893_c0_seq2.p1	Ec-14_002550.3	Hypothetical leucine-rich repeat protein	GO:0003743;GO:0005515;GO:0005852;GO:0006413	PTHR27000: ; IPR003591: Leucine-rich repeat, typical subtype; IPR001611: Leucine-rich repeat; SM00365: Leucine-rich repeat, SDS22-like subfamily; IPR032675: Leucine-rich repeat domain, L domain-like; Coil:	NA
comp26135_c0_seq2.p1	Ec-14_002570.1	Nucleic acid-binding, OB-fold	GO:0003676	IPR012340: Nucleic acid-binding, OB-fold; PTHR13989:	NA
comp12216_c0_seq1.p1	Ec-14_002590.1	Replication factor Mcm10	n/a;n/a;n/a	IPR015408: Zinc finger, Mcm10/DnaG-type; IPR015411: Replication factor Mcm10, C-terminal; PTHR13454:	NA
comp30604_c0_seq4.p1	Ec-14_002640.1	Winged helix-turn-helix DNA-binding domain	GO:0007154;GO:0035556;GO:0035091;GO:0005515	IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001683: Phox homologous domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000591: DEP domain	NA
comp24656_c0_seq2.p2	Ec-14_002650.1	G-patch domain	GO:0003676	PTHR21032: ; IPR000467: G-patch domain; Coil: ; IPR025239: Domain of unknown function DUF4187; SignalP-TM:	NA
comp27828_c0_seq1.p1	Ec-14_002660.1	TB2/DP1/HVA22-related protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004345: TB2/DP1/HVA22-related protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24656_c0_seq1.p1	Ec-14_002670.1	Peptidase M20, dimerisation domain	GO:0016787;GO:0046983	PTHR11014: ; IPR001261: ArgE/DapE/ACY1/CPG2/YscS, conserved site; IPR002933: Peptidase M20; IPR010159: N-acyl-L-amino-acid amidohydrolase; SSF53187: ; G3DSA:3.40.630.10: ; IPR011650: Peptidase M20, dimerisation domain	NA
comp25460_c0_seq1.p1	Ec-14_002690.1	Zinc finger, RING/FYVE/PHD-type	GO:0005515;GO:0008270	SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type	NA
comp31545_c0_seq2.p3	Ec-14_002700.1	Dolichol phosphate-mannose biosynthesis regulatory protein	GO:0030176;GO:0009059	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR15039: ; IPR009914: Dolichol phosphate-mannose biosynthesis regulatory; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32786_c0_seq5.p1	Ec-14_002710.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28866_c0_seq3.p1	Ec-14_002720.1	Armadillo-type fold	GO:0005488	IPR026971: Condensin subunit 1/Condensin-2 complex subunit D3; IPR011989: Armadillo-like helical; PF12717: non-SMC mitotic condensation complex subunit 1; IPR016024: Armadillo-type fold; IPR024324: Condensin complex, subunit 1, N-terminal	NA
comp31545_c0_seq2.p2	Ec-14_002740.1	peptidyl-prolyl cis-trans isomerase 1	GO:0016853	PTHR10657: ; SSF54534: ; G3DSA:3.10.50.40: ; IPR000297: Peptidyl-prolyl cis-trans isomerase, PpiC-type; PTHR10657:SF4:	NA
comp27019_c0_seq2.p1	Ec-14_002750.1	Putative retinoblastoma	GO:0005634;GO:0051726	IPR002719: Retinoblastoma-associated protein, B-box; IPR028309: Retinoblastoma protein family; IPR015652: Retinoblastoma-related protein; IPR013763: Cyclin-like; IPR024599: Retinoblastoma-associated protein, N-terminal; IPR002720: Retinoblastoma-associated protein, A-box	KOG1010
comp13064_c0_seq1.p1	Ec-14_002770.1	FeS cluster biogenesis	n/a;n/a;n/a	PTHR10072:SF46: ; SIGNAL_PEPTIDE: Signal peptide region; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10072: ; IPR000361: FeS cluster biogenesis; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24220_c0_seq3.p1	Ec-14_002790.1	Mef2, mitochondrial translation elongation factor EF-G	GO:0003924;GO:0005525	IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:2.40.30.10: ; IPR000795: Translation factor, GTP-binding domain; SignalP-TM: ; IPR035517: Translation elongation factor EFG/EF2, domain IV; G3DSA:3.30.70.870: ; IPR005225: Small GTP-binding protein domain; IPR000640: Translation elongation factor EFG, V domain; PTHR23115: ; IPR031157: Tr-type G domain, conserved site; IPR020568: Ribosomal protein S5 domain 2-type fold; PF00009: Elongation factor Tu GTP binding domain; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup; IPR009022: Elongation factor G, III-V domain; IPR009000: Translation protein, beta-barrel domain	NA
comp26986_c0_seq3.p1	Ec-14_002800.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32238_c1_seq3.p1	Ec-14_002810.1	Putative NIN-like transcription factor	n/a;n/a;n/a	IPR003035: RWP-RK domain; PTHR32002:	NA
comp31453_c0_seq5.p2	Ec-14_002820.1	decarboxylase	GO:0003824	IPR008286: Orn/Lys/Arg decarboxylase, C-terminal; SIGNAL_PEPTIDE: Signal peptide region; IPR000310: Orn/Lys/Arg decarboxylase, major domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR015424: Pyridoxal phosphate-dependent transferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR11751: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	NA
comp31453_c0_seq5.p1	Ec-14_002830.1	DNA photolyase, N-terminal	n/a;n/a;n/a	IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; IPR006050: DNA photolyase, N-terminal	NA
comp31344_c1_seq2.p1	Ec-14_002840.1	hypothetical protein	GO:0031177	NA	NA
comp27609_c0_seq2.p2	Ec-14_002860.1	Taxilin family	GO:0019905	IPR026183: Taxilin family; Coil:	NA

comp12188_c0_seq1.p1	Ec-14_006130.1	Inositol monophosphatase	GO:0046854	G3DSA:3.30.540.10: ; IPR020550: Inositol monophosphatase, conserved site; IPR000760: Inositol monophosphatase; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.40.190.80: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF56655: ; SignalP-noTM: ; IPR006239: 3(2),5 -bisphosphate nucleotidase HAL2; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR020583: Inositol monophosphatase, metal-binding site	NA
comp12250_c0_seq1.p1	Ec-14_006140.1	SRPRB, beta subunit of the signal recognition particle receptor	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR19326: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR019009: Signal recognition particle receptor, beta subunit; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26623_c0_seq1.p1	Ec-14_006150.1	Concanavalin A-like lectin/glucanase domain	n/a;n/a;n/a	SSF54928: ; IPR000504: RNA recognition motif domain; IPR001079: Galectin, carbohydrate recognition domain; IPR012677: Nucleotide-binding alpha-beta plait domain; IPR013320: Concanavalin A-like lectin/glucanase domain	NA
comp30985_c0_seq1.p1	Ec-14_006170.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	NA
comp31555_c0_seq17.p1	Ec-14_006180.1	Ribosomal protein L27	GO:0005840;GO:0005622;GO:0006412;GO:0003735	G3DSA:2.40.50.100: ; IPR001684: Ribosomal protein L27; SSF110324: ; IPR018261: Ribosomal protein L27, conserved site; SignalP-TM:	NA
comp31555_c0_seq4.p1	Ec-14_006190.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil: ; IPR020636: Calcium/calmodulin-dependent/calcium-dependent protein kinase	NA
comp15129_c0_seq2.p1	Ec-14_006200.1	Isochorismatase-like	GO:0008152;GO:0003824	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR14119: ; IPR000868: Isochorismatase-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12011_c0_seq1.p2	Ec-14_006210.1	Zinc finger, RING-type	GO:0005515;GO:0008270	PTHR22765: ; SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type	NA
comp12011_c0_seq1.p1	Ec-14_006220.1	MYST-type histone acetyltransferase and chromo domain protein	GO:0005634;GO:0006355;GO:0016747	NA	NA
comp27569_c0_seq2.p1	Ec-14_006230.1	Amino-acid N-acetyltransferase	GO:0004042;GO:0006526;GO:0005737	NA	KOG2436
comp29215_c0_seq1.p3	Ec-14_006240.1	Prefoldin subunit 2	GO:0006457;GO:0016272;GO:0051082	IPR002777: Prefoldin beta-like; IPR009053: Prefoldin; IPR027235: Prefoldin subunit 2; Coil:	NA
comp30956_c0_seq3.p1	Ec-14_006250.1	aspartyl protease	GO:0004190;GO:0006508	IPR021109: Aspartic peptidase domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001461: Aspartic peptidase; IPR001969: Aspartic peptidase, active site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30956_c0_seq3.p2	Ec-14_006280.1	Glycyl-tRNA Synthetase	GO:0004820;GO:0005524;GO:0006426;GO:0005737;GO:000166;GO:0006418;GO:0004812	SSF55681: ; IPR002314: Aminoacyl-tRNA synthetase, class II (G/ H/ P/ S), conserved domain; IPR027031: Glycyl-tRNA synthetase/DNA polymerase subunit gamma-2; IPR002315: Glycyl-tRNA synthetase; IPR009068: S15/NS1, RNA-binding; G3DSA:3.30.930.10: ; IPR000738: WHEP-TRS	KOG2298
comp29390_c0_seq2.p1	Ec-14_006300.1	Protein arginine N-methyltransferase	GO:0008168;GO:0006479	NA	NA
comp32034_c1_seq2.p2	Ec-14_006310.1	Nucleotide-sugar transporter	GO:0005351;GO:0000139;GO:0008643;GO:0016021	SSF103481: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007271: Nucleotide-sugar transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32034_c1_seq11.p1	Ec-14_006320.1	Armadillo-type fold	GO:0005488	IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold	NA
comp26369_c0_seq3.p1	Ec-14_006330.1	Ribosomal protein S15	GO:0003735;GO:0005622;GO:0005840;GO:0006412	IPR012606: Ribosomal protein S13/S15, N-terminal; IPR000589: Ribosomal protein S15; PTHR11885: ; IPR009068: S15/NS1, RNA-binding	NA
comp25013_c0_seq2.p1	Ec-14_006380.1	Protein kinase-like domain	GO:0016772	SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.90.1200.10: ; PTHR12149: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011009: Protein kinase-like domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016477: Fructosamine/Ketosamine-3-kinase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31919_c0_seq4.p1	Ec-14_006390.1	Zinc finger FYVE domain-containing protein	GO:0008270	IPR002921: Fungal lipase-like domain; IPR000306: FYVE zinc finger; IPR017455: Zinc finger, FYVE-related; IPR029058: Alpha/Beta hydrolase fold; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR21493: ; IPR011011: Zinc finger, FYVE/PHD-type	NA
comp32426_c0_seq1.p1	Ec-14_006400.1	Nucleotide-diphospho-sugar transferases	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13632: Glycosyl transferase family group 2; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR029044: Nucleotide-diphospho-sugar transferases; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24284_c0_seq1.p1	Ec-14_006410.1	Fringe-like	GO:0016020;GO:0016757	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR23033: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR003378: Fringe-like	NA
comp30426_c0_seq1.p1	Ec-14_006420.1	Mitochondrial import inner membrane translocase subunit TIM22 homolog	GO:0005743;GO:0008565;GO:0015031	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR14110: ; IPR003397: Mitochondrial inner membrane translocase subunit Tim17/Tim22/Tim23/peroxisomal protein PMP24; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3225
comp21566_c0_seq1.p1	Ec-14_006430.2	Nucleotide-binding alpha-beta plait domain	GO:0000166	IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp29828_c0_seq1.p1	Ec-14_006440.1	O-phosphoseryl-tRNA(Sec) selenium transferase	GO:0003824	IPR015424: Pyridoxal phosphate-dependent transferase; IPR019872: O-phosphoseryl-tRNA(Sec) selenium transferase; IPR008829: Soluble liver antigen/liver pancreas antigen; Coil: ; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	NA
comp24844_c0_seq3.p1	Ec-14_006450.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28031_c0_seq1.p1	Ec-14_006460.1	GTP diphosphokinase	GO:0015969	PTHR21262: ; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; PF13328: HD domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF81301: ; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.30.460.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF109604: ; IPR018247: EF-Hand 1, calcium-binding site; SIGNAL_PEPTIDE: Signal peptide region; SSF47473: ; IPR007685: RelA/SpoT; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-noTM:	NA
comp31092_c0_seq3.p1	Ec-14_006470.1	Armadillo-like helical	GO:0005488	IPR011989: Armadillo-like helical; SignalP-TM:	NA
comp29844_c0_seq1.p1	Ec-14_006490.3	Magnesium chelatase subunit H, putative chloroplast precursor	GO:0015995;GO:0016851	PTHR23304:SF109: ; IPR003672: CobN/magnesium chelatase; SIGNAL_PEPTIDE: Signal peptide region; IPR022571: Magnesium chelatase, subunit H, N-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR23304: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30644_c0_seq1.p1	Ec-14_006500.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp11664_c0_seq1.p1	Ec-14_006510.1	Autophagy-related protein 18	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR11227:	NA
comp11664_c0_seq2.p2	Ec-14_006520.1	Centromeric protein E, putative	GO:0007018;GO:0005524;GO:0008017;GO:0003777	IPR019821: Kinesin motor domain, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR027640: Kinesin-like protein; Coil: ; IPR001752: Kinesin motor domain	NA
comp25005_c0_seq1.p1	Ec-14_006530.1	enoyl-Coenzyme A hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	GO:0020037;GO:0006118;GO:0055114;GO:0006979;GO:0004601;GO:0006631;GO:0003857;GO:0016491	PTHR23309: ; IPR029045: ClpP/crotonase-like domain; SSF51735: ; IPR008927: 6-phosphogluconate dehydrogenase C-terminal domain-like; IPR013328: 6-phosphogluconate dehydrogenase, domain 2; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006176: 3-hydroxyacyl-CoA dehydrogenase, NAD binding; IPR006108: 3-hydroxyacyl-CoA dehydrogenase, C-terminal; IPR001753: Crotonase superfamily; IPR016040: NAD(P)-binding domain	KOG1683
comp29374_c1_seq4.p1	Ec-14_006540.1	MAPK related serine/threonine protein kinase	GO:0004672;GO:0005524;GO:0006468	PTHR24055: ; IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10:	KOG0661
comp29374_c1_seq3.p1	Ec-14_006550.1	Chlorophyll synthase, putative chloroplast precursor	GO:0004659;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR011799: Chlorophyll synthase, ChlG; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11048: ; SignalP-noTM: ; IPR006372: Bacteriochlorophyll/chlorophyll synthetase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR000537: UbiA prenyltransferase family; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp40539_c0_seq1.p1	Ec-14_006560.1	PAS domain	GO:0004871;GO:0007165	IPR000014: PAS domain; G3DSA:1.20.5.170: ; G3DSA:3.30.450.20:	NA
comp34522_c0_seq1.p1	Ec-14_006570.1	Transmembrane transporter protein, chloroquine resistant	GO:0055085;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR31326: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34130_c0_seq1.p1	Ec-14_006580.1	acetylornithine aminotransferase	GO:0003824;GO:0008483;GO:0030170	IPR004636: Acetylornithine/Succinylornithine transaminase family; IPR005814: Aminotransferase class-III; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR015424: Pyridoxal phosphate-dependent transferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2	NA
comp27256_c0_seq3.p1	Ec-14_006590.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	SSF54928: ; PTHR24012: ; PF14259: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain); IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; Coil:	NA
comp24006_c0_seq3.p1	Ec-14_006605.1	hypothetical protein	NA	Coil:	NA
comp26854_c0_seq1.p1	Ec-14_006620.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013083: Zinc finger, RING/FYVE/PHD-type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26292_c0_seq1.p1	Ec-14_006630.1	Histidyl-tRNA Synthetase Similar to Histidine Ammonia-Lyase	GO:0016841;GO:0009058;GO:0006418;GO:0004812	IPR008948: L-Aspartase-like; G3DSA:1.20.200.10: ; IPR006195: Aminoacyl-tRNA synthetase, class II; IPR001106: Aromatic amino acid lyase; IPR024083: Fumarase/histidase, N-terminal; IPR015807: Histidine-tRNA ligase; SSF55681: ; PF13393: Histidyl-tRNA synthetase; G3DSA:3.30.930.10: ; IPR004154: Anticodon-binding; IPR004516: Histidine-tRNA ligase/ATP phosphoribosyltransferase regulatory subunit	KOG0222
comp31793_c0_seq1.p1	Ec-14_006640.1	Armadillo-type fold	GO:0005488	IPR021843: Protein of unknown function DUF3437; IPR011989: Armadillo-like helical; PTHR32170: ; IPR016024: Armadillo-type fold	NA
comp34334_c0_seq1.p1	Ec-14_006650.1	Ribosomal protein L17	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR000456: Ribosomal protein L17; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31743_c0_seq4.p1	Ec-14_006670.1	PUB domain	GO:0016020;GO:0016560;GO:0005777;GO:0005515;GO:0005778	IPR018997: PUB domain; IPR006785: Peroxisome membrane anchor protein Pex14p, N-terminal; SSF143503: ; IPR025655: Peroxisomal membrane protein 14	NA
comp20653_c1_seq1.p1	Ec-14_006680.1	Dual-specificity tyrosine-phosphorylation regulated kinase	NA	PTHR24058:SF17: ; IPR017441: Protein kinase, ATP binding site; PTHR24058: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	KOG0667
comp12313_c0_seq1.p1	Ec-14_006690.1	Cytochrome P450	GO:0005506;GO:0016705;GO:0020037;GO:0055114	IPR001128: Cytochrome P450; PTHR24291:SF46: ; IPR017972: Cytochrome P450, conserved site; IPR002401: Cytochrome P450, E-class, group I; SignalP-TM: ; PTHR24291:	KOG0157
comp21095_c0_seq1.p1	Ec-14_006700.1	Cytochrome P450	GO:0020037;GO:0005506;GO:0055114;GO:0016705	IPR001128: Cytochrome P450; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR017972: Cytochrome P450, conserved site; IPR002401: Cytochrome P450, E-class, group I; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR24290: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0157
comp31743_c0_seq4.p2	Ec-14_006710.1	Putative DP transcription factor	GO:0005667;GO:0007049	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR003316: E2F/DP family, winged-helix DNA-binding domain; IPR014889: Transcription factor DP, C-terminal; SSF46785: ; IPR015648: Transcription factor DP; SSF144074: ; Coil:	KOG2578
comp32353_c2_seq26.p1	Ec-14_006750.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13432: Tetratricopeptide repeat; PF13371: Tetratricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; IPR013105: Tetratricopeptide TPR2; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; PTHR23083: ; IPR019734: Tetratricopeptide repeat	NA
comp16609_c0_seq1.p1	Ec-14_006760.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32319_c0_seq18.p1	Ec-14_006770.1	High mobility group, SNF2 and SLIDE domain protein	GO:0005524	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR009071: High mobility group box domain; IPR000330: SNF2-related; IPR015195: SLIDE domain; IPR009057: Homeodomain-like; IPR014001: Helicase superfamily 1/2, ATP-binding domain; PTHR10799: ; Coil: ; IPR001650: Helicase, C-terminal	NA
comp11981_c0_seq2.p1	Ec-14_006780.1	isovaleryl-CoA dehydrogenase	GO:0016627;GO:0055114	IPR013786: Acyl-CoA dehydrogenase/oxidase, N-terminal; IPR009100: Acyl-CoA dehydrogenase/oxidase, N-terminal and middle domain; IPR006091: Acyl-CoA oxidase/dehydrogenase, central domain; IPR006089: Acyl-CoA dehydrogenase, conserved site; G3DSA:1.20.140.10: ; IPR009075: Acyl-CoA dehydrogenase/oxidase C-terminal; PTHR10909:	KOG0141
comp28781_c0_seq1.p1	Ec-14_006790.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; PTHR23082: ; IPR019734: Tetratricopeptide repeat; SignalP-TM:	NA
comp34161_c0_seq1.p1	Ec-14_006810.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003677;GO:0005524;GO:0005634;GO:0006270	IPR012340: Nucleic acid-binding, OB-fold; IPR001208: Mini-chromosome maintenance, DNA-dependent ATPase; IPR018525: Mini-chromosome maintenance, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR008048: DNA replication licensing factor Mcm; PTHR11630: ; G3DSA:3.30.1640.10: ; IPR027925: MCM N-terminal domain	NA
comp28672_c0_seq3.p1	Ec-14_006820.2	Hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp33721_c0_seq1.p1	Ec-14_006830.1	DnaJ-like/ Sec63 translocase subunit	GO:0006457;GO:0031072;GO:0005515;GO:0051082	IPR014756: Immunoglobulin E-set; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001623: DnaJ domain; SSF158702: ; G3DSA:1.10.3380.10: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004179: Sec63 domain; G3DSA:1.10.150.20: ; IPR027137: Translocation protein Sec63; IPR000008: C2 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31962_c0_seq2.p1	Ec-14_006840.1	Na+/H+ antiporter, NhaC-like	GO:0016021	IPR018461: Na+/H+ antiporter, NhaC-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28623_c0_seq3.p1	Ec-14_006850.1	Armadillo-type fold	GO:0005488	IPR024095: Vesicle tethering protein p115-like; IPR016024: Armadillo-type fold; Coil:	NA
comp29913_c0_seq1.p3	Ec-14_006890.1	Prefoldin	GO:0006457;n/a;GO:0016272	IPR004127: Prefoldin alpha-like; IPR009053: Prefoldin; IPR016655: Prefoldin subunit 3; Coil:	NA
comp29913_c0_seq1.p1	Ec-14_006910.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp86976_c0_seq1.p1	Ec-14_006920.1	Forkhead-associated (FHA) domain	GO:0007018;GO:0005524;GO:0008017;GO:0005515;GO:0003777	IPR008984: SMAD/FHA domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR027640: Kinesin-like protein; IPR028763: Kinesin-like protein KIF12; Coil: ; IPR001752: Kinesin motor domain; IPR000253: Forkhead-associated (FHA) domain	NA
comp30974_c0_seq5.p1	Ec-14_006930.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28511_c1_seq1.p1	Ec-14_006940.1	ENTH/VHS	n/a;n/a;n/a	IPR002014: VHS; IPR018205: VHS subgroup; G3DSA:1.20.58.160: ; Coil: ; IPR008942: ENTH/VHS; PTHR13856: ; SSF89009:	NA
comp28511_c0_seq1.p1	Ec-14_006950.1	FAD dependent oxidoreductase	GO:0050660;GO:0055114;GO:0016491	PTHR13847: ; IPR006076: FAD dependent oxidoreductase; G3DSA:3.50.50.60: ; IPR012727: Glycine oxidase ThiO; G3DSA:3.30.9.10: ; SSF51905: ; SSF54373:	NA
comp28511_c0_seq1.p6	Ec-14_006960.1	Small nuclear ribonucleoprotein-associated protein D3	GO:0006396;GO:0030529;GO:0016071	IPR001163: Ribonucleoprotein LSM domain; G3DSA:2.30.30.100: ; IPR027141: Like-Sm (LSM) domain containing protein, LSm4/SmD1/SmD3; IPR010920: Like-Sm (LSM) domain; IPR006649: Ribonucleoprotein LSM domain, eukaryotic/archaea-type	NA
comp25131_c0_seq2.p2	Ec-14_006970.1	ERV/ALR sulfhydryl oxidase domain	GO:0055114;GO:0016972;GO:0045454	PTHR22897: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; IPR017937: Thioredoxin, conserved site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017905: ERV/ALR sulfhydryl oxidase domain; SignalP-noTM: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31343_c0_seq12.p1	Ec-14_006980.1	Ribosomal protein L1-like	GO:0006396;n/a;GO:0003723	IPR023674: Ribosomal protein L1-like; PTHR23105: ; IPR016095: Ribosomal protein L1, 3-layer alpha/beta-sandwich; IPR028364: Ribosomal protein L1/ribosomal biogenesis protein; Coil: ; IPR016094: Ribosomal protein L1, 2-layer alpha/beta-sandwich	NA
comp29620_c0_seq3.p1	Ec-14_006990.2	Nascent polypeptide-associated complex NAC domain	n/a;n/a;n/a	PTHR10351: ; IPR002715: Nascent polypeptide-associated complex NAC domain	NA
comp23639_c1_seq2.p1	Ec-14_007000.1	Protein of unknown function DUF1394	n/a;n/a;n/a	IPR009828: Protein of unknown function DUF1394	NA
comp34435_c0_seq1.p1	Ec-14_007010.1	ATPase, F1 complex, gamma subunit	GO:0015986;GO:0045261;GO:0046933;GO:0046961	IPR000131: ATPase, F1 complex, gamma subunit; G3DSA:1.10.287.80: ; IPR023632: ATPase, F1 complex, gamma subunit conserved site; IPR023633: ATPase, F1 complex, gamma subunit domain; PIRSF039089: ; G3DSA:3.40.1380.10:	NA
comp25980_c0_seq2.p1	Ec-15_000050.1	Protein of unknown function DUF1517	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR010903: Protein of unknown function DUF1517; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26751_c0_seq3.p1	Ec-15_000060.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	PTHR24622: ; SSF54928: ; IPR000504: RNA recognition motif domain; PR01228: Eggshell protein signature; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp34288_c0_seq1.p1	Ec-15_000070.1	EF-hand domain pair	GO:0005509	IPR002180: 6,7-dimethyl-8-ribityllumazine synthase; PF13833: EF-hand domain pair; IPR018247: EF-Hand 1, calcium-binding site; PTHR10891: ; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; SSF47473:	NA
comp13056_c0_seq1.p1	Ec-15_000100.1	MutS protein homolog 2A	GO:0005524;GO:0006298;GO:0030983	G3DSA:1.10.1420.10: ; IPR007861: DNA mismatch repair protein MutS, clamp; IPR007696: DNA mismatch repair protein MutS, core; IPR000432: DNA mismatch repair protein MutS, C-terminal; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR11361: ; Coil: ; IPR011184: DNA mismatch repair MutS	KOG0219
comp28989_c0_seq1.p1	Ec-15_000120.1	Adenylate kinase family protein	GO:0016787	SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000850: Adenylate kinase/UMP-CMP kinase; PF00406: Adenylate kinase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR015797: NUDIX hydrolase domain-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR13622: ; IPR000086: NUDIX hydrolase domain	NA
comp30973_c0_seq1.p1	Ec-15_000130.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp30541_c0_seq3.p1	Ec-15_000140.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR002885: Pentatricopeptide repeat; Coil: ; PTHR24015: ; SignalP-TM:	NA
comp29351_c0_seq1.p2	Ec-15_000150.1	2Fe-2S ferredoxin-type domain	GO:0009055;GO:0051536	IPR001041: 2Fe-2S ferredoxin-type domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012675: Beta-grasp domain; PTHR23426: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001055: Adrenodoxin; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33188_c0_seq22.p1	Ec-15_000170.1	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19456_c0_seq1.p1	Ec-15_000190.1	Alpha/Beta hydrolase fold	GO:0004806;GO:0006629	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002921: Fungal lipase-like domain; IPR029058: Alpha/Beta hydrolase fold; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; PTHR21493: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp27426_c0_seq2.p1	Ec-15_000250.1	Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain	GO:0055114;GO:0016491	G3DSA:3.50.50.60: ; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	NA
comp28164_c0_seq3.p1	Ec-15_000260.2	hypothetical protein	n/a;n/a;n/a	G3DSA:1.20.1000.10: ; Coil:	NA
comp30311_c0_seq3.p1	Ec-15_000290.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp12869_c0_seq1.p1	Ec-15_000300.1	translation initiation factor eIF3 f subunit	GO:0005515	IPR000555: JAB1/MPN/MOV34 metalloenzyme domain; IPR027531: Eukaryotic translation initiation factor 3 subunit F; IPR024969: Rpn11/EIF3F C-terminal domain; PTHR10540:	NA
comp29351_c0_seq1.p1	Ec-15_000310.1	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11671_c0_seq1.p1	Ec-15_000320.1	Ubiquitin-related domain	n/a;n/a;n/a	G3DSA:3.10.20.90: ; IPR029071: Ubiquitin-related domain; IPR001012: UBX domain; IPR006155: Machado-Joseph disease protein MJD; PTHR14159:	NA
comp33629_c0_seq1.p1	Ec-15_000350.1	DNA repair helicase	NA	PTHR11274: ; IPR006935: Helicase/UvrB domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001161: Helicase Ercc3; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; PF13625: Helicase conserved C-terminal domain	NA
comp48732_c0_seq1.p1	Ec-15_000360.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp31489_c0_seq10.p1	Ec-15_000410.2	Homeodomain-like	GO:0003677	NA	NA
comp31489_c0_seq10.p2	Ec-15_000420.1	conserved unknown protein	GO:0000786;GO:0003677;GO:0006334;n/a	Coil:	NA
comp19425_c0_seq3.p1	Ec-15_000440.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32921_c1_seq8.p2	Ec-15_000450.1	Glycolate Oxidase	GO:0003973;GO:0005777;GO:0055114;GO:0010181;GO:0009853;GO:0016491	IPR013785: Aldolase-type TIM barrel; IPR008259: FMN-dependent alpha-hydroxy acid dehydrogenase, active site; PTHR10578: ; IPR000262: FMN-dependent dehydrogenase; SSF51395: ; IPR012133: Alpha-hydroxy acid dehydrogenase, FMN-dependent	KOG0538
comp19972_c0_seq2.p1	Ec-15_000470.1	MscS Mechanosensitive ion channel	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26948_c0_seq1.p1	Ec-15_000480.1	UBA-like	GO:0005515;GO:0008242	IPR000449: Ubiquitin-associated domain/translation elongation factor EF-Ts, N-terminal; SSF54001: ; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase; PTHR24006: ; IPR016652: Ubiquitinyl hydrolase; IPR015940: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote; IPR018200: Ubiquitin specific protease, conserved site; SSF57850: ; G3DSA:1.10.8.10: ; IPR028889: Ubiquitin specific protease domain; IPR009060: UBA-like	NA
comp27127_c0_seq1.p1	Ec-15_000490.1	Light harvesting complex protein	GO:0009765;GO:0016020	SIGNAL_PEPTIDE: Signal peptide region; IPR022796: Chlorophyll A-B binding protein; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023329: Chlorophyll a/b binding protein domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001344: Chlorophyll A-B binding protein, plant; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31350_c0_seq8.p1	Ec-15_000500.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp31350_c0_seq10.p1	Ec-15_000510.1	Putative subunit of the Anaphase Promoting Complex	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; PTHR19918: ; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain	KOG0305
comp30351_c3_seq1.p1	Ec-15_000520.1	SNF2-related, helicase, ISW1, SANT and SLIDE domain protein	GO:0003677;GO:0005524;GO:0016589;GO:0043044;GO:0016887	NA	NA
comp34111_c0_seq1.p1	Ec-15_000530.1	centrin	GO:0005509	PF13833: EF-hand domain pair; IPR018247: EF-Hand 1, calcium-binding site; IPR000629: ATP-dependent RNA helicase DEAD-box, conserved site; PTHR23050: ; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; SSF47473:	KOG0028
comp29548_c0_seq3.p1	Ec-15_000550.1	Rab11C, RAB family GTPase	GO:0005622;GO:0007264;GO:0005525	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR005225: Small GTP-binding protein domain; IPR001806: Small GTPase superfamily; IPR020849: Small GTPase superfamily, Ras type; IPR003579: Small GTPase superfamily, Rab type; PS51419: small GTPase Rab1 family profile.; PTHR24073:	NA
comp27222_c0_seq1.p1	Ec-15_000570.1	YihA6, YihA/EngB-like GTPase	n/a;GO:0005622;GO:0005525;GO:0000917	IPR027417: P-loop containing nucleoside triphosphate hydrolase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006073: GTP binding domain; IPR019987: GTP-binding protein, ribosome biogenesis, YsxC; IPR030393: EngB-type guanine nucleotide-binding (G) domain; Coil: ; PTHR11649: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30996_c0_seq3.p1	Ec-15_000580.1	Exportin/Importin, Cse1-like	GO:0006886	PTHR10997: ; IPR001494: Importin-beta, N-terminal domain; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold; Coil: ; IPR013713: Exportin/Importin, Cse1-like; PTHR10997:SF18:	NA
comp17465_c0_seq1.p1	Ec-15_000600.1	Hypoxia induced protein, domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR12297: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR007667: Hypoxia induced protein, domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12324_c0_seq1.p1	Ec-15_000630.1	WSC-domain containing protein	NA	IPR013994: Carbohydrate-binding WSC, subgroup; PTHR19297: ; IPR002889: Carbohydrate-binding WSC; IPR025975: Polysaccharide lyase	NA
comp30611_c0_seq3.p1	Ec-15_000650.1	Histone-fold	GO:0046982;GO:0005488	IPR011442: Domain of unknown function DUF1546; IPR009072: Histone-fold; IPR016024: Armadillo-type fold; IPR004823: TATA box binding protein associated factor (TAF); PTHR10221:	NA
comp20248_c0_seq2.p1	Ec-15_000670.1	NAD(P)-binding domain	GO:0003824;GO:0003854;GO:0005488;GO:0006694;GO:0008152	SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR15020: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PF13460: NADH(P)-binding	NA
comp26196_c0_seq2.p1	Ec-15_000680.1	Putative ATP-dependent helicase YFR038W	GO:0003677;GO:0005524	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014001: Helicase superfamily 1/2, ATP-binding domain; PTHR10799: ; IPR001650: Helicase, C-terminal; Coil: ; IPR000330: SNF2-related, N-terminal domain	NA
comp32412_c1_seq2.p1	Ec-15_000690.1	Kinesin-like protein	GO:0007018;GO:0005524;GO:0008017;GO:0003777;GO:0005871	IPR019821: Kinesin motor domain, conserved site; IPR027640: Kinesin-like protein; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR001752: Kinesin motor domain	NA
comp19944_c0_seq1.p1	Ec-15_000700.1	protein kinase	GO:0004871;GO:0007165	NA	NA
comp31861_c0_seq4.p1	Ec-15_000720.1	FYVE zinc finger	GO:0046872	IPR000306: FYVE zinc finger; IPR017455: Zinc finger, FYVE-related; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; IPR007461: Ysc84 actin-binding domain; PTHR15629:	NA
comp25115_c0_seq2.p1	Ec-15_000730.1	38 kDa ribosome-associated protein precursor	GO:0003824;GO:0050662	IPR001509: NAD-dependent epimerase/dehydratase, N-terminal domain; SSF51735: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016040: NAD(P)-binding domain; G3DSA:3.90.25.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR10366:	NA
comp32428_c0_seq9.p1	Ec-15_000750.1	dihydrodipicolinate reductase	GO:0005737;GO:0055114;GO:0009089;GO:0008839	SSF51735: ; IPR023940: Dihydrodipicolinate reductase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000846: Dihydrodipicolinate reductase, N-terminal; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR022663: Dihydrodipicolinate reductase, C-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; IPR011859: Dihydrodipicolinate reductase, plant-type; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24291_c0_seq1.p1	Ec-15_000760.3	WD40-repeat-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR15052:SF2: ; Coil: ; PTHR15052:	NA
comp29924_c0_seq3.p1	Ec-15_000780.1	conserved unknown protein	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002076: ELO family; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3071
comp29924_c0_seq3.p2	Ec-15_000790.1	GOLD	GO:0006810;GO:0016021	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR009038: GOLD; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34030_c0_seq1.p1	Ec-15_000800.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp12713_c0_seq2.p1	Ec-15_000810.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp32850_c0_seq11.p1	Ec-15_000820.1	HAD-like domain	GO:0000287;GO:0005737;GO:0008253;n/a	IPR006434: Pyrimidine 5'-nucleotidase, eukaryotic; IPR023214: HAD-like domain	NA
comp32255_c0_seq10.p1	Ec-15_000830.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24681_c0_seq1.p1	Ec-15_000840.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28205_c0_seq1.p1	Ec-15_000850.1	hypothetical protein	n/a;n/a;n/a	IPR010736: Sperm-tail PG-rich repeat	NA
comp12077_c0_seq1.p1	Ec-15_000870.1	Membrane-associated, eicosanoid/glutathione metabolism (MAPEG) protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF161084: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023352: Membrane associated eicosanoid/glutathione metabolism-like domain; IPR001129: Membrane-associated, eicosanoid/glutathione metabolism (MAPEG) protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29294_c0_seq2.p1	Ec-15_000880.1	RNA pseudouridylate synthase domain-containing protein (C-terminal) RNA pseudouridylate synthase dom	GO:0003723;GO:0001522;GO:0016866;GO:0009451	IPR020103: Pseudouridine synthase, catalytic domain; SSF55174: ; IPR006145: Pseudouridine synthase, RsuA/RluB/C/D/E/F; PTHR21600: ; IPR002942: RNA-binding S4 domain; IPR000748: Pseudouridine synthase, RsuA/RluB/E/F; IPR018496: Pseudouridine synthase, RsuA/RluB/E/F, conserved site	NA
comp29280_c0_seq2.p1	Ec-15_000900.1	V-ATPase proteolipid subunit	GO:0033179;GO:0015991;GO:0015078	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10263: ; G3DSA:1.20.120.610: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR002379: V-ATPase proteolipid subunit C-like domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011555: V-ATPase proteolipid subunit C, eukaryotic; IPR000245: V-ATPase proteolipid subunit; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12557_c0_seq1.p1	Ec-15_001040.1	Protein of unknown function DUF1348	n/a;n/a;n/a	SSF54427: ; SIGNAL_PEPTIDE: Signal peptide region; IPR009783: Protein of unknown function DUF1348; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR31757: ; G3DSA:3.10.450.50: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp13248_c0_seq1.p1	Ec-15_001090.1	Pectin lyase fold/virulence factor	GO:0003723;GO:0004809;GO:0008033;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002905: tRNA methyltransferase, Trm1; SIGNAL_PEPTIDE: Signal peptide region; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR10631:SF3: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29971_c0_seq1.p1	Ec-15_001110.2	Pumilio RNA-binding repeat	GO:0003723	IPR001313: Pumilio RNA-binding repeat; IPR011989: Armadillo-like helical; PTHR12537: ; IPR016024: Armadillo-type fold; PTHR12537:SF12:	NA
comp29535_c0_seq8.p1	Ec-15_001120.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp12801_c0_seq1.p1	Ec-15_001130.1	Phox homologous domain	GO:0035091	IPR000449: Ubiquitin-associated domain/translation elongation factor EF-Ts, N-terminal; IPR015940: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote; G3DSA:1.10.8.10: ; IPR001683: Phox homologous domain; IPR009060: UBA-like	NA
comp32538_c0_seq11.p1	Ec-15_001220.1	transposase	n/a;n/a;n/a	PF13358: DDE superfamily endonuclease; PF13551: Winged helix-turn helix; Coil:	NA
comp30715_c0_seq3.p1	Ec-15_001230.1	Exostosin-like	GO:0016020;n/a;GO:0008146;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004263: Exostosin-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR005331: Sulfotransferase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11062:	NA
comp24866_c0_seq1.p1	Ec-15_001250.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	PTHR10108:SF714: ; PF13489: Methyltransferase domain; SIGNAL_PEPTIDE: Signal peptide region; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR10108: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27343_c0_seq2.p2	Ec-15_001270.1	Proteasome alpha-subunit, N-terminal domain	GO:0004175;GO:0019773;GO:0004298;GO:0006511	IPR029055: Nucleophile aminohydrolases, N-terminal; IPR016050: Proteasome beta-type subunit, conserved site; IPR000426: Proteasome alpha-subunit, N-terminal domain; IPR001353: Proteasome, subunit alpha/beta; PTHR11599: ; IPR023332: Proteasome A-type subunit	NA
comp27343_c0_seq2.p1	Ec-15_001280.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp31107_c0_seq1.p1	Ec-15_001290.1	DDH domain	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR004097: DHHA2 domain; G3DSA:3.90.1640.10: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001667: DDH domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF64182: ; PTHR12112: ; SignalP-noTM: ; PTHR12112:SF22: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20728_c0_seq1.p1	Ec-15_001300.3	katanin p80 subunit	n/a;n/a;n/a	IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR19845: ; IPR028021: Katanin p80 subunit, C-terminal; IPR026962: Katanin p80 subunit B1; IPR020472: G-protein beta WD-40 repeat	KOG0267
comp27831_c0_seq1.p1	Ec-15_001310.1	Protein of unknown function DUF974	n/a;n/a;n/a	IPR010378: Protein of unknown function DUF974	NA
comp27798_c0_seq2.p1	Ec-15_001320.2	Tetratricopeptide repeat containing protein	NA	PF13424: Tetratricopeptide repeat; IPR017441: Protein kinase, ATP binding site; IPR011990: Tetratricopeptide-like helical domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR001245: Serine-threonine/tyrosine-protein kinase catalytic domain; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; PTHR23257: ; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	NA
comp24845_c0_seq1.p1	Ec-15_001330.1	Ferredoxin-dependent bilin reductase	GO:0010024;GO:0055114;GO:0050897;GO:0016636	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR009249: Ferredoxin-dependent bilin reductase; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31588_c0_seq11.p3	Ec-15_001340.2	conserved unknown protein	n/a;n/a;n/a	PTHR13166: ; PTHR13166:SF4: ; IPR008011: Complex 1 LYR protein	NA
comp32562_c1_seq9.p1	Ec-15_001350.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; IPR002110: Ankyrin repeat; PTHR24188:	NA
comp24739_c0_seq2.p1	Ec-15_001360.1	Fanconi anemia complex, subunit FancL, WD-repeat containing domain	GO:0005249;GO:0006813;GO:0008076	PF11793: FANCL C-terminal domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR026848: E3 ubiquitin-protein ligase FANCL; IPR019162: Fanconi anemia complex, subunit FancL, WD-repeat containing domain; PTHR13206: ; IPR020467: Potassium channel, voltage dependent, Kv1.4	NA
comp27023_c0_seq1.p1	Ec-15_001370.1	Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain	GO:0003824;GO:0055114;GO:0009396;GO:0004488	IPR020631: Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain; SSF51735: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR020630: Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain; IPR020867: Tetrahydrofolate dehydrogenase/cyclohydrolase, conserved site; G3DSA:3.40.192.10: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10025: ; SSF53223: ; IPR016040: NAD(P)-binding domain; IPR000672: Tetrahydrofolate dehydrogenase/cyclohydrolase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32103_c0_seq12.p3	Ec-15_001380.1	Ribonuclease P/MRP protein subunit	GO:0008033;GO:0004540	SIGNAL_PEPTIDE: Signal peptide region; PTHR13004: ; SSF160350: ; IPR016819: Ribonuclease P/MRP protein subunit Pop5; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002759: Ribonuclease P/MRP protein subunit	NA
comp32276_c1_seq12.p1	Ec-15_001390.1	Tetraspanin/Peripherin	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018499: Tetraspanin/Peripherin; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25528_c0_seq1.p1	Ec-15_001420.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25528_c0_seq2.p1	Ec-15_001420.2	Tetratricopeptide-like helical domain	GO:0005515	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29461_c0_seq5.p1	Ec-15_001430.1	ICP0-binding domain of Ubiquitin-specific protease 7	n/a;n/a;n/a	NA	NA
comp24896_c0_seq1.p2	Ec-15_001450.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp24896_c0_seq1.p1	Ec-15_001460.1	Adenylate cyclase-associated CAP, C-terminal	GO:0003779;GO:0007010	IPR006599: CARP motif; IPR016098: Cyclase-associated protein CAP/septum formation inhibitor MinC, C-terminal; IPR017901: C-CAP/cofactor C-like domain; IPR013912: Adenylate cyclase-associated CAP, C-terminal	NA
comp31667_c2_seq3.p1	Ec-15_001470.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0005694;GO:0006259	IPR010935: SMCs flexible hinge; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR003395: RecF/RecN/SMC, N-terminal; PTHR18937: ; IPR024704: Structural maintenance of chromosomes protein	NA
comp24437_c0_seq2.p1	Ec-15_001480.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp28567_c0_seq1.p1	Ec-15_001500.3	Zn(2)-C6 fungal-type DNA-binding domain	GO:0000981;GO:0005634;GO:0006355;GO:0008270	IPR001138: Zn(2)-C6 fungal-type DNA-binding domain	NA
comp15986_c0_seq1.p1	Ec-15_001540.1	Hypothetical protein	n/a;n/a;n/a	IPR001138: Zn(2)-C6 fungal-type DNA-binding domain	NA
comp29716_c0_seq1.p1	Ec-15_001550.1	CCAAT-binding factor	GO:0005488	IPR011989: Armadillo-like helical; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR12048: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005612: CCAAT-binding factor; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27580_c0_seq1.p1	Ec-15_001570.3	Zinc finger, RING/FYVE/PHD-type	GO:0003676	IPR003034: SAP domain; Coil: ; IPR001876: Zinc finger, RanBP2-type	NA
comp12629_c0_seq1.p1	Ec-15_001580.1	Thioredoxin-like fold	n/a;n/a;n/a	IPR006844: Magnesium transporter protein 1; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR021149: Oligosaccharyl transferase complex, subunit OST3/OST6; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32609_c0_seq17.p1	Ec-15_001600.1	DNA gyrase subunit A	GO:0003677;GO:0005524;GO:0005694;GO:0003916;GO:0006265	IPR002205: DNA topoisomerase, type IIA, subunit A/C-terminal; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR10169: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR024946: Arginine repressor C-terminal-like domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR006691: DNA gyrase/topoisomerase IV, subunit A, C-terminal beta-pinwheel; G3DSA:2.120.10.90: ; SIGNAL_PEPTIDE: Signal peptide region; IPR013758: DNA topoisomerase, type IIA, subunit A/ C-terminal, alpha-beta; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005743: DNA gyrase, subunit A; Coil: ; SSF101904: ; IPR013760: DNA topoisomerase, type IIA-like domain	NA
comp153978_c0_seq1.p1	Ec-15_001620.1	C2 domain	GO:0005515	PTHR10774: ; IPR001202: WW domain; Coil: ; IPR000008: C2 domain; IPR000048: IQ motif, EF-hand binding site; G3DSA:2.20.70.10:	NA
comp20818_c0_seq1.p1	Ec-15_001630.1	DNA helicase (DNA repair), Rad3 type	n/a;GO:0005524;GO:0006139;GO:0008026;GO:0003676;GO:0016818	PTHR11472: ; IPR014013: Helicase, superfamily 1/2, ATP-binding domain, DinG/Rad3-type; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR006554: Helicase-like, DEXD box c2 type; IPR006555: ATP-dependent helicase, C-terminal; IPR010614: DEAD2; IPR014001: Helicase superfamily 1/2, ATP-binding domain; Coil: ; IPR013020: DNA helicase (DNA repair), Rad3 type	NA
comp24142_c0_seq1.p1	Ec-15_001640.1	Mog1/PsbP, alpha/beta/alpha sandwich	n/a;n/a;n/a	PTHR31407: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR016123: Mog1/PsbP, alpha/beta/alpha sandwich; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002683: Photosystem II PsbP, oxygen evolving complex; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27030_c0_seq2.p1	Ec-15_001650.1	WW domain	GO:0005515	IPR001202: WW domain; G3DSA:2.20.70.10:	NA
comp30790_c3_seq6.p1	Ec-15_001680.1	Alpha/Beta hydrolase fold	GO:0016787	IPR029058: Alpha/Beta hydrolase fold; PTHR17630: ; IPR002925: Dienelactone hydrolase	NA
comp27490_c0_seq4.p1	Ec-15_001700.1	Six-bladed beta-propeller, TolB-like	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011042: Six-bladed beta-propeller, TolB-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF63825: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26436_c0_seq3.p1	Ec-15_001710.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp25409_c0_seq1.p1	Ec-15_001720.1	Carbohydrate sulfotransferase-related	GO:0016051;GO:0008146;GO:0016021	IPR018011: Carbohydrate sulfotransferase-related; IPR005331: Sulfotransferase	NA
comp31844_c0_seq6.p2	Ec-15_001750.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31844_c0_seq8.p1	Ec-15_001770.1	EEIG1/EHBP1 N-terminal domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32468_c3_seq1.p1	Ec-15_001780.1	Inositol monophosphatase	GO:0046854	IPR020550: Inositol monophosphatase, conserved site; G3DSA:3.30.540.10: ; PTHR20854:SF5: ; IPR000760: Inositol monophosphatase; SSF56655: ; G3DSA:3.40.190.80: ; IPR006240: 3(2),5 -bisphosphate nucleotidase, bacterial; IPR020583: Inositol monophosphatase, metal-binding site	NA
comp29337_c0_seq2.p1	Ec-15_001800.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp25409_c0_seq1.p2	Ec-15_001830.1	Alpha/beta hydrolase fold	GO:0004091;n/a	IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; PTHR10794: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR022742: Serine aminopeptidase, S33; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR012020: AB-hydrolase ABHD1/2/3; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25958_c0_seq1.p1	Ec-15_001840.1	cation chanel protein, possibly calcium-activated BK potassium channel, alpha subunit	GO:0016020;GO:0006813;GO:0008152;GO:0015269;GO:0016740	PTHR10027: ; G3DSA:1.10.287.70: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF81324: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005821: Ion transport domain; IPR016040: NAD(P)-binding domain; IPR003091: Potassium channel; IPR003929: Potassium channel, calcium-activated, BK, alpha subunit; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11763_c0_seq1.p1	Ec-15_001850.1	putative S-adenosylmethionine-dependent methyltransferase	NA	PTHR18895: ; IPR004398: RNA methyltransferase, RsmD; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20498_c0_seq1.p2	Ec-15_001860.1	Actin family	GO:0005515	IPR029909: Actin-related protein 1 family; G3DSA:3.30.420.40: ; G3DSA:3.90.640.10: ; IPR004000: Actin family; IPR020902: Actin/actin-like conserved site; SSF53067:	NA
comp31205_c1_seq1.p1	Ec-15_001880.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR000863: Sulfotransferase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR19297:	NA
comp31205_c1_seq1.p2	Ec-15_001890.1	PsbQ-like domain	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR023222: PsbQ-like domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28120_c0_seq2.p2	Ec-15_001900.1	Phosphatidate cytidylyltransferase	GO:0016020;GO:0016772	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR13773: ; PF01148: Cytidylyltransferase family; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1440
comp29164_c0_seq2.p1	Ec-15_001960.1	GDP-L-galactose/GDP-D-glucose phosphorylase	GO:0080048	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR026506: GDP-L-galactose/GDP-D-glucose phosphorylase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31246_c0_seq1.p1	Ec-15_001970.1	Vacuolar protein sorting-associated protein 13	GO:0005509	IPR026847: Vacuolar protein sorting-associated protein 13; IPR009543: Vacuolar protein sorting-associated protein 13 domain; IPR015412: Autophagy-related, C-terminal; Coil: ; IPR010482: Peroxin/Dysferlin domain; IPR026854: Vacuolar protein sorting-associated protein 13A N-terminal domain	NA
comp47957_c0_seq1.p1	Ec-15_001990.1	Radial spoke 3	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; Coil: ; IPR009290: Radial spoke 3; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29152_c0_seq4.p1	Ec-15_002010.3	MORN motif	n/a;n/a;n/a	G3DSA:2.20.110.10: ; PTHR23084: ; SSF82185: ; IPR003409: MORN motif; SignalP-TM:	NA
comp34836_c0_seq1.p1	Ec-15_002020.1	HAD-superfamily hydrolase, subfamily IIA	GO:0008152;GO:0016791	PTHR19288: ; IPR006349: 2-phosphoglycolate phosphatase, eukaryotic; IPR023214: HAD-like domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023215: Nitrophenylphosphatase-like domain; IPR006357: HAD-superfamily hydrolase, subfamily IIA; PF13242: HAD-hydrolase-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR19288:SF6:	NA
comp34410_c0_seq1.p1	Ec-15_002100.1	RNA recognition motif domain	GO:0003676	PF13893: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain); SSF54928: ; PF14259: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain); IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; PTHR15608: ; Coil: ; IPR025640: Domain of unknown function DUF4339	NA
comp74439_c0_seq1.p1	Ec-15_002120.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp26899_c0_seq1.p1	Ec-15_002130.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	GO:0016192;GO:0016021	G3DSA:1.20.5.110: ; IPR010908: Longin domain; IPR001388: Synaptobrevin; IPR011012: Longin-like domain; SSF58038: ; PTHR21136:	KOG0861
comp26224_c0_seq3.p1	Ec-15_002140.1	putative multispanning membrane protein	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004240: Nonaspanin (TM9SF); TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31338_c0_seq12.p1	Ec-15_002160.1	Amine oxidase	GO:0016491;GO:0055114	SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.90.660.10: ; PTHR10742: ; SSF54373: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002937: Amine oxidase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023753: FAD/NAD(P)-binding domain	NA
comp26743_c0_seq3.p1	Ec-15_002170.1	RNA methylase	GO:0008168;GO:0032259;GO:0003676	NA	NA
comp26743_c0_seq4.p3	Ec-15_002190.1	flagellar associated protein	GO:0042073	IPR022088: Intraflagellar transport complex B protein 46	NA
comp28456_c0_seq2.p1	Ec-15_002200.1	LISK family protein kinase	GO:0004672;GO:0005524;GO:0006468	IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; PTHR23257: ; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	NA
comp28456_c0_seq2.p2	Ec-15_002210.1	Peptidyl-prolyl cis-trans isomerase, FKBP-type	GO:0006457	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; PF13371: Tetratricopeptide repeat; IPR013026: Tetratricopeptide repeat-containing domain; IPR023566: Peptidyl-prolyl cis-trans isomerase, FKBP-type; IPR019734: Tetratricopeptide repeat	NA
comp26683_c0_seq2.p1	Ec-15_002230.1	Phox homologous domain	GO:0035091	IPR001478: PDZ domain; IPR001683: Phox homologous domain	NA
comp26683_c0_seq2.p2	Ec-15_002240.1	Histidine phosphatase superfamily, clade-1	n/a;n/a;n/a	IPR013078: Histidine phosphatase superfamily, clade-1; IPR029033: Histidine phosphatase superfamily	NA
comp99457_c0_seq1.p1	Ec-15_002250.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp31537_c0_seq2.p1	Ec-15_002260.2	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; PTHR24361: ; IPR011009: Protein kinase-like domain	NA
comp25206_c0_seq3.p2	Ec-15_002280.1	Nucleic acid-binding, OB-fold	GO:0003723;GO:0006413;GO:0003743	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR012340: Nucleic acid-binding, OB-fold; IPR006196: RNA-binding domain, S1, IF1 type; IPR004368: Translation initiation factor IF-1; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp33144_c0_seq15.p1	Ec-15_002290.1	AGC-kinase, C-terminal	GO:0004674;GO:0005524;GO:0006468	SSF50729: ; G3DSA:3.30.200.20: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; IPR011009: Protein kinase-like domain; IPR001849: Pleckstrin homology domain; IPR000961: AGC-kinase, C-terminal; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; IPR011993: Pleckstrin homology-like domain; G3DSA:1.10.510.10: ; PTHR24354:	NA
comp33144_c0_seq15.p2	Ec-15_002300.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32200_c0_seq1.p1	Ec-15_002320.1	conserved unknown protein	GO:0005488	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32898_c0_seq10.p2	Ec-15_002330.1	Phosphotyrosyl phosphatase activator, PTPA	GO:0019211	SSF140984: ; IPR004327: Phosphotyrosyl phosphatase activator, PTPA	NA
comp32898_c0_seq8.p1	Ec-15_002340.1	Phox homologous domain	GO:0035091	SSF50729: ; IPR017441: Protein kinase, ATP binding site; IPR013761: Sterile alpha motif/pointed domain; G3DSA:3.30.200.20: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; IPR001245: Serine-threonine/tyrosine-protein kinase catalytic domain; IPR001683: Phox homologous domain; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR001849: Pleckstrin homology domain; PTHR23257: ; IPR000719: Protein kinase domain; IPR011993: Pleckstrin homology-like domain; G3DSA:1.10.510.10:	NA
comp34381_c0_seq1.p1	Ec-15_002350.1	Thioredoxin-like fold	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR012336: Thioredoxin-like fold	NA
comp33076_c0_seq28.p2	Ec-15_002360.1	Glutamyl-tRNA Synthetase, chloroplast precursor	GO:0000166;GO:0004812;GO:0005524;GO:0005737;GO:0006412;GO:0006418	IPR001412: Aminoacyl-tRNA synthetase, class I, conserved site; IPR020061: Glutamyl/glutaminyl-tRNA synthetase, class Ib, alpha-bundle domain; IPR004527: Glutamate-tRNA ligase, bacterial/mitochondrial; SIGNAL_PEPTIDE: Signal peptide region; IPR008925: Aminoacyl-tRNA synthetase, class I, anticodon-binding; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR020058: Glutamyl/glutaminyl-tRNA synthetase, class Ib, catalytic domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR000924: Glutamyl/glutaminyl-tRNA synthetase; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF52374: ; SignalP-noTM: ; IPR020751: Aminoacyl-tRNA synthetase, class I, anticodon-binding domain, subdomain 2; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:3.90.800.10:	KOG1149
comp33076_c0_seq9.p1	Ec-15_002370.1	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	GO:0055114;GO:0016491	IPR000103: Pyridine nucleotide-disulphide oxidoreductase, class-II; SIGNAL_PEPTIDE: Signal peptide region; PR00368: FAD-dependent pyridine nucleotide reductase signature; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR22912: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.50.50.60: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	NA
comp27560_c0_seq3.p2	Ec-15_002390.1	BolA protein	n/a;n/a;n/a	G3DSA:3.30.70.1500: ; PTHR12735: ; IPR002634: BolA protein	NA
comp27560_c0_seq3.p1	Ec-15_002400.1	dUTPase-like	GO:0009117;GO:0016787;GO:0046080	IPR008180: Deoxyuridine triphosphate nucleotidohydrolase/Deoxycytidine triphosphate deaminase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR029054: dUTPase-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR008181: Deoxyuridine triphosphate nucleotidohydrolase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11241: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27560_c0_seq5.p1	Ec-15_002420.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp26985_c0_seq1.p1	Ec-15_002450.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp26985_c0_seq1.p2	Ec-15_002460.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30365_c0_seq3.p1	Ec-15_002480.1	Peptidase M16, N-terminal	GO:0003824;GO:0046872	IPR001431: Peptidase M16, zinc-binding site; IPR007863: Peptidase M16, C-terminal domain; SIGNAL_PEPTIDE: Signal peptide region; IPR011765: Peptidase M16, N-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011249: Metalloenzyme, LuxS/M16 peptidase-like; IPR011237: Peptidase M16 domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; PTHR11851: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31024_c0_seq7.p1	Ec-15_002530.1	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR005135: Endonuclease/exonuclease/phosphatase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR15822:	NA
comp32671_c0_seq14.p2	Ec-15_002540.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020	PTHR24089: ; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier	NA
comp33281_c0_seq2.p1	Ec-15_002560.1	C2 domain	GO:0005515	IPR026847: Vacuolar protein sorting-associated protein 13; IPR009543: Vacuolar protein sorting-associated protein 13 domain; IPR001478: PDZ domain; Coil: ; IPR000008: C2 domain; IPR026854: Vacuolar protein sorting-associated protein 13A N-terminal domain	NA
comp32435_c0_seq2.p1	Ec-15_002570.1	conserved unknown protein	GO:0016020;n/a;GO:0005044	IPR001190: SRCR domain; PTHR15688: ; Coil:	NA
comp28074_c0_seq1.p1	Ec-15_002580.1	MAGE homology domain	n/a;n/a;n/a	IPR002190: MAGE homology domain	NA
comp33041_c0_seq3.p1	Ec-15_002620.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003677;GO:0005524	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; PTHR10799: ; IPR000330: SNF2-related	NA
comp32671_c0_seq14.p1	Ec-15_002630.1	WD40 repeat	GO:0005515	PTHR19877: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; PTHR19877:SF1: ; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp28824_c0_seq3.p2	Ec-15_002640.1	Peptidyl-prolyl cis-trans isomerase, FKBP-type	GO:0006457	G3DSA:3.10.50.40: ; SSF54534: ; SIGNAL_PEPTIDE: Signal peptide region; IPR001478: PDZ domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023566: Peptidyl-prolyl cis-trans isomerase, FKBP-type; IPR001179: Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0549
comp28824_c0_seq3.p1	Ec-15_002650.1	putative type II topoisomerase	n/a;n/a;n/a	PTHR35698:SF1: ; PTHR35698:	NA
comp24187_c0_seq2.p1	Ec-15_002670.1	Histone-like bacterial DNA-binding protein	GO:0003677	IPR000119: Histone-like bacterial DNA-binding protein; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR010992: Integration host factor (IHF)-like DNA-binding domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR020816: Histone-like DNA-binding protein, conserved site	NA
comp28824_c0_seq3.p3	Ec-15_002720.1	Ribosomal protein L1/ribosomal biogenesis protein	GO:0003735;GO:0005622;GO:0005840;GO:0006412	IPR005878: Ribosomal protein L1, bacterial-type; PTHR23105:SF51: ; SignalP-TM: ; IPR023674: Ribosomal protein L1-like; PTHR23105: ; IPR016095: Ribosomal protein L1, 3-layer alpha/beta-sandwich; Coil: ; IPR028364: Ribosomal protein L1/ribosomal biogenesis protein; IPR016094: Ribosomal protein L1, 2-layer alpha/beta-sandwich	NA
comp12824_c0_seq1.p1	Ec-15_002740.1	Ribosomal protein L13	GO:0003735;GO:0005840;GO:0006412	IPR023564: Ribosomal protein L13 domain; IPR005823: Ribosomal protein L13, bacterial-type; IPR005822: Ribosomal protein L13; SignalP-TM:	NA
comp32119_c0_seq9.p1	Ec-15_002760.1	PDZ domain	GO:0005515	IPR009003: Trypsin-like cysteine/serine peptidase domain; IPR025926: PDZ-like domain; PTHR22939: ; IPR001478: PDZ domain; G3DSA:2.40.10.10:	NA
comp30190_c0_seq2.p1	Ec-15_002770.1	ATPase, AAA-type, core	GO:0005524	PTHR23076: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003959: ATPase, AAA-type, core; IPR003593: AAA+ ATPase domain; IPR003960: ATPase, AAA-type, conserved site; G3DSA:1.10.8.60: ; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29441_c0_seq1.p1	Ec-15_002790.1	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR22847: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; Coil:	NA
comp27085_c0_seq1.p2	Ec-15_002800.3	hypothetical protein	n/a;n/a;n/a	NA	NA
comp32019_c1_seq3.p1	Ec-15_002810.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PTHR23271: ; IPR011990: Tetratricopeptide-like helical domain; IPR003107: HAT (Half-A-TPR) repeat; IPR013949: U3 small nucleolar RNA-associated protein 6	NA
comp56162_c0_seq1.p2	Ec-15_002820.1	Glutathione-dependent formaldehyde-activating enzyme/centromere protein V	GO:0008152;GO:0016846	IPR006913: Glutathione-dependent formaldehyde-activating enzyme/centromere protein V; IPR011057: Mss4-like	NA
comp25030_c0_seq1.p1	Ec-15_002850.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0031072	PTHR24077: ; IPR001623: DnaJ domain; IPR018253: DnaJ domain, conserved site	NA
comp32374_c4_seq13.p1	Ec-15_002870.3	Glycosyl transferase, family 14	GO:0008375;GO:0016020	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; IPR003406: Glycosyl transferase, family 14; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp21834_c0_seq1.p2	Ec-15_002890.3	ADF-H/Gelsolin-like domain	GO:0003779;GO:0005622	SSF55753: ; PTHR10829: ; PTHR10829:SF2: ; IPR029006: ADF-H/Gelsolin-like domain; IPR002108: Actin-depolymerising factor homology domain	NA
comp31563_c1_seq1.p1	Ec-15_002920.1	Copper amine oxidase, C-terminal	GO:0055114;GO:0008131;GO:0005507;GO:0048038;GO:0009308	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR016182: Copper amine oxidase, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015801: Copper amine oxidase, N2/N3-terminal; IPR015800: Copper amine oxidase, N2-terminal; IPR015802: Copper amine oxidase, N3-terminal; IPR000269: Copper amine oxidase; IPR015798: Copper amine oxidase, C-terminal; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19716_c0_seq2.p1	Ec-15_002930.1	WD40/YVTN repeat-like-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; IPR020472: G-protein beta WD-40 repeat; PTHR22841:	NA
comp26077_c0_seq1.p1	Ec-15_002940.1	Actin-related protein	GO:0005515	IPR030054: Actin-related protein 6; G3DSA:3.90.640.10: ; G3DSA:3.30.420.40: ; IPR004000: Actin family; Coil: ; SSF53067:	NA
comp16795_c0_seq1.p1	Ec-15_002950.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777	IPR019821: Kinesin motor domain, conserved site; IPR027640: Kinesin-like protein; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR001752: Kinesin motor domain	NA
comp33392_c0_seq1.p1	Ec-15_002960.2	TRAM/LAG1/CLN8 homology domain	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006634: TRAM/LAG1/CLN8 homology domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19594_c0_seq1.p1	Ec-15_003010.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26460_c0_seq1.p1	Ec-15_003020.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp13073_c0_seq1.p1	Ec-15_003030.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; PF13414: TPR repeat; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; PTHR22904:	NA
comp24366_c0_seq1.p1	Ec-15_003040.1	UDP-sulfoquinovose synthase, plastid precursor	GO:0003824;GO:0005488;GO:0008152	IPR001509: NAD-dependent epimerase/dehydratase, N-terminal domain; SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; G3DSA:3.90.25.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR10366:	KOG1371
comp32586_c0_seq2.p1	Ec-15_003050.1	UBA-like	GO:0005515	IPR015940: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote; G3DSA:3.80.10.10: ; G3DSA:1.10.8.10: ; SSF52058: ; PTHR23125: ; IPR006553: Leucine-rich repeat, cysteine-containing subtype; Coil: ; PF13516: Leucine Rich repeat; IPR009060: UBA-like	NA
comp25253_c1_seq1.p1	Ec-15_003070.1	Thioredoxin-like fold	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24619_c0_seq1.p1	Ec-15_003090.1	Ubiquitin-associated domain/translation elongation factor EF-Ts, N-terminal	GO:0005515	G3DSA:3.10.20.90: ; PTHR10621: ; IPR015940: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote; IPR000449: Ubiquitin-associated domain/translation elongation factor EF-Ts, N-terminal; G3DSA:1.10.8.10: ; IPR029071: Ubiquitin-related domain; IPR004806: UV excision repair protein Rad23; IPR000626: Ubiquitin-like; IPR015360: XPC-binding domain; IPR009060: UBA-like	NA
comp33829_c0_seq1.p1	Ec-15_003110.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp26834_c0_seq2.p2	Ec-15_003120.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp26834_c0_seq2.p1	Ec-15_003130.1	flagellar radial spoke protein 16	GO:0006457;GO:0051082	PTHR24078: ; IPR008971: HSP40/DnaJ peptide-binding; IPR002939: Chaperone DnaJ, C-terminal; IPR001623: DnaJ domain; IPR018253: DnaJ domain, conserved site; G3DSA:2.60.260.20:	KOG0714
comp22969_c0_seq1.p1	Ec-15_003150.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24031: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR014014: RNA helicase, DEAD-box type, Q motif; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0326
comp22969_c0_seq1.p2	Ec-15_003160.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp19216_c0_seq1.p1	Ec-15_003170.1	WD40-repeat-containing domain	GO:0005515	PTHR10971: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp31544_c0_seq18.p1	Ec-15_003230.3	Hypothetical leucine rich repeat protein	GO:0005515	PTHR27000: ; IPR001611: Leucine-rich repeat; IPR032675: Leucine-rich repeat domain, L domain-like	NA
comp34531_c0_seq1.p1	Ec-15_003250.1	Uncharacterised protein family UPF0016	GO:0016020	IPR001727: Uncharacterised protein family UPF0016; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR12608:SF1: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31424_c0_seq6.p1	Ec-15_003260.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp30746_c0_seq3.p1	Ec-15_003265.1	hypothetical protein	NA	IPR009071: High mobility group box domain; mobidb-lite: consensus disorder prediction; cd00084: HMG-box	NA
comp32531_c1_seq10.p1	Ec-15_003280.2	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp14899_c0_seq2.p1	Ec-15_003310.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp20099_c0_seq1.p1	Ec-15_003360.1	Tetratricopeptide TPR1	GO:0005515	IPR001440: Tetratricopeptide repeat 1; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; PTHR22904: ; IPR019734: Tetratricopeptide repeat	NA
comp33024_c1_seq34.p2	Ec-15_003370.1	conserved unknown protein	GO:0003779;GO:0007010	NA	NA
comp26312_c0_seq1.p1	Ec-15_003380.1	IQ motif, EF-hand binding site	GO:0005515	G3DSA:1.10.287.70: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11537:SF137: ; IPR028325: Voltage-gated potassium channel; IPR000048: IQ motif, EF-hand binding site; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF81324: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005821: Ion transport domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30443_c0_seq4.p1	Ec-15_003410.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp12003_c0_seq1.p1	Ec-15_003420.1	nucleotidyltransferase family protein	GO:0007154;GO:0035091;GO:0005515	PTHR23092: ; IPR001683: Phox homologous domain	NA
comp30184_c0_seq6.p1	Ec-15_003440.1	Uracil-DNA glycosylase-like	n/a;n/a;n/a	SM00987: UreE urease accessory protein, C-terminal domain; IPR005273: Uracil-DNA glycosylase, family 4 domain; IPR005122: Uracil-DNA glycosylase-like	NA
comp30872_c0_seq8.p1	Ec-15_003460.1	Calcium-activated outward-rectifying potassium channel, putative	n/a;GO:0005249;GO:0005774;GO:0030007;GO:0071805	PTHR11003: ; G3DSA:1.10.287.70: ; IPR003280: Two pore domain potassium channel; IPR018247: EF-Hand 1, calcium-binding site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; SSF47473: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF81324: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013099: Two pore domain potassium channel domain; IPR031144: Two pore domain potassium channel, plant; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1418
comp12084_c0_seq3.p1	Ec-15_003470.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33985_c0_seq1.p1	Ec-15_003510.1	expressed unknown protein	GO:0003700;GO:0005622;GO:0006355;GO:0043565	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32798_c0_seq5.p1	Ec-15_003520.1	Zc3h12a-like Ribonuclease NYN domain protein	GO:0016020;GO:0055085;GO:0015238;GO:0015297;GO:0006855	IPR021869: Ribonuclease Zc3h12a-like; IPR002885: Pentatricopeptide repeat; PTHR13547:	NA
comp30260_c0_seq1.p1	Ec-15_003530.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0006470	IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C	NA
comp32527_c0_seq32.p1	Ec-15_003540.1	Methyltransferase TRM13	GO:0008168;GO:0008033	PTHR12998: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR022776: TRM13/UPF0224 family, U11-48K-like CHHC zinc finger domain; IPR007871: Methyltransferase TRM13	NA

comp32667_c0_seq14.p1	Ec-15_003560.1	PFtsY, plastid signal recognition particle receptor	GO:0005525;GO:0006614	IPR013822: Signal recognition particle, SRP54 subunit, helical bundle; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; G3DSA:1.20.120.140: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR000897: Signal recognition particle, SRP54 subunit, GTPase domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11564:	NA
comp29097_c0_seq2.p1	Ec-15_003600.2	Zinc finger, CCCH-type	GO:0046872	IPR000571: Zinc finger, CCCH-type; IPR013785: Aldolase-type TIM barrel; SIGNAL_PEPTIDE: Signal peptide region; SSF51395: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001269: tRNA-dihydrouridine synthase; PTHR11082:SF8: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR018517: tRNA-dihydrouridine synthase, conserved site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12323_c0_seq1.p1	Ec-15_003630.1	ATPase, AAA-type, core	GO:0005524	IPR019489: Clp ATPase, C-terminal; IPR003959: ATPase, AAA-type, core; IPR003593: AAA+ ATPase domain; G3DSA:1.10.8.10: ; IPR004491: Heat shock protein HslU; G3DSA:1.10.8.60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR11262:	NA
comp27726_c0_seq1.p1	Ec-15_003640.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020;GO:0055085	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR24089: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023395: Mitochondrial carrier domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33999_c0_seq1.p1	Ec-15_003660.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp26608_c0_seq2.p1	Ec-15_003670.1	Rossmann-like alpha/beta/alpha sandwich fold	n/a;GO:0006529;GO:0004066	IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; SSF52402: ; PTHR11807: ; IPR001962: Asparagine synthase	NA
comp12322_c0_seq1.p1	Ec-15_003680.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp24953_c0_seq1.p1	Ec-15_003690.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PTHR23004: ; IPR011990: Tetratricopeptide-like helical domain; IPR010323: Protein of unknown function DUF924; G3DSA:1.20.58.320:	NA
comp32615_c1_seq8.p1	Ec-15_003720.1	Casein kinase (serine/threonine/tyrosine protein kinase)	GO:0006468;GO:0004672;GO:0016772	PTHR11909: ; IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:1.10.510.10: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain	KOG1164
comp26939_c1_seq2.p1	Ec-15_003730.1	NAD(P)-binding domain	GO:0008641;GO:0006512;GO:0006464	PTHR10953: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009036: Molybdenum cofactor biosynthesis, MoeB; SignalP-noTM: ; IPR000594: UBA/THIF-type NAD/FAD binding fold; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR000011: Ubiquitin/SUMO-activating enzyme E1	NA
comp27786_c0_seq3.p1	Ec-15_003750.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp30848_c0_seq3.p1	Ec-15_003770.1	Heat shock protein 70	NA	PTHR19375: ; IPR018181: Heat shock protein 70, conserved site; G3DSA:3.30.420.40: ; IPR013126: Heat shock protein 70 family; Coil: ; G3DSA:3.30.30.30: ; SSF53067:	NA
comp28496_c0_seq1.p1	Ec-15_003830.1	Protein phosphatase 2A regulatory subunit	GO:0005509	PTHR12085: ; IPR018247: EF-Hand 1, calcium-binding site; IPR011992: EF-hand domain pair; SSF47473:	KOG2562
comp27258_c0_seq3.p1	Ec-15_003860.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp88273_c0_seq1.p1	Ec-15_003890.1	Hypothetical leucine rich repeat protein	GO:0005515	SIGNAL_PEPTIDE: Signal peptide region; PTHR10552: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR032675: Leucine-rich repeat domain, L domain-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29919_c0_seq1.p1	Ec-15_003920.1	Molybdenum cofactor biosynthesis, MoeB	n/a;n/a;n/a	IPR000127: Ubiquitin-activating enzyme repeat; PTHR10953: ; IPR023280: Ubiquitin-like 1 activating enzyme, catalytic cysteine domain; IPR019572: Ubiquitin-activating enzyme; IPR009036: Molybdenum cofactor biosynthesis, MoeB; IPR016040: NAD(P)-binding domain; Coil: ; IPR018965: Ubiquitin-activating enzyme e1, C-terminal	NA
comp20896_c0_seq2.p1	Ec-15_003930.1	TB2/DP1/HVA22-related protein	n/a;GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000008: C2 domain; IPR004345: TB2/DP1/HVA22-related protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30444_c0_seq2.p1	Ec-15_003940.1	Pre-mRNA-splicing factor 38	GO:0003676	SSF63748: ; G3DSA:2.30.30.140: ; IPR005037: Pre-mRNA-splicing factor 38; Coil: ; PTHR23142:SF2: ; IPR002999: Tudor domain	NA
comp25077_c0_seq1.p1	Ec-15_003950.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp22302_c0_seq1.p1	Ec-15_003960.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0009058	SSF53756: ; IPR011990: Tetratricopeptide-like helical domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR001296: Glycosyl transferase, family 1; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR12526: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; G3DSA:3.40.50.2000: ; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24355_c0_seq1.p1	Ec-15_003970.1	Jumonji and demethylase NO66 domain protein	n/a;n/a;n/a	NA	NA
comp29763_c0_seq1.p1	Ec-15_003980.1	CRAL-TRIO domain	GO:0005524;GO:0016887;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011074: CRAL/TRIO, N-terminal domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001251: CRAL-TRIO domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.10.8.20: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR23324:	NA
comp12384_c0_seq1.p1	Ec-15_004000.1	ubiquitin-conjugating enzyme 1	GO:0005515	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; IPR000449: Ubiquitin-associated domain/translation elongation factor EF-Ts, N-terminal; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023313: Ubiquitin-conjugating enzyme, active site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR015940: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR24067: ; G3DSA:1.10.8.10: ; SM00212: Ubiquitin-conjugating enzyme E2, catalytic domain homologues; IPR000608: Ubiquitin-conjugating enzyme E2; IPR009060: UBA-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp18214_c0_seq1.p1	Ec-15_004050.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp25076_c0_seq3.p1	Ec-15_004060.2	Nucleophile aminohydrolases, N-terminal	GO:0004298;GO:0005839;GO:0006511;GO:0051603	IPR029055: Nucleophile aminohydrolases, N-terminal; IPR000426: Proteasome alpha-subunit, N-terminal domain; PTHR11599: ; IPR001353: Proteasome, subunit alpha/beta; PTHR11599:SF11:	NA
comp26833_c0_seq1.p1	Ec-15_004120.1	Glutamate ammonia ligase	GO:0003824	IPR027302: Glutamine synthetase, N-terminal conserved site; IPR008146: Glutamine synthetase, catalytic domain; IPR008147: Glutamine synthetase, beta-Grasp; PTHR20852: ; SSF55931: ; IPR014746: Glutamine synthetase/guanido kinase, catalytic domain; IPR027303: Glutamine synthetase, glycine-rich site	KOG0683
comp12666_c0_seq2.p1	Ec-15_004140.1	3,8-divinyl protochlorophyllide a 8-vinyl reductase, putative chloroplast precursor	GO:0003824;GO:0005488;GO:0008152	SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR14194: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; PF13460: NADH(P)-binding; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32520_c1_seq2.p1	Ec-15_004150.1	Ribosomal protein S5 domain 2-type fold, subgroup	GO:0005840;n/a;GO:0005622;GO:0006412;GO:0003735	IPR000754: Ribosomal protein S9; IPR020568: Ribosomal protein S5 domain 2-type fold; IPR020574: Ribosomal protein S9, conserved site; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup	NA
comp28537_c0_seq2.p1	Ec-15_004170.1	Fumarylacetoacetase, C-terminal-related	GO:0008152;GO:0003824	IPR011234: Fumarylacetoacetase, C-terminal-related; IPR002529: Fumarylacetoacetase, C-terminal; PTHR11820:	NA
comp20151_c0_seq2.p1	Ec-15_004180.1	PPP domain	GO:0016787	SSF48452: ; IPR029052: Metallo-dependent phosphatase-like; IPR001440: Tetratricopeptide TPR1; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; PIRSF033096: ; IPR011236: Serine/threonine protein phosphatase 5; IPR011990: Tetratricopeptide-like helical domain; PTHR11668: ; IPR013235: PPP domain; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; IPR006186: Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase	NA
comp32523_c0_seq1.p1	Ec-15_004200.1	Domain of unknown function DUF4211	n/a;n/a;n/a	Coil: ; IPR025451: Domain of unknown function DUF4211	NA
comp32081_c0_seq4.p1	Ec-15_004210.1	AEC family transporter: auxin efflux	GO:0016021;GO:0055085	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR31651: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR31651:SF3: ; IPR004776: Auxin efflux carrier	NA
comp33989_c0_seq1.p1	Ec-15_004230.1	1-deoxy-D-xylulose 5-phosphate synthase, chloroplast precursor	GO:0003824;GO:0008152	IPR005476: Transketolase, C-terminal; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR005475: Transketolase-like, pyrimidine-binding domain; IPR020826: Transketolase binding site; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11624: ; IPR005477: Deoxyxylulose-5-phosphate synthase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR005474: Transketolase, N-terminal; SIGNAL_PEPTIDE: Signal peptide region; IPR009014: Transketolase, C-terminal/Pyruvate-ferredoxin oxidoreductase, domain II; IPR029061: Thiamin diphosphate-binding fold; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-noTM:	KOG0523
comp21139_c0_seq2.p1	Ec-15_004240.1	Ribosomal protein L2, C-terminal	GO:0003735;GO:0005840;GO:0006412	IPR012340: Nucleic acid-binding, OB-fold; IPR002171: Ribosomal protein L2; IPR014722: Ribosomal protein L2 domain 2; IPR008991: Translation protein SH3-like domain; IPR022669: Ribosomal protein L2, C-terminal; IPR022671: Ribosomal protein L2, conserved site; IPR022666: Ribosomal Proteins L2, RNA binding domain; IPR014726: Ribosomal protein L2, domain 3	NA
comp34995_c0_seq1.p1	Ec-15_004250.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp24773_c0_seq3.p1	Ec-15_004260.1	WD40/YVTN repeat-like-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; PTHR22850: ; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp30773_c0_seq5.p1	Ec-15_004340.1	ABC1 family protein	NA	IPR004147: UbiB domain; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.30.200.20: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011009: Protein kinase-like domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10566: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28890_c1_seq1.p1	Ec-15_004350.2	Putative 5-3 exonuclease	GO:0003676;GO:0004527	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR004859: Putative 5-3 exonuclease; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR027073: 5'-3' exoribonuclease; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30576_c0_seq2.p1	Ec-15_004360.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	IPR020683: Ankyrin repeat-containing domain	NA
comp28984_c0_seq2.p1	Ec-15_004370.2	expressed unknown protein	n/a;n/a;n/a	IPR023214: HAD-like domain	NA
comp30823_c0_seq4.p1	Ec-15_004400.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003677;GO:0005524;GO:0006259;GO:0008094	IPR020588: DNA recombination and repair protein RecA-like, ATP-binding domain; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PF13481: AAA domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR22942: ; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32605_c0_seq1.p1	Ec-15_004420.1	Pleckstrin homology-like domain	GO:0005515	SSF50729: ; PTHR12482: ; IPR013761: Sterile alpha motif/pointed domain; IPR029058: Alpha/Beta hydrolase fold; IPR001660: Sterile alpha motif domain; IPR007751: Domain of unknown function DUF676, lipase-like; IPR001478: PDZ domain; IPR003961: Fibronectin type III; IPR001849: Pleckstrin homology domain; IPR013783: Immunoglobulin-like fold; IPR011993: Pleckstrin homology-like domain	NA
comp22995_c0_seq3.p1	Ec-15_004430.1	Light harvesting complex protein	GO:0009765;GO:0016020	SIGNAL_PEPTIDE: Signal peptide region; IPR022796: Chlorophyll A-B binding protein; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023329: Chlorophyll a/b binding protein domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001344: Chlorophyll A-B binding protein, plant; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12308_c0_seq2.p1	Ec-15_004440.1	C2 domain	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000008: C2 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19352_c0_seq1.p1	Ec-15_004450.1	Nucleic acid-binding, OB-fold	GO:0000049	IPR012340: Nucleic acid-binding, OB-fold; IPR002547: tRNA-binding domain; PTHR11586:	NA
comp30336_c0_seq1.p1	Ec-15_004460.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002885: Pentatricopeptide repeat; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; Coil: ; PTHR24015: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31054_c0_seq6.p1	Ec-15_004510.1	Acetyltransferase (GNAT) domain protein	n/a;n/a;n/a	NA	NA
comp32110_c0_seq4.p1	Ec-15_004530.1	cleavage and polyadenylation specificity factor CG10110-PA	GO:0005634;GO:0009058;GO:0003824;GO:0030170;GO:0003676	NA	NA
comp32110_c0_seq16.p1	Ec-15_004530.2	cleavage and polyadenylation specificity factor CG10110-PA	GO:0003824;GO:0009058;GO:0030170	PF10433: Mono-functional DNA-alkylating methyl methanesulfonate N-term; PTHR10644:SF2: ; PTHR10644:	NA
comp27518_c0_seq2.p1	Ec-15_004550.1	mitochondrial carrier protein-like	GO:0006810;GO:0016020;GO:0005488	PTHR24089: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002067: Mitochondrial carrier protein; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023395: Mitochondrial carrier domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR018108: Mitochondrial substrate/solute carrier	NA
comp31083_c0_seq1.p1	Ec-15_004560.1	Histone deacetylase domain protein	n/a;n/a;n/a	NA	NA
comp31865_c0_seq3.p1	Ec-15_004570.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005515;n/a	PF13086: AAA domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR026852: Helicase Sen1-like; PF13087: AAA domain; PTHR10887: ; IPR003593: AAA+ ATPase domain; IPR001202: WW domain; Coil: ; G3DSA:2.20.70.10:	NA
comp26343_c0_seq1.p1	Ec-15_004590.1	Clustered mitochondria protein, N-terminal	n/a;GO:0005515	PF12807: Translation initiation factor eIF3 subunit 135; PF13424: Tetratricopeptide repeat; SSF48452: ; IPR023231: GSKIP domain; IPR011990: Tetratricopeptide-like helical domain; PTHR12601: ; IPR028275: Clustered mitochondria protein, N-terminal; SignalP-TM: ; IPR025697: CLU domain; IPR013026: Tetratricopeptide repeat-containing domain; Coil: ; IPR019734: Tetratricopeptide repeat	NA
comp30664_c0_seq3.p1	Ec-15_004610.2	WW domain	GO:0005515	IPR001202: WW domain; Coil: ; SignalP-TM: ; G3DSA:2.20.70.10:	NA
comp26357_c0_seq2.p1	Ec-15_004630.1	Ubiquitin-conjugating enzyme/RWD-like	GO:0019787;GO:0043687;GO:0051246	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; PTHR24067: ; SM00212: Ubiquitin-conjugating enzyme E2, catalytic domain homologues; IPR000608: Ubiquitin-conjugating enzyme E2; Coil:	NA
comp30091_c0_seq3.p1	Ec-15_004640.1	GYF	GO:0005515	PTHR13138: ; Coil: ; IPR003169: GYF domain	NA
comp35462_c0_seq1.p2	Ec-15_004650.1	Ubiquitin-related domain	GO:0006464;GO:0005515	G3DSA:3.10.20.90: ; IPR029071: Ubiquitin-related domain; IPR000626: Ubiquitin-like	NA
comp31727_c1_seq2.p1	Ec-15_004670.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32483_c0_seq4.p1	Ec-15_004700.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21278_c0_seq1.p1	Ec-15_004750.1	Asparagine synthase (glutamine-hydrolyzing)	GO:0004066;GO:0006529	IPR000583: Class II glutamine amidotransferase domain; IPR006426: Asparagine synthase, glutamine-hydrolyzing; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; PTHR11772: ; IPR029055: Nucleophile aminohydrolases, N-terminal; SSF52402: ; IPR001962: Asparagine synthase; IPR017932: Glutamine amidotransferase type 2 domain	KOG0571
comp30476_c0_seq3.p4	Ec-15_004760.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30476_c0_seq3.p7	Ec-15_004770.1	thioredoxin O	n/a;GO:0045454	IPR005746: Thioredoxin; PR00421: Thioredoxin family signature; IPR013766: Thioredoxin domain; IPR012336: Thioredoxin-like fold; IPR017937: Thioredoxin, conserved site	NA
comp30476_c0_seq3.p1	Ec-15_004790.1	RIO-like kinase	GO:0003824;GO:0005524	IPR018934: RIO domain; IPR017407: Serine/threonine-protein kinase Rio1; G3DSA:3.30.200.20: ; IPR000687: RIO kinase; IPR011009: Protein kinase-like domain; PTHR10593: ; G3DSA:1.10.510.10: ; Coil: ; IPR018935: RIO kinase, conserved site	NA
comp40693_c0_seq1.p2	Ec-15_004830.1	PDZ domain	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004088: K Homology domain, type 1; IPR001478: PDZ domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24699_c0_seq1.p1	Ec-15_004890.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp34382_c0_seq1.p1	Ec-15_004940.1	Clathrin assembly complex, medium subunit	GO:0006886;GO:0016192;GO:0030131	IPR028565: Mu homology domain; PTHR11998: ; IPR018240: Clathrin adaptor, mu subunit, conserved site; IPR001392: Clathrin adaptor, mu subunit; IPR008968: Clathrin adaptor, mu subunit, C-terminal; G3DSA:2.60.40.1170: ; G3DSA:3.30.450.60: ; IPR022775: AP complex, mu/sigma subunit; IPR011012: Longin-like domain	KOG0937
comp9986_c0_seq1.p1	Ec-15_004960.1	FAR1 DNA binding domain	n/a;n/a;n/a	IPR004330: FAR1 DNA binding domain	NA
comp21199_c0_seq1.p1	Ec-15_004970.1	gamma tubulin	GO:0003924;GO:0005525;GO:0043234;GO:0051258;n/a	IPR002454: Gamma tubulin; IPR017975: Tubulin, conserved site; IPR000217: Tubulin; IPR003008: Tubulin/FtsZ, GTPase domain; IPR023123: Tubulin, C-terminal; IPR018316: Tubulin/FtsZ, 2-layer sandwich domain; IPR008280: Tubulin/FtsZ, C-terminal	KOG1374
comp21199_c0_seq1.p2	Ec-15_004975.1	hypothetical protein	NA	SIGNAL_PEPTIDE: Signal peptide region; IPR019329: NADH:ubiquinone oxidoreductase, ESSS subunit; mobidb-lite: consensus disorder prediction; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32067_c0_seq4.p1	Ec-15_004990.1	Ankyrin Repeat Transient Receptor Potential Channel	GO:0070588;GO:0016020;GO:0005515;GO:0005262	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10582: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR002153: Transient receptor potential channel, canonical; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020683: Ankyrin repeat-containing domain; IPR005821: Ion transport domain; Coil: ; IPR002110: Ankyrin repeat; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3676
comp31323_c0_seq4.p1	Ec-16_000010.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp32156_c0_seq8.p1	Ec-16_000030.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001650: Helicase, C-terminal; PTHR14950:	KOG0354
comp28896_c0_seq1.p1	Ec-16_000040.1	Armadillo-type fold	GO:0005488	IPR007015: DNA polymerase V; IPR016024: Armadillo-type fold	NA
comp24394_c0_seq3.p1	Ec-16_000050.1	Ubiquitin conjugation factor E4, core	GO:0000151;GO:0006511;GO:0016567;GO:0034450	IPR019474: Ubiquitin conjugation factor E4, core; IPR003613: U box domain; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR13931:	NA
comp31643_c0_seq3.p3	Ec-16_000080.1	HAD-like domain	n/a;n/a;n/a	IPR023214: HAD-like domain	NA
comp31643_c0_seq3.p1	Ec-16_000090.1	similar to Zinc finger protein	GO:0005515;GO:0008270	PTHR12389: ; SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011989: Armadillo-like helical	NA
comp30151_c0_seq5.p1	Ec-16_000110.1	Ribosomal protein L29e	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR002673: Ribosomal protein L29e	NA
comp20366_c0_seq2.p1	Ec-16_000120.1	expressed unknown protein	NA	NA	NA
comp31966_c1_seq11.p1	Ec-16_000130.1	DEAD box helicase	GO:0003676;GO:0004386	PTHR13710: ; IPR011991: Winged helix-turn-helix DNA-binding domain; IPR011545: DEAD/DEAH box helicase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR032284: ATP-dependent DNA helicase RecQ, zinc-binding domain; PTHR13710:SF70: ; IPR004589: DNA helicase, ATP-dependent, RecQ type; IPR002464: DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal	KOG0351
comp24769_c0_seq1.p1	Ec-16_000150.1	Peptidase C2, calpain, large subunit, domain III	GO:0004198;GO:0005622;GO:0006508	G3DSA:2.60.120.380: ; SSF54001: ; IPR001300: Peptidase C2, calpain, catalytic domain; IPR022684: Peptidase C2, calpain family; IPR022683: Peptidase C2, calpain, domain III; G3DSA:3.90.70.10: ; IPR022682: Peptidase C2, calpain, large subunit, domain III; IPR007330: MIT; PTHR10183:	NA
comp21159_c0_seq1.p1	Ec-16_000190.1	T-complex protein 1, gamma subunit	GO:0006457;GO:0005524;GO:0051082	IPR017998: Chaperone tailless complex polypeptide 1 (TCP-1); IPR012719: T-complex protein 1, gamma subunit; IPR027410: TCP-1-like chaperonin intermediate domain; IPR027409: GroEL-like apical domain; IPR002194: Chaperonin TCP-1, conserved site; IPR002423: Chaperonin Cpn60/TCP-1 family; SSF54849: ; IPR027413: GroEL-like equatorial domain; SSF48592:	KOG0364
comp13220_c0_seq1.p2	Ec-16_000210.1	ubiquitin UbiA	GO:0005515	G3DSA:3.10.20.90: ; PTHR10666: ; IPR001975: Ribosomal protein L40e; IPR019956: Ubiquitin; IPR011332: Zinc-binding ribosomal protein; IPR029071: Ubiquitin-related domain; IPR000626: Ubiquitin-like	NA
comp21442_c0_seq1.p1	Ec-16_000220.1	Ubiquitin-conjugating enzyme/RWD-like	GO:0006464;GO:0006512;GO:0015031	PTHR23306: ; IPR016135: Ubiquitin-conjugating enzyme/RWD-like; PTHR23306:SF3: ; SSF140111: ; IPR008883: Ubiquitin E2 variant, N-terminal; Coil: ; IPR017916: Steadiness box (SB) domain	NA
comp26539_c0_seq2.p1	Ec-16_000240.1	Haem peroxidase	GO:0020037;GO:0055114;GO:0006979;GO:0004601	G3DSA:1.10.520.10: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR019794: Peroxidase, active site; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR010255: Haem peroxidase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002207: Plant ascorbate peroxidase; G3DSA:1.10.420.10: ; IPR019793: Peroxidases heam-ligand binding site; PTHR31356: ; IPR002016: Haem peroxidase, plant/fungal/bacterial; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25070_c0_seq1.p1	Ec-16_000260.1	Peptidase C65, otubain	n/a;n/a;n/a	IPR003323: OTU domain; SSF54001: ; IPR019400: Peptidase C65, otubain; PTHR12931:	NA
comp31558_c0_seq1.p1	Ec-16_000270.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24015: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002885: Pentatricopeptide repeat; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32951_c0_seq35.p1	Ec-16_000310.1	Ubiquitin E2 variant, N-terminal	GO:0006464;GO:0015031	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR23306: ; IPR016135: Ubiquitin-conjugating enzyme/RWD-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR008883: Ubiquitin E2 variant, N-terminal; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30903_c0_seq2.p1	Ec-16_000370.1	EsV-1-7 domain protein	NA	NA	NA
comp12610_c0_seq1.p1	Ec-16_000400.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp28148_c0_seq1.p1	Ec-16_000410.1	Pre-mRNA-splicing factor 38	n/a;n/a;n/a	IPR005037: Pre-mRNA-splicing factor 38	NA
comp27058_c0_seq1.p1	Ec-16_000420.1	Cytidine deaminase-like	GO:0003824	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:3.40.140.10: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016193: Cytidine deaminase-like; IPR002125: Cytidine and deoxycytidylate deaminases, zinc-binding; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33144_c2_seq1.p1	Ec-16_000430.1	Heat Shock transcription factor	GO:0005634;GO:0006355;GO:0043565;GO:0003700	NA	NA
comp17420_c0_seq1.p1	Ec-16_000480.1	flagellar outer dynein arm light chain 2	n/a;n/a;n/a	IPR005334: Tctex-1	KOG4108
comp24637_c0_seq2.p1	Ec-16_000490.1	NUDIX hydrolase domain-like	GO:0016787	PTHR22769: ; IPR015797: NUDIX hydrolase domain-like; IPR020084: NUDIX hydrolase, conserved site; IPR000086: NUDIX hydrolase domain; SignalP-TM:	NA
comp28891_c0_seq1.p1	Ec-16_000510.1	UbiB domain	n/a;n/a;n/a	IPR004147: UbiB domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011009: Protein kinase-like domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR10566: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; G3DSA:1.10.510.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24988_c0_seq2.p1	Ec-16_000520.1	Short-chain dehydrogenase/reductase SDR	GO:0008152;GO:0016491	SSF51735: ; IPR020904: Short-chain dehydrogenase/reductase, conserved site; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002198: Short-chain dehydrogenase/reductase SDR; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR24316: ; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33040_c0_seq7.p1	Ec-16_000530.1	Concanavalin A-like lectin/glucanase domain	NA	IPR000859: CUB domain; IPR010606: Mib-herc2; IPR001870: B30.2/SPRY domain; PF13385: Concanavalin A-like lectin/glucanases superfamily; IPR013320: Concanavalin A-like lectin/glucanase domain; PTHR11254: ; SSF159034: ; PF15711: Interleukin-like EMT inducer; PTHR11254:SF328: ; Coil: ; IPR000569: HECT domain; G3DSA:3.30.2160.10: ; IPR006558: LamG-like jellyroll fold	NA
comp12488_c0_seq2.p1	Ec-16_000540.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR002885: Pentatricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; PTHR24015:	NA
comp32177_c4_seq1.p1	Ec-16_000550.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0003723;GO:0006364;GO:0008757;n/a	PTHR22807: ; G3DSA:3.30.70.1170: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR011023: Nop2p; IPR023267: RNA (C5-cytosine) methyltransferase; IPR001678: SAM-dependent methyltransferase RsmB/NOP2-type; IPR023273: RNA (C5-cytosine) methyltransferase, NOP2; IPR018314: Bacterial Fmu (Sun)/eukaryotic nucleolar NOL1/Nop2p, conserved site; Coil:	NA
comp31080_c0_seq1.p3	Ec-16_000610.2	Helicase superfamily 1/2, ATP-binding domain	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; SSF158702: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal	KOG0950
comp31097_c1_seq2.p1	Ec-16_000620.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR002885: Pentatricopeptide repeat; PTHR24015:	NA
comp32154_c0_seq14.p1	Ec-16_000625.1	hypothetical protein	GO:0005515	IPR011990: Tetratricopeptide-like helical domain; IPR002885: Pentatricopeptide repeat; mobidb-lite: consensus disorder prediction; IPR033443: Pentacotripeptide-repeat region of PROPR; PTHR24015:	NA
comp25991_c0_seq1.p2	Ec-16_000630.1	Peptidase T1A, proteasome beta-subunit	GO:0004175;GO:0051603;GO:0004298;GO:0005839	IPR029055: Nucleophile aminohydrolases, N-terminal; IPR016050: Proteasome beta-type subunit, conserved site; IPR001353: Proteasome, subunit alpha/beta; IPR000243: Peptidase T1A, proteasome beta-subunit; PTHR11599: ; IPR023333: Proteasome B-type subunit	NA
comp31231_c0_seq9.p1	Ec-16_000650.1	Signal recognition particle, SRP54 subunit, helical bundle	GO:0006810;GO:0006614;GO:0005525	IPR013822: Signal recognition particle, SRP54 subunit, helical bundle; IPR007222: Signal recognition particle receptor, alpha subunit, N-terminal; IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:1.20.120.140: ; IPR003593: AAA+ ATPase domain; IPR000897: Signal recognition particle, SRP54 subunit, GTPase domain; PTHR11564: ; IPR011012: Longin-like domain	NA
comp31231_c0_seq9.p2	Ec-16_000660.1	RNA-binding protein, putative	GO:0000166	PTHR24012: ; SSF54928: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp25942_c0_seq3.p1	Ec-16_000690.1	Immunoglobulin-like fold	n/a;GO:0005515	IPR014756: Immunoglobulin E-set; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002909: IPT domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013783: Immunoglobulin-like fold; PTHR22727: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29755_c0_seq3.p2	Ec-16_000700.1	Zinc finger, RING-CH-type	GO:0005515;GO:0008270	SSF57850: ; IPR008984: SMAD/FHA domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011016: Zinc finger, RING-CH-type; IPR000253: Forkhead-associated (FHA) domain; PTHR23012:	NA
comp30093_c0_seq2.p2	Ec-16_000740.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13424: Tetratricopeptide repeat; PTHR19959: ; IPR011990: Tetratricopeptide-like helical domain	NA
comp12840_c0_seq1.p2	Ec-16_000760.3	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp30093_c0_seq2.p1	Ec-16_000770.1	DNA-directed RNA polymerase, phage-type	GO:0003677;GO:0006351;GO:0003899	IPR024075: DNA-directed RNA polymerase, helix hairpin domain; SSF56672: ; IPR029262: DNA-directed RNA polymerase N-terminal domain; G3DSA:1.10.150.20: ; G3DSA:1.10.287.280: ; Coil: ; IPR002092: DNA-directed RNA polymerase, phage-type; G3DSA:3.30.70.370:	NA
comp30804_c0_seq4.p1	Ec-16_000800.1	Rab-GTPase-TBC domain	GO:0005097;GO:0032313	G3DSA:1.10.8.270: ; PTHR22957: ; IPR000195: Rab-GTPase-TBC domain	NA
comp30804_c0_seq4.p2	Ec-16_000810.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;GO:0018024	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR013110: Histone methylation DOT1	NA
comp30804_c0_seq4.p3	Ec-16_000820.1	GPN-loop GTPase	GO:0000166	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR004130: GPN-loop GTPase; IPR030228: GPN-loop GTPase 3	NA
comp12223_c0_seq1.p1	Ec-16_000830.1	Metallo-dependent phosphatase-like	n/a;n/a;n/a	IPR029052: Metallo-dependent phosphatase-like; PTHR24032:	NA
comp28628_c0_seq3.p1	Ec-16_000840.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR12176: ; IPR013216: Methyltransferase type 11	NA
comp27381_c0_seq1.p1	Ec-16_000850.1	TPR domain-containing protein	GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013105: Tetratricopeptide TPR2; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR23083:	NA
comp29407_c0_seq3.p1	Ec-16_000990.1	C2 domain	GO:0005515	PTHR10774: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; IPR000008: C2 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20619_c0_seq1.p1	Ec-16_001000.1	Aconitate hydratase,	GO:0008152	IPR006248: Aconitase, mitochondrial-like; IPR001030: Aconitase/3-isopropylmalate dehydratase large subunit, alpha/beta/alpha domain; IPR018136: Aconitase family, 4Fe-4S cluster binding site; IPR000573: Aconitase A/isopropylmalate dehydratase small subunit, swivel domain; IPR015932: Aconitase/3-isopropylmalate dehydratase large subunit, alpha/beta/alpha, subdomain 2; IPR015928: Aconitase/3-isopropylmalate dehydratase, swivel; IPR015937: Aconitase/isopropylmalate dehydratase; IPR015931: Aconitase/3-isopropylmalate dehydratase large subunit, alpha/beta/alpha, subdomain 1/3	KOG0453
comp19549_c0_seq3.p1	Ec-16_001010.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp24383_c0_seq1.p1	Ec-16_001030.1	mRNA decapping complex protein	GO:0005515	PTHR15598: ; IPR019775: WD40 repeat, conserved site; SIGNAL_PEPTIDE: Signal peptide region; IPR001680: WD40 repeat; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20942_c0_seq1.p1	Ec-16_001080.2	Ankyrin repeat-containing domain	n/a;n/a;n/a	IPR020683: Ankyrin repeat-containing domain; PTHR24123: ; IPR002110: Ankyrin repeat	NA
comp24325_c0_seq2.p1	Ec-16_001110.1	TRAPP III complex, Trs85	n/a;n/a;n/a	NA	NA
comp30647_c0_seq3.p1	Ec-16_001150.1	Single-stranded nucleic acid binding R3H	GO:0003676	IPR007502: Helicase-associated domain; IPR011545: DEAD/DEAH box helicase domain; IPR011709: Domain of unknown function DUF1605; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR18934: ; IPR001374: Single-stranded nucleic acid binding R3H; IPR031083: ATP-dependent RNA helicase YTHDC2-related; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal	NA
comp32504_c1_seq19.p1	Ec-16_001160.1	YCII-related	NA	IPR011008: Dimeric alpha-beta barrel; G3DSA:3.30.70.1060: ; IPR005545: YCII-related	NA
comp32655_c2_seq2.p1	Ec-16_001170.1	expressed unknown protein	GO:0008152;GO:0016491;GO:0055114	Coil:	NA
comp33635_c0_seq1.p2	Ec-16_001180.1	Hypothetical leucine rich repeat protein	GO:0005515	SM00364: Leucine-rich repeats, bacterial type; G3DSA:3.80.10.10: ; IPR003591: Leucine-rich repeat, typical subtype; IPR001611: Leucine-rich repeat; SSF52047: ; PTHR23155:	NA
comp34045_c0_seq1.p1	Ec-16_001200.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp19955_c0_seq1.p1	Ec-16_001210.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28124_c0_seq2.p1	Ec-16_001220.1	Phox homologous domain	GO:0035091	IPR001478: PDZ domain; IPR001683: Phox homologous domain	NA
comp28837_c0_seq2.p1	Ec-16_001250.1	Trifunctional enzyme subunit alpha	GO:0003824;GO:0005488;GO:0008152	PTHR23309: ; IPR018376: Enoyl-CoA hydratase/isomerase, conserved site; SSF51735: ; IPR008927: 6-phosphogluconate dehydrogenase C-terminal domain-like; IPR013328: 6-phosphogluconate dehydrogenase, domain 2; IPR029045: ClpP/crotonase-like domain; IPR006176: 3-hydroxyacyl-CoA dehydrogenase, NAD binding; IPR006108: 3-hydroxyacyl-CoA dehydrogenase, C-terminal; IPR001753: Crotonase superfamily; IPR006180: 3-hydroxyacyl-CoA dehydrogenase, conserved site; IPR016040: NAD(P)-binding domain	KOG1683
comp24170_c0_seq1.p1	Ec-16_001260.1	cryptochrome 1	GO:0006281;GO:0003913	G3DSA:1.25.40.80: ; G3DSA:1.10.579.10: ; IPR005101: DNA photolyase, FAD-binding/Cryptochrome, C-terminal; PTHR11455:	KOG0133
comp27161_c0_seq2.p1	Ec-16_001270.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; IPR011333: BTB/POZ fold; PTHR24198: ; IPR000210: BTB/POZ-like; G3DSA:3.30.710.10: ; Coil: ; IPR002110: Ankyrin repeat	NA
comp30347_c0_seq1.p1	Ec-16_001290.1	DEAD/DEAH box helicase domain	GO:0005524;GO:0003676	NA	NA
comp12960_c0_seq2.p1	Ec-16_001300.1	UAA transporter	GO:0055085	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF103481: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013657: UAA transporter; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10778: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26873_c0_seq1.p1	Ec-16_001320.1	Phosphatidic acid phosphatase type 2/haloperoxidase	GO:0016020;GO:0003824	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10165: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000326: Phosphatidic acid phosphatase type 2/haloperoxidase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26615_c0_seq1.p1	Ec-16_001360.1	HECT	GO:0004842;GO:0005515	IPR020683: Ankyrin repeat-containing domain; IPR000569: HECT; IPR011011: Zinc finger, FYVE/PHD-type; G3DSA:3.30.2160.10: ; IPR002110: Ankyrin repeat; PTHR11254:	NA
comp32944_c0_seq12.p3	Ec-16_001370.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp32944_c0_seq2.p2	Ec-16_001380.3	Frataxin/CyaY	GO:0008199;GO:0016226	IPR002908: Frataxin/CyaY	NA
comp19517_c0_seq1.p1	Ec-16_001420.3	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp34726_c0_seq1.p1	Ec-16_001430.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; IPR002110: Ankyrin repeat; PTHR24188:	NA
comp31091_c2_seq1.p1	Ec-16_001440.1	Zinc finger, PHD-finger	GO:0005515	PTHR10615: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR001965: Zinc finger, PHD-type; PTHR10615:SF100: ; IPR011011: Zinc finger, FYVE/PHD-type; Coil: ; IPR019787: Zinc finger, PHD-finger	NA
comp24929_c0_seq1.p1	Ec-16_001450.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR019410: Nicotinamide N-methyltransferase-like; PTHR14704:	NA
comp32935_c4_seq3.p1	Ec-16_001460.1	60S ribosomal protein L12	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR020783: Ribosomal protein L11, C-terminal; IPR020784: Ribosomal protein L11, N-terminal; IPR020785: Ribosomal protein L11, conserved site; IPR000911: Ribosomal protein L11/L12	NA
comp26871_c0_seq1.p1	Ec-16_001470.1	Ribosomal protein S5 domain 2-type fold	GO:0003723;GO:0004654;GO:0006402;GO:0005739	IPR012340: Nucleic acid-binding, OB-fold; IPR015847: Exoribonuclease, phosphorolytic domain 2; IPR003029: Ribosomal protein S1, RNA-binding domain; IPR015848: Polyribonucleotide nucleotidyltransferase, RNA-binding domain; IPR027408: PNPase/RNase PH domain; IPR004088: K Homology domain, type 1; IPR022967: RNA-binding domain, S1; IPR001247: Exoribonuclease, phosphorolytic domain 1; IPR020568: Ribosomal protein S5 domain 2-type fold; IPR012162: Polyribonucleotide nucleotidyltransferase	NA
comp28516_c1_seq1.p1	Ec-16_001480.1	dynein heavy chain	n/a;GO:0007018;GO:0003777	IPR004273: Dynein heavy chain domain; PF12774: Hydrolytic ATP binding site of dynein motor region D1; IPR011704: ATPase, dynein-related, AAA domain; PF12781: ATP-binding dynein motor region D5; IPR013602: Dynein heavy chain, domain-2; PF12775: P-loop containing dynein motor region D3; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR013594: Dynein heavy chain, domain-1; IPR024317: Dynein heavy chain, P-loop containing D4 domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR024743: Dynein heavy chain, coiled coil stalk; Coil: ; IPR026983: Dynein heavy chain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3595
comp30298_c0_seq11.p1	Ec-16_001490.1	expressed unknown protein	GO:0031177	Coil:	NA
comp32794_c0_seq4.p2	Ec-16_001500.1	UBA-like	GO:0005515	NA	NA
comp32794_c0_seq4.p3	Ec-16_001510.1	Armadillo-type fold	GO:0005488	NA	NA
comp11715_c0_seq1.p1	Ec-16_001520.1	Microtubule-associated anchor protein involved in autophagy and membrane trafficking	NA	G3DSA:3.10.20.90: ; IPR029071: Ubiquitin-related domain; IPR004241: Autophagy protein Atg8 ubiquitin-like	KOG1654
comp22437_c0_seq1.p1	Ec-16_001550.1	Branched-chain alpha-ketoacid dehydrogenase kinase/Pyruvate dehydrogenase kinase, N-terminal	n/a;n/a;n/a	IPR018955: Branched-chain alpha-ketoacid dehydrogenase kinase/Pyruvate dehydrogenase kinase, N-terminal; IPR003594: Histidine kinase-like ATPase, C-terminal domain; PTHR11947: ; SignalP-TM:	NA
comp32093_c0_seq3.p1	Ec-16_001640.1	Vacuolar protein sorting-associated protein 13 domain	GO:0008104;n/a	IPR026847: Vacuolar protein sorting-associated protein 13; IPR015412: Autophagy-related, C-terminal; IPR009543: Vacuolar protein sorting-associated protein 13 domain	NA
comp32093_c0_seq3.p2	Ec-16_001650.1	C2H2 zinc finger protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; mobidb-lite: consensus disorder prediction; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25074_c0_seq1.p1	Ec-16_001660.1	NHPX subunit of the C/D ribonucleoprotein complex	GO:0042254;GO:0003723;GO:0005730;GO:0030529	NA	NA
comp27495_c0_seq1.p1	Ec-16_001670.1	Mpv17/PMP22	GO:0016021	IPR007248: Mpv17/PMP22; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34985_c0_seq1.p1	Ec-16_001680.1	Putative Glutathione S-transferase	n/a;GO:0005515	IPR004046: Glutathione S-transferase, C-terminal; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR004045: Glutathione S-transferase, N-terminal; PTHR11260: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR010987: Glutathione S-transferase, C-terminal-like; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0876
comp30734_c0_seq1.p1	Ec-16_001700.3	MIT	n/a;n/a;n/a	IPR007330: MIT	NA
comp34082_c0_seq1.p1	Ec-16_001710.1	G-protein, beta subunit	n/a;GO:0005515	IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR016346: Guanine nucleotide-binding protein, beta subunit; IPR001632: G-protein, beta subunit; IPR020472: G-protein beta WD-40 repeat; PIRSF002394: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; Coil:	NA
comp33905_c0_seq1.p1	Ec-16_001720.1	Carbohydrate sulfotransferase-related	GO:0016051;GO:0008146;GO:0016021	IPR018011: Carbohydrate sulfotransferase-related; IPR005331: Sulfotransferase	NA
comp31827_c0_seq6.p1	Ec-16_001730.2	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20867_c0_seq2.p1	Ec-16_001740.1	Tissue inhibitor of metalloproteinases-like, OB-fold	GO:0005515	IPR008993: Tissue inhibitor of metalloproteinases-like, OB-fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; G3DSA:2.40.50.120: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp11930_c0_seq1.p1	Ec-16_001760.1	Histidinol dehydrogenase	GO:0051287;GO:0055114;GO:0000105;GO:0008270;GO:0004399	IPR016161: Aldehyde/histidinol dehydrogenase; G3DSA:3.40.50.1980: ; IPR022695: Histidinol dehydrogenase, monofunctional; PTHR21256: ; IPR001692: Histidinol dehydrogenase, conserved site; IPR012131: Histidinol dehydrogenase	KOG2697
comp30560_c0_seq4.p1	Ec-16_001780.1	P-type ATPase, cytoplasmic domain N	GO:0000166	NA	NA
comp24891_c0_seq1.p1	Ec-16_001790.1	Luc7-related	GO:0003729;GO:0005685;GO:0006376	Coil: ; IPR004882: Luc7-related	NA
comp11842_c0_seq1.p1	Ec-16_001820.1	Ribosomal protein S18	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR001648: Ribosomal protein S18	NA
comp31896_c2_seq8.p1	Ec-16_001850.1	LisH dimerisation motif, subgroup	n/a;n/a;n/a	IPR024964: CTLH/CRA C-terminal to LisH motif domain; IPR006595: CTLH, C-terminal LisH motif; IPR006594: LIS1 homology motif; PTHR12864: ; IPR013144: CRA domain	NA
comp33004_c0_seq22.p1	Ec-16_001860.1	DNA-binding domain	GO:0003677;GO:0006355;GO:0003700	NA	NA
comp29207_c0_seq2.p1	Ec-16_001890.1	NAD(P)-binding domain	GO:0003824;GO:0005488;GO:0008152	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; PTHR14097: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32106_c0_seq9.p1	Ec-16_001910.1	hypothetical protein	NA	Coil:	NA
comp30989_c0_seq2.p1	Ec-16_001920.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp16539_c0_seq1.p1	Ec-16_001950.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp11801_c0_seq2.p1	Ec-16_001960.1	formaldehyde dehydrogenase	GO:0055114;GO:0008270;GO:0016491	SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013149: Alcohol dehydrogenase, C-terminal; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011032: GroES (chaperonin 10)-like; IPR016040: NAD(P)-binding domain; IPR013154: Alcohol dehydrogenase GroES-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002085: Alcohol dehydrogenase superfamily, zinc-type	KOG0022
comp29181_c0_seq7.p1	Ec-16_001970.1	Probable phytol kinase, chloroplast precursor, carboxyterminal half	GO:0016020;GO:0016772	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PF01148: Cytidylyltransferase family; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR32523: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29181_c0_seq7.p2	Ec-16_002000.1	RNase L inhibitor RLI, possible metal-binding domain	n/a;n/a;n/a	IPR022968: Ribosome biogenesis protein; IPR007177: Domain of unknown function DUF367; IPR007209: RNase L inhibitor RLI, possible metal-binding domain	NA
comp32106_c0_seq7.p2	Ec-16_002010.1	Putative cell division cycle 20. Subunit or the Anaphase Promoting Complex	GO:0005515	PTHR19918:SF8: ; PTHR19918: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; Coil:	KOG0305
comp20595_c0_seq1.p1	Ec-16_002030.1	Heat shock protein 40 like protein	GO:0031072;GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; IPR001623: DnaJ domain; IPR018253: DnaJ domain, conserved site; PTHR24078: ; PF13414: TPR repeat; IPR013105: Tetratricopeptide TPR2; IPR013026: Tetratricopeptide repeat-containing domain; Coil: ; IPR019734: Tetratricopeptide repeat	NA
comp30399_c0_seq2.p1	Ec-16_002040.1	Lipase maturation factor	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009613: Lipase maturation factor; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR14463:	NA
comp31585_c0_seq1.p2	Ec-16_002050.1	Zinc finger, C2H2, LYAR-type	n/a;n/a;n/a	IPR014898: Zinc finger, C2H2, LYAR-type; PTHR13100: ; SSF57667:	NA
comp21450_c0_seq2.p1	Ec-16_002060.1	FAD-binding, type 2, subdomain 1	GO:0008762;GO:0050660;GO:0003824;GO:0055114;GO:0016491	IPR016167: FAD-binding, type 2, subdomain 1; SignalP-TM: ; IPR016166: FAD-binding, type 2; IPR016171: Vanillyl-alcohol oxidase, C-terminal subdomain 2; IPR004113: FAD-linked oxidase, C-terminal; PTHR11748: ; IPR016169: CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2; IPR016164: FAD-linked oxidase-like, C-terminal; IPR006094: FAD linked oxidase, N-terminal	NA
comp12853_c0_seq1.p1	Ec-16_002070.1	putative serine esterase	NA	PTHR12482: ; IPR029058: Alpha/Beta hydrolase fold; IPR007751: Domain of unknown function DUF676, lipase-like	NA
comp20187_c0_seq1.p1	Ec-16_002090.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp25172_c0_seq1.p1	Ec-16_002100.1	50S ribosomal protein L20	GO:0005840;GO:0003723;GO:0006412;GO:0005622;GO:0003735;GO:0019843	G3DSA:1.10.1900.20: ; SSF74731: ; PD002389: RIBOSOMAL RRNA-BINDING RNA-BINDING RIBONUCLEOPROTEIN L20 50S L20 CHLOROPLAST BACTERIAL ORGANELLE; Coil: ; IPR005813: Ribosomal protein L20	NA
comp23536_c0_seq2.p1	Ec-16_002120.1	3-isopropylmalate dehydrogenase	GO:0000287;GO:0016616;GO:0008152;GO:0051287;GO:0055114;GO:0003862	IPR004429: Isopropylmalate dehydrogenase; IPR001804: Isocitrate and isopropylmalate dehydrogenases family; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR019818: Isocitrate/isopropylmalate dehydrogenase, conserved site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF53659: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR024084: Isopropylmalate dehydrogenase-like domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0785
comp21191_c0_seq3.p1	Ec-16_002130.1	pyruvate dehydrogenase kinase isoform 2; PDK2	GO:0016310;GO:0016772	IPR005467: Signal transduction histidine kinase, core; IPR018955: Branched-chain alpha-ketoacid dehydrogenase kinase/Pyruvate dehydrogenase kinase, N-terminal; IPR003594: Histidine kinase-like ATPase, C-terminal domain; PTHR11947: ; IPR004358: Signal transduction histidine kinase-related protein, C-terminal	NA
comp12012_c0_seq2.p1	Ec-16_002140.1	TAFII55 protein, conserved region	GO:0005669;GO:0006367	PTHR12228: ; IPR006751: TAFII55 protein, conserved region	NA
comp27996_c0_seq2.p1	Ec-16_002150.1	SPX, N-terminal	n/a;n/a;n/a	IPR004331: SPX domain; PTHR10783:	NA
comp29455_c0_seq3.p1	Ec-16_002160.1	Lyso-phosphatidylcholine acyltransferase	GO:0016746;GO:0006644	SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.40.1130.10: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000872: Tafazzin; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002123: Phospholipid/glycerol acyltransferase; SSF69593: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp34344_c0_seq1.p1	Ec-16_002190.1	Mitochondrial import inner membrane translocase subunit TIM23 homolog	GO:0005743;GO:0008565;GO:0015031	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR15371: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003397: Mitochondrial inner membrane translocase subunit Tim17/Tim22/Tim23/peroxisomal protein PMP24; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3324
comp30774_c0_seq2.p1	Ec-16_002210.1	Haloacid dehalogenase-like hydrolase	NA	NA	NA
comp20999_c0_seq1.p1	Ec-16_002230.1	cleavage-associated kinase	n/a;n/a;n/a	IPR000595: Cyclic nucleotide-binding domain; PTHR24349: ; IPR017441: Protein kinase, ATP binding site; G3DSA:3.30.200.20: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; IPR011992: EF-hand domain pair; SSF47473: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000719: Protein kinase domain; IPR018490: Cyclic nucleotide-binding-like; G3DSA:1.10.510.10: ; Coil: ; IPR014710: RmlC-like jelly roll fold; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0032
comp31501_c0_seq2.p1	Ec-16_002260.1	PCI/PINT associated module	GO:0000502;GO:0030234;GO:0042176;n/a	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR000717: Proteasome component (PCI) domain; PTHR10758:SF2: ; PTHR10758: ; IPR013143: PCI/PINT associated module; IPR013586: 26S proteasome regulatory subunit, C-terminal	NA
comp28602_c0_seq1.p1	Ec-16_002270.1	conserved unknown protein	NA	PTHR17901:SF14: ; IPR010033: HAD-superfamily phosphatase, subfamily IIIC; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR023214: HAD-like domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR010036: Magnesium-dependent phosphatase-1, eukaryotic/archaeal type; IPR024734: Magnesium-dependent phosphatase-1, eukaryotic type; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33043_c0_seq4.p1	Ec-16_002320.1	Hypothetical protein	n/a;n/a;n/a	PTHR11439:SF185: ; IPR001584: Integrase, catalytic core; IPR012337: Ribonuclease H-like domain; PTHR11439:	NA
comp29265_c0_seq1.p1	Ec-16_002330.2	Ammonium transporter	GO:0008519;GO:0016020;GO:0072488	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001905: Ammonium transporter; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11730:SF6: ; IPR018047: Ammonium transporter, conserved site; IPR024041: Ammonium transporter AmtB-like domain; IPR029020: Ammonium/urea transporter; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30402_c0_seq2.p1	Ec-16_002340.1	DNA helicase	GO:0005524;GO:0006281;GO:0004386;GO:0003678;GO:0000723	IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR23274: ; IPR003840: DNA helicase; IPR010285: DNA helicase Pif1-like	NA
comp32814_c0_seq10.p1	Ec-16_002350.1	FYVE zinc finger	GO:0046872	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR000306: FYVE zinc finger; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017455: Zinc finger, FYVE-related; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32954_c2_seq5.p1	Ec-16_002360.2	Hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31501_c0_seq2.p3	Ec-16_002380.1	Autophagy-related protein 1010	n/a;n/a;n/a	IPR012445: Autophagy-related protein 1010; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR13292:SF0: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33083_c0_seq3.p1	Ec-16_002380.3	Autophagy-related protein 1010	n/a;n/a;n/a	PF14223: gag-polypeptide of LTR copia-type	NA
comp26255_c0_seq2.p1	Ec-16_002390.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020	PTHR24089: ; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier	NA
comp20385_c0_seq1.p1	Ec-16_002420.1	pyruvate dehydrogenase kinase	GO:0005524	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR003594: Histidine kinase-like ATPase, C-terminal domain; PTHR11947: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR018955: Branched-chain alpha-ketoacid dehydrogenase kinase/Pyruvate dehydrogenase kinase, N-terminal	NA
comp30199_c0_seq1.p1	Ec-16_002430.1	P-loop containing nucleoside triphosphate hydrolase	n/a;GO:0003677;GO:0005524	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR010003: HARP domain; IPR001876: Zinc finger, RanBP2-type; IPR000330: SNF2-related; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF90209: ; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; PTHR10799: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19552_c0_seq1.p1	Ec-16_002440.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	SSF54928: ; PTHR24012: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp30772_c1_seq1.p1	Ec-16_002470.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32069_c0_seq8.p1	Ec-16_002520.1	Endonuclease/exonuclease/phosphatase	n/a;GO:0005515	IPR000300: Inositol polyphosphate-related phosphatase; PTHR11200: ; IPR005135: Endonuclease/exonuclease/phosphatase; IPR000008: C2 domain	NA
comp32069_c0_seq7.p2	Ec-16_002530.1	hypothetical protein	NA	IPR005135: Endonuclease/exonuclease/phosphatase	NA
comp32935_c0_seq3.p1	Ec-16_002540.1	Methionyl-tRNA synthetase	GO:0005524;GO:0004825;GO:0005737;GO:0006418;GO:0000166;GO:0006412;GO:0004812	SIGNAL_PEPTIDE: Signal peptide region; IPR015413: Methionyl/Leucyl tRNA synthetase; PTHR11946: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR009080: Aminoacyl-tRNA synthetase, class 1a, anticodon-binding; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; G3DSA:2.170.220.10: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF52374: ; IPR014758: Methionyl-tRNA synthetase; IPR023457: Methionine-tRNA synthetase, type 2; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0436
comp24592_c0_seq2.p1	Ec-16_002560.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020	PTHR24089: ; IPR002067: Mitochondrial carrier protein; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier	NA
comp26805_c1_seq1.p1	Ec-16_002590.1	divergent RAB-like GTPase	GO:0005622;GO:0007264;GO:0005525	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; IPR020849: Small GTPase superfamily, Ras type; IPR003579: Small GTPase superfamily, Rab type; PS51419: small GTPase Rab1 family profile.; PTHR24073:	NA
comp33271_c2_seq6.p1	Ec-16_002610.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; Coil: ; IPR002110: Ankyrin repeat	NA
comp29906_c0_seq5.p1	Ec-16_002620.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp30301_c0_seq4.p1	Ec-16_002630.1	Peptidase M18	GO:0006508;GO:0004177;GO:0008270	SSF53187: ; SSF101821: ; G3DSA:3.40.630.10: ; IPR001948: Peptidase M18	NA
comp11978_c0_seq1.p1	Ec-16_002640.1	Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain	GO:0055114;GO:0016491	IPR000103: Pyridine nucleotide-disulphide oxidoreductase, class-II; IPR005982: Thioredoxin reductase; PR00368: FAD-dependent pyridine nucleotide reductase signature; PTHR22912: ; SignalP-TM: ; IPR008255: Pyridine nucleotide-disulphide oxidoreductase, class-II, active site; IPR001327: Pyridine nucleotide-disulphide oxidoreductase, NAD-binding domain; G3DSA:3.50.50.60: ; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	NA
comp31076_c2_seq1.p1	Ec-16_002650.1	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	n/a;GO:0005515	IPR000408: Regulator of chromosome condensation, RCC1; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR22870: ; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020683: Ankyrin repeat-containing domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp24811_c0_seq1.p1	Ec-16_002680.1	Ca2+/calmodulin-dependent protein kinase kinase beta and related serine/threonine protein kinases	GO:0016772	IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; PTHR24347:SF1: ; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil: ; IPR020636: Calcium/calmodulin-dependent/calcium-dependent protein kinase	KOG0585
comp25422_c0_seq1.p1	Ec-16_002690.2	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp29737_c0_seq1.p1	Ec-16_002710.1	Regulator of chromosome condensation, RCC1	n/a;n/a;n/a	PTHR22870: ; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II; IPR000408: Regulator of chromosome condensation, RCC1; PF13540: Regulator of chromosome condensation (RCC1) repeat	NA
comp32812_c1_seq7.p1	Ec-16_002740.1	Nucleophile aminohydrolases, N-terminal	n/a;n/a;n/a	IPR013994: Carbohydrate-binding WSC, subgroup; IPR002889: Carbohydrate-binding WSC; IPR026869: Putative glutamine amidotransferase type 2; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029055: Nucleophile aminohydrolases, N-terminal; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11907: ; IPR017932: Glutamine amidotransferase type 2 domain	NA
comp26902_c0_seq2.p1	Ec-16_002750.1	Protein of unknown function DUF1180	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR009565: Protein of unknown function DUF1180; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28853_c0_seq1.p1	Ec-16_002770.1	Zinc finger, PHD-finger	GO:0005515	IPR019786: Zinc finger, PHD-type, conserved site; IPR001965: Zinc finger, PHD-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; Coil: ; IPR019787: Zinc finger, PHD-finger	NA
comp30181_c0_seq1.p1	Ec-16_002790.1	Transcription elongation factor S-II, central domain	GO:0006351	IPR017890: Transcription elongation factor S-IIM; PTHR11477: ; IPR003618: Transcription elongation factor S-II, central domain	NA
comp86466_c0_seq1.p1	Ec-16_002820.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp26945_c0_seq1.p1	Ec-16_002850.1	PIN domain-like	n/a;n/a;n/a	IPR006984: rRNA-processing protein Fcf1/Utp23; PTHR12416: ; IPR029060: PIN domain-like	NA
comp34750_c0_seq1.p1	Ec-16_002860.1	TVP18/Calcium channel flower	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR019365: TVP18/Calcium channel flower; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24343_c0_seq1.p1	Ec-16_002870.1	Cystathionine beta-synthase	GO:0004122;GO:0006520	IPR001216: Cysteine synthase/cystathionine beta-synthase, pyridoxal-phosphate attachment site; G3DSA:3.10.580.10: ; IPR001926: Tryptophan synthase beta subunit-like PLP-dependent enzyme; IPR000644: CBS domain; SSF54631: ; PTHR10314: ; G3DSA:3.40.50.1100:	KOG1252
comp32434_c0_seq6.p1	Ec-16_002880.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp30875_c0_seq3.p1	Ec-16_002890.1	Major facilitator superfamily domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020846: Major facilitator superfamily domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR19432:SF35: ; G3DSA:1.20.1250.20: ; PTHR19432: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30875_c0_seq3.p2	Ec-16_002900.1	haloacid dehalogenase-like hydrolase	NA	PTHR18901: ; IPR023214: HAD-like domain; SignalP-TM:	NA
comp32531_c1_seq8.p6	Ec-16_002930.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp33070_c0_seq1.p1	Ec-16_002940.1	Uracil-DNA glycosylase-like	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR005122: Uracil-DNA glycosylase-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR13235: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12314_c0_seq1.p1	Ec-16_002950.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30223_c0_seq2.p1	Ec-16_002950.2	hypothetical protein	n/a;n/a;n/a	NA	NA
comp63433_c0_seq1.p1	Ec-16_002960.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp69201_c0_seq1.p1	Ec-16_002970.1	Vasohibin	GO:0005737;GO:0045765	PTHR15750: ; IPR028131: Vasohibin	NA
comp29876_c0_seq1.p1	Ec-16_002980.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp32044_c0_seq5.p1	Ec-16_002990.1	Possible rho or cAMP PK	GO:0004672;GO:0005524;GO:0006468	IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PTHR24362: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	KOG0612
comp26977_c0_seq5.p2	Ec-16_003000.1	Nucleoid-associated protein YbaB	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR004401: Nucleoid-associated protein YbaB family	NA
comp19982_c0_seq2.p1	Ec-16_003010.1	N-carbamoylputrescine amidase	GO:0006596;GO:0006807;GO:0050126;GO:0016810	IPR003010: Carbon-nitrogen hydrolase; PTHR23088:	KOG0806
comp24225_c0_seq2.p1	Ec-16_003020.1	NUDIX hydrolase domain	GO:0016787	PTHR11839: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR020084: NUDIX hydrolase, conserved site; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR015797: NUDIX hydrolase domain-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000086: NUDIX hydrolase domain	NA
comp32582_c0_seq14.p1	Ec-16_003040.1	Quinonprotein alcohol dehydrogenase-like superfamily	n/a;n/a;n/a	PF13637: Ankyrin repeats (many copies); IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; PTHR24133: ; SSF141571: ; IPR020683: Ankyrin repeat-containing domain; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily; IPR002110: Ankyrin repeat	NA
comp30755_c0_seq3.p1	Ec-16_003060.4	Peptidase C2, calpain, large subunit, domain III	GO:0004198;GO:0005622;GO:0006508	SSF54001: ; G3DSA:3.90.70.10: ; G3DSA:2.60.120.380: ; IPR022682: Peptidase C2, calpain, large subunit, domain III; Coil: ; PTHR10183: ; IPR001300: Peptidase C2, calpain, catalytic domain	NA
comp26977_c0_seq5.p1	Ec-16_003070.1	P-loop containing nucleoside triphosphate hydrolase	GO:0000166	IPR003593: AAA+ ATPase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR030230: GPN-loop GTPase 1; Coil: ; IPR004130: GPN-loop GTPase	NA
comp29827_c0_seq2.p1	Ec-16_003090.1	Rhodanese-like domain	n/a;n/a;n/a	PTHR22778: ; IPR001763: Rhodanese-like domain; PTHR22778:SF21: ; IPR022111: Rhodanase, C-terminal	NA
comp26477_c0_seq2.p1	Ec-16_003110.1	ABC-2 type transporter	GO:0016020	IPR003439: ABC transporter-like; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013525: ABC-2 type transporter; IPR017871: ABC transporter, conserved site; PTHR19241:	NA

comp31642_c1_seq2.p1	Ec-16_003660.1	Mitochondrial transcription termination factor	GO:0006355;GO:0003690;GO:0005515;GO:0005739	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR003690: Mitochodrial transcription termination factor; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp29746_c0_seq6.p1	Ec-16_003690.1	Major facilitator superfamily	GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24003: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28825_c0_seq2.p2	Ec-16_003700.1	N2227-like	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR012901: N2227-like; PTHR12303:	NA
comp33296_c0_seq1.p1	Ec-16_003710.1	lipase	GO:0003824;GO:0004806;GO:0006629	IPR002921: Fungal lipase-like domain; IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR21493: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	no relat
comp19654_c0_seq1.p1	Ec-16_003720.1	Armadillo-like helical	GO:0043248;GO:0005488	IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold; IPR019538: 26S proteasome non-ATPase regulatory subunit 5	NA
comp12426_c0_seq1.p1	Ec-16_003740.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp25046_c0_seq1.p1	Ec-16_003750.1	Transmembrane protein Tvp38/TMEM64-like	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015414: Transmembrane protein TMEM64/TMEM41; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR12677:SF5: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR032816: SNARE associated Golgi protein	KOG3140
comp24922_c0_seq2.p1	Ec-16_003770.1	DNA recombination and repair protein Rad51, C-terminal	GO:0003677;GO:0005524;GO:0006259;GO:0008094	IPR020588: DNA recombination and repair protein RecA-like, ATP-binding domain; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR013632: DNA recombination and repair protein Rad51, C-terminal; PTHR22942:	NA
comp22777_c0_seq1.p1	Ec-16_003780.1	Domain of unknown function DUF1336	n/a;n/a;n/a	IPR009769: Domain of unknown function DUF1336; PTHR31558:	NA
comp11867_c0_seq1.p1	Ec-16_003790.1	Pleckstrin homology-like domain	GO:0016020;GO:0006897	SSF50729: ; IPR012466: Adaptin ear-binding coat-associated protein 1 NECAP-1; IPR011993: Pleckstrin homology-like domain; Coil: ; PTHR12847:	NA
comp32232_c0_seq7.p1	Ec-16_003800.1	Scaffold protein Nfu/NifU, N-terminal	GO:0005506	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR011989: Armadillo-like helical; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR014824: Scaffold protein Nfu/NifU, N-terminal; IPR016024: Armadillo-type fold; PF13646: HEAT repeats; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32232_c0_seq7.p2	Ec-16_003830.1	Phosphoribosyltransferase-like	n/a;n/a;n/a	PTHR10285: ; IPR029057: Phosphoribosyltransferase-like	NA
comp27575_c0_seq1.p1	Ec-16_003850.1	C-type lectin fold	n/a;n/a;n/a	IPR016187: C-type lectin fold; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR23150: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005532: Sulfatase-modifying factor enzyme; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp19463_c0_seq2.p1	Ec-16_003860.1	Nuclear fusion protein, KAR5	n/a;n/a;n/a	PTHR33538: ; IPR007292: Nuclear fusion protein, KAR5; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR33538:SF2: ; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30844_c0_seq5.p1	Ec-16_003880.1	Tetratricopeptide-like helical domain	GO:0005515	IPR011990: Tetratricopeptide-like helical domain; IPR013935: TRAPP II complex, Trs120; PTHR21512:	NA
comp32333_c3_seq17.p1	Ec-16_003890.1	Domain of unknown function DUF221	GO:0016020	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF13967: Late exocytosis, associated with Golgi transport; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003864: Domain of unknown function DUF221; PTHR13018: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32333_c3_seq18.p2	Ec-16_003910.1	conserved unknown protein	GO:0019089	NA	NA
comp20033_c0_seq1.p1	Ec-16_003940.1	Elongated TPR repeat-containing domain	GO:0006457	IPR023114: Elongated TPR repeat-containing domain	NA

comp19927_c0_seq1.p1	Ec-17_003180.1	SANT domain protein	n/a;n/a;n/a
comp31912_c0_seq2.p2	Ec-17_003190.1	MaoC-like domain	GO:0008152;GO:0016491
comp32970_c1_seq1.p1	Ec-17_003200.1	Molecular chaperones HSP70/HSC70, HSP70 superfamily	n/a;n/a;n/a
comp32945_c5_seq3.p1	Ec-17_003210.1	expressed unknown protein	n/a;n/a;n/a
comp19614_c0_seq1.p1	Ec-17_003230.1	expressed unknown protein	n/a;n/a;n/a
comp32932_c0_seq1.p1	Ec-17_003240.1	expressed unknown protein	n/a;n/a;n/a
comp26645_c0_seq1.p1	Ec-17_003250.1	Serine type protease, similar to Protease Do-like 1, chloroplast precursor	GO:0005515
comp31841_c1_seq1.p1	Ec-17_003270.1	Zinc finger, CCCH-type	GO:0046872
comp24692_c0_seq1.p1	Ec-17_003290.1	Cupin-like domain protein	n/a;n/a;n/a
comp31587_c0_seq2.p1	Ec-17_003300.1	serine/threonine protein phosphatase	GO:0016787
comp26432_c0_seq1.p1	Ec-17_003350.1	expressed unknown protein	n/a;n/a;n/a
comp26432_c0_seq1.p3	Ec-17_003360.1	expressed unknown protein	n/a;n/a;n/a
comp30621_c0_seq3.p1	Ec-17_003380.1	similar to TPR, partial	NA
comp30583_c0_seq9.p1	Ec-17_003420.1	Histidine phosphatase superfamily	n/a;n/a;n/a
comp19581_c0_seq1.p1	Ec-17_003450.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168
comp29633_c1_seq2.p1	Ec-17_003460.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0000981;GO:0005634;GO:0006355;GO:0008270
comp22132_c0_seq2.p1	Ec-17_003470.1	expressed unknown protein	n/a;n/a;n/a
comp12651_c0_seq1.p1	Ec-17_003490.1	Zinc finger, RanBP2-type	GO:0008270
comp24759_c0_seq1.p1	Ec-17_003500.1	GPI mannosyltransferase, family GT76	GO:0006506;GO:0016758;GO:0016021;GO:0005789
comp30983_c0_seq3.p2	Ec-17_003520.1	solanesyl diphosphate synthase-like protein	GO:0008299
comp24759_c0_seq1.p4	Ec-17_003530.1	RNA pseudouridylate synthase domain containing 1	GO:0003723;GO:0001522;GO:0009451;GO:0009982
comp31059_c0_seq3.p1	Ec-17_003580.1	RNA recognition motif 2	GO:0000166
comp13078_c0_seq1.p1	Ec-17_003590.1	Zinc finger, RING-type	GO:0005515;GO:0008270
comp31955_c0_seq6.p4	Ec-17_003600.1	expressed unknown protein	n/a;n/a;n/a
comp29729_c0_seq11.p1	Ec-17_003610.1	Major facilitator superfamily	GO:0055085;GO:0016021
comp21227_c0_seq1.p1	Ec-17_003620.1	Mitochondrial substrate/solute carrier	GO:0005488;GO:0006810;GO:0016020
comp32408_c0_seq1.p1	Ec-17_003630.1	Short-chain dehydrogenase/reductase SDR	GO:0008152;GO:0016491
comp27721_c0_seq2.p1	Ec-17_003640.1	CRAL-TRIO domain	GO:0005215;GO:0005622;GO:0006810
comp20374_c0_seq1.p1	Ec-17_003680.2	Ankyrin repeat-containing domain	n/a;n/a;n/a
comp28663_c0_seq1.p1	Ec-17_003690.1	Tetratricopeptide-like helical domain	GO:0005515
comp26197_c1_seq4.p1	Ec-17_003700.2	Ribonucleotide reductase, class I , alpha subunit	GO:0055114
comp31261_c0_seq12.p1	Ec-17_003710.1	hypothetical protein	GO:0005509
comp25720_c0_seq1.p1	Ec-17_003710.2	hypothetical protein	GO:0005509
comp27291_c0_seq1.p2	Ec-17_003720.1	Uridine kinase like	GO:0005524;GO:0016773
comp27291_c0_seq1.p1	Ec-17_003730.1	expressed unknown protein	n/a;n/a;n/a
comp26535_c0_seq2.p1	Ec-17_003740.1	Ribonuclease HII/HIII	GO:0003723;GO:0004523;GO:0003676
comp29022_c0_seq1.p1	Ec-17_003760.1	CRAL-TRIO domain	n/a;n/a;n/a
comp26212_c0_seq1.p1	Ec-17_003820.1	Amino acid transporter, transmembrane	n/a;n/a;n/a
comp27724_c0_seq2.p1	Ec-17_003840.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0016887
comp27593_c0_seq2.p1	Ec-17_003860.1	DEAD box helicase	n/a;n/a;n/a
comp20146_c0_seq1.p1	Ec-17_003880.1	conserved unknown protein	GO:0003702;GO:0005215;GO:0005488;GO:0005673;GO:0006367;GO:0006810
comp32851_c1_seq10.p1	Ec-17_003910.1	Major facilitator superfamily	GO:0055085;GO:0016021
comp31421_c0_seq1.p1	Ec-17_003920.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp33133_c1_seq3.p1	Ec-17_003930.2	protein phosphatase 2C	NA
comp31260_c0_seq6.p3	Ec-17_003940.3	TLDc domain	GO:0016998
comp62954_c0_seq1.p1	Ec-17_003950.1	calmodulin-like myosin-light chain	GO:0003676
comp30979_c0_seq1.p1	Ec-17_003970.1	glutaminyl-tRNA synthase	GO:0016884;GO:0006412
comp32427_c0_seq10.p1	Ec-17_003980.2	expressed unknown protein	n/a;n/a;n/a
comp15026_c0_seq2.p1	Ec-17_003990.1	Nucleotide-diphospho-sugar transferases	n/a;n/a;n/a
comp28351_c1_seq1.p1	Ec-17_004010.1	ATP-dependent helicase, C-terminal	GO:0005524;GO:0006139;GO:0008026;GO:0003676;GO:0016818
comp31887_c0_seq7.p1	Ec-17_004030.2	conserved unknown protein	n/a;n/a;n/a
comp30979_c0_seq8.p1	Ec-17_004060.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp11057_c0_seq1.p2	Ec-17_004070.1	Ribosomal protein S30	GO:0005840;GO:0005622;GO:0006412;GO:0003735
comp24228_c0_seq2.p1	Ec-17_004080.1	Pentatricopeptide repeat	n/a;n/a;n/a
comp11686_c0_seq1.p1	Ec-17_004090.1	cathepsin B-like proteinase	GO:0006508;GO:0004197
comp10241_c0_seq1.p1	Ec-17_004110.1	expressed unknown protein	n/a;n/a;n/a
comp13691_c0_seq1.p1	Ec-17_004120.1	Protein of unknown function DUF4558	n/a;n/a;n/a
comp29321_c1_seq2.p1	Ec-17_004130.1	ribosomal protein rpS22, plastidal	GO:0044238
comp23759_c0_seq3.p1	Ec-17_004140.1	conserved unknown protein	n/a;n/a;n/a
comp12762_c0_seq1.p1	Ec-17_004150.1	Amine oxidase	GO:0055114;GO:0016491
comp30953_c0_seq5.p1	Ec-17_004160.1	Bromodomain	GO:0005515
comp12614_c0_seq2.p1	Ec-17_004170.1	expressed unknown protein	n/a;n/a;n/a
comp25751_c0_seq2.p1	Ec-17_004180.1	conserved unknown protein	NA
comp24237_c0_seq2.p1	Ec-17_004210.1	Calcium-dependent protein kinase 2 (PfCDPK2)	GO:0005524;GO:0006468;GO:0004672
comp24970_c0_seq3.p1	Ec-17_004220.2	expressed unknown protein	n/a;n/a;n/a
comp28262_c0_seq1.p1	Ec-17_004230.1	peptidase S1 and S6, chymotrypsin/Hap	NA
comp37155_c0_seq1.p1	Ec-17_004280.1	viral A-type inclusion protein	n/a;n/a;n/a
comp27139_c0_seq4.p1	Ec-17_004350.1	Sodium/solute symporter	GO:0005215;GO:0006810;GO:0016020;GO:0055085
comp27374_c0_seq1.p2	Ec-17_004360.2	Galactose-binding domain-like	n/a;n/a;n/a
comp25441_c0_seq1.p1	Ec-18_000010.1	hypothetical protein	n/a;n/a;n/a
comp33650_c0_seq1.p1	Ec-18_000020.1	Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase	GO:0016787
comp27319_c0_seq2.p1	Ec-18_000030.1	RGS domain	GO:0038032
comp31087_c0_seq2.p1	Ec-18_000040.1	expressed unknown protein	n/a;n/a;n/a
comp31571_c1_seq6.p1	Ec-18_000060.2	Immunoglobulin E-set	n/a;n/a;n/a
comp11950_c0_seq1.p1	Ec-18_000080.2	dihydrolipoamide acetyltransferase	n/a;n/a;n/a
comp28637_c0_seq2.p1	Ec-18_000110.1	Truncated protein kinase domain protein	NA
comp32252_c0_seq5.p1	Ec-18_000160.1	Ribonuclease H-like domain	GO:0003676
comp31826_c0_seq1.p1	Ec-18_000180.1	WD40/YVTN repeat-like-containing domain	GO:0005515
comp26119_c0_seq1.p1	Ec-18_000200.1	hypothetical protein	n/a;n/a;n/a
comp30666_c0_seq10.p1	Ec-18_000260.1	NAD(P)-binding domain	GO:0008152;GO:0016491
comp12625_c0_seq2.p1	Ec-18_000290.1	Thioredoxin-like fold	n/a;n/a;n/a
comp20280_c0_seq1.p1	Ec-18_000300.1	Protein of unknown function DUF1415	n/a;n/a;n/a
comp31042_c0_seq1.p1	Ec-18_000310.1	expressed unknown protein	n/a;n/a;n/a
comp26161_c0_seq1.p1	Ec-18_000320.1	expressed unknown protein	n/a;n/a;n/a
comp30895_c0_seq3.p1	Ec-18_000330.1	conserved unknown protein	n/a;n/a;n/a
comp30895_c0_seq2.p1	Ec-18_000350.1	conserved unknown protein	n/a;n/a;n/a
comp27849_c0_seq3.p1	Ec-18_000380.1	Hypothetical leucine rich repeat protein	NA
comp11819_c0_seq1.p1	Ec-18_000430.1	Frataxin/CyaY	GO:0008199;GO:0016226
comp29853_c0_seq4.p1	Ec-18_000440.1	expressed unknown protein	n/a;n/a;n/a
comp30655_c0_seq1.p1	Ec-18_000450.1	RlpA-like double-psi beta-barrel domain	n/a;n/a;n/a
comp32090_c1_seq11.p1	Ec-18_000460.1	2-Isopropylmalate synthase	GO:0003852;GO:0009098
comp31078_c0_seq2.p1	Ec-18_000480.3	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a
comp29196_c0_seq1.p1	Ec-18_000480.5	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a
comp31601_c0_seq6.p1	Ec-18_000490.1	TLDc domain	GO:0007165;GO:0005622
comp10897_c0_seq1.p1	Ec-18_000500.1	cAMP-dependent protein kinase regulatory subunit	GO:0001932;GO:0005952;GO:0008603
comp2362_c0_seq1.p1	Ec-18_000510.1	Helicase, C-terminal	n/a;n/a;n/a
comp28924_c0_seq3.p1	Ec-18_000530.1	Fatty acid desaturase	GO:0006629
comp34012_c0_seq1.p1	Ec-18_000540.1	expressed unknown protein	n/a;n/a;n/a
comp24767_c0_seq1.p1	Ec-18_000560.1	diacylglycerol kinase	GO:0004143;GO:0007205
comp26633_c0_seq1.p2	Ec-18_000600.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp26133_c0_seq2.p1	Ec-18_000610.1	Extracellular Endonuclease, subunit A	GO:0003676;GO:0016787;GO:0046872
comp26633_c0_seq1.p1	Ec-18_000620.1	Inositol-pentakisphosphate 2-kinase	GO:0035299;GO:0005524
comp26363_c0_seq1.p1	Ec-18_000650.1	Ankyrin Repeat Transient Receptor Potential Channel	GO:0016020;GO:0070588;n/a;GO:0055085;GO:0006811;GO:0005216;GO:0034704;GO:0005262
comp27714_c0_seq1.p1	Ec-18_000680.1	putative: silimar to centromere/kinetochore protein zw10 homolog	GO:0005634;GO:0000775;GO:0007067
comp26529_c0_seq1.p1	Ec-18_000720.1	Villin/Gelsolin	GO:0003779;GO:0007010
comp20712_c0_seq1.p1	Ec-18_000730.1	WD40/YVTN repeat-like-containing domain	GO:0005515
comp31169_c0_seq14.p1	Ec-18_000740.1	Immunoglobulin E-set	GO:0000287;GO:0004427;GO:0005737;GO:0005515;GO:0006796
comp32209_c2_seq3.p1	Ec-18_000760.3	FYVE zinc finger protein	GO:0005622;GO:0008270
comp29354_c0_seq1.p2	Ec-18_000770.1	Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain	GO:0000413;GO:0003755;GO:0006457
comp29354_c0_seq1.p1	Ec-18_000780.1	FNIP	n/a;n/a;n/a
comp29354_c0_seq1.p3	Ec-18_000790.1	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	n/a;n/a;n/a
comp32030_c1_seq2.p1	Ec-18_000800.1	Protein kinase-like domain	GO:0016772
comp21402_c0_seq1.p1	Ec-18_000830.1	expressed unknown protein	n/a;n/a;n/a
comp26733_c0_seq2.p2	Ec-18_000840.1	expressed unknown protein	n/a;n/a;n/a
comp26733_c0_seq2.p1	Ec-18_000850.1	Epoxide hydrolase-like	GO:0003824
comp31550_c0_seq38.p2	Ec-18_000860.2	Legume lectin domain	GO:0030246
comp31550_c0_seq38.p1	Ec-18_000870.2	Serine/threonine protein kinase	GO:0016772
comp12354_c0_seq2.p1	Ec-18_000910.1	Gamma-tocopherol methyltransferase	GO:0008152;GO:0008168
comp13504_c0_seq2.p1	Ec-18_000910.2	Gamma-tocopherol methyltransferase	GO:0008152;GO:0008168
comp34530_c0_seq1.p1	Ec-18_000930.1	Protein of unknown function DUF3727	n/a;n/a;n/a
comp21779_c0_seq2.p1	Ec-18_000940.1	EsV-1-7 domain protein	NA
comp33890_c0_seq1.p1	Ec-18_000990.1	geranyl-diphosphate synthase	GO:0008299
comp32648_c0_seq2.p1	Ec-18_001010.1	FNIP	n/a;n/a;n/a
comp22226_c0_seq4.p1	Ec-18_001020.1	Hypothetical protein	n/a;n/a;n/a
comp16284_c0_seq2.p1	Ec-18_001040.1	Heat shock protein 90	GO:0005524
comp30618_c0_seq4.p1	Ec-18_001050.2	conserved unknown protein	n/a;n/a;n/a
comp30618_c0_seq2.p1	Ec-18_001050.3	conserved unknown protein	n/a;n/a;n/a
comp38092_c0_seq1.p1	Ec-18_001060.1	EsV-1-7 domain protein	n/a;n/a;n/a
comp27042_c0_seq1.p1	Ec-18_001100.1	expressed unknown protein	n/a;n/a;n/a
comp29139_c0_seq1.p2	Ec-18_001120.2	Actin-related protein 2/3 complex subunit 3	GO:0005515
comp11998_c0_seq1.p1	Ec-18_001150.1	Glycoside hydrolase superfamily	n/a;n/a;n/a
comp24987_c0_seq1.p1	Ec-18_001160.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a
comp31565_c0_seq6.p3	Ec-18_001200.1	HAD-like domain	GO:0016787;n/a
comp31565_c0_seq5.p1	Ec-18_001210.1	Peptidase S9, prolyl oligopeptidase, catalytic domain	GO:0004252;GO:0008236;GO:0006508
comp31906_c1_seq3.p1	Ec-18_001220.1	expressed unknown protein	n/a;n/a;n/a
comp35213_c0_seq1.p1	Ec-18_001280.1	HSP20-like chaperone	n/a;n/a;n/a
comp30747_c0_seq3.p1	Ec-18_001290.1	mannitol 1-phosphate dehydrogenase	n/a;n/a;n/a
comp32294_c1_seq11.p2	Ec-18_001300.1	CDP-diacylglycerol—inositol 3-phosphatidyltransferase	GO:0008654;GO:0016020;GO:0016780
comp29666_c0_seq3.p1	Ec-18_001310.1	Pyruvate, phosphate dikinase	GO:0016310;GO:0003824;GO:0016772
comp28912_c0_seq1.p1	Ec-18_001320.1	Protein of unknown function DUF901	n/a;n/a;n/a
comp30192_c0_seq3.p1	Ec-18_001330.1	Major facilitator superfamily domain	n/a;n/a;n/a
comp24849_c0_seq1.p1	Ec-18_001350.1	hypothetical protein	GO:0004657;GO:0005509;GO:0006560;GO:0006562
comp20324_c0_seq1.p1	Ec-18_001370.1	hypothetical protein	n/a;n/a;n/a
comp32953_c4_seq21.p1	Ec-18_001410.1	conserved unknown protein	n/a;n/a;n/a
comp26352_c0_seq1.p1	Ec-18_001420.1	DNA primase large subunit, eukaryotic/archaeal	GO:0006269;GO:0003896
comp24940_c0_seq3.p1	Ec-18_001490.1	Hypothetical protein	n/a;n/a;n/a
comp24940_c0_seq4.p2	Ec-18_001500.1	CoA-binding	GO:0048037
comp13353_c0_seq1.p1	Ec-18_001520.1	hypothetical protein	n/a;n/a;n/a
comp32737_c1_seq11.p1	Ec-18_001570.1	Phosphoserine phosphatase	GO:0008152;GO:0016791
comp30332_c0_seq1.p1	Ec-18_001590.1	SAC3/GANP/Nin1/mts3/eIF-3 p25	n/a;n/a;n/a
comp20157_c0_seq1.p1	Ec-18_001600.1	Vacuolar Processing Enzyme	GO:0008233;GO:0006508;GO:0004197
comp32858_c2_seq19.p1	Ec-18_001620.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;GO:0008757;GO:0008152;GO:0008119;GO:0005737
comp31455_c0_seq2.p1	Ec-18_001660.1	Heat Shock transcription factor	GO:0005634;GO:0006355;GO:0043565;GO:0003700
comp32591_c1_seq4.p1	Ec-18_001665.1	hypothetical protein	GO:0005509
comp21298_c0_seq2.p1	Ec-18_001670.1	Ragulator complex protein LAMTOR3	GO:0032006
comp34010_c0_seq1.p1	Ec-18_001680.1	Ribosomal protein L7/L12	GO:0005840;GO:0005622;GO:0006412;GO:0003735
comp24819_c0_seq1.p1	Ec-18_001690.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp26542_c0_seq1.p1	Ec-18_001700.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	GO:0016020;GO:0016192;GO:0005515
comp31379_c0_seq14.p1	Ec-18_001710.1	conserved unknown protein	n/a;n/a;n/a
comp11939_c0_seq1.p1	Ec-18_001730.1	Light harvesting complex protein	GO:0009765;GO:0016020
comp34346_c0_seq1.p1	Ec-18_001740.1	Light harvesting complex protein	GO:0009765;GO:0016020
comp32181_c1_seq7.p1	Ec-18_001750.1	Uncharacterised GTP-binding protein, C-terminal	n/a;n/a;n/a
comp28992_c0_seq4.p1	Ec-18_001760.1	Basic-leucine zipper domain	GO:0006355;GO:0043565;GO:0003700
comp28992_c0_seq4.p2	Ec-18_001770.1	SET domain protein	GO:0005515
comp20348_c0_seq2.p1	Ec-18_001780.1	similar to U3 small nucleolar RNA interacting protein 2	GO:0005515
comp20348_c0_seq2.p2	Ec-18_001790.1	Hypothetical protein	n/a;n/a;n/a
comp26681_c0_seq2.p1	Ec-18_001800.1	Tetratricopeptide-like helical domain	GO:0005515
comp24305_c0_seq2.p1	Ec-18_001810.1	FCH domain	n/a;n/a;n/a
comp28782_c0_seq2.p1	Ec-18_001810.2	FCH domain	n/a;n/a;n/a
comp31126_c0_seq3.p1	Ec-18_001820.1	Armadillo-type fold	GO:0005488
comp31469_c0_seq4.p1	Ec-18_001830.1	Zinc finger, RING/FYVE/PHD-type	n/a;GO:0007165;GO:0016567;GO:0004842;GO:0006955
comp29256_c0_seq1.p1	Ec-18_001840.1	CBF1-interacting co-repressor CIR, N-terminal domain	n/a;n/a;n/a
comp20706_c0_seq1.p1	Ec-18_001850.1	Phytoene desaturase, chloroplast precursor	GO:0009055;GO:0006118;GO:0055114;GO:0016491
comp27329_c0_seq4.p1	Ec-18_001860.1	conserved unknown protein	n/a;n/a;n/a
comp33019_c1_seq20.p1	Ec-18_001870.1	Tyrosyl-tRNA synthetase	GO:0005524;GO:0005737;GO:0006418;GO:0000166;GO:0006412;GO:0004831;GO:0004812
comp29036_c1_seq3.p1	Ec-18_001880.1	Uncharacterised protein family UPF0016	GO:0016020
comp32867_c0_seq4.p1	Ec-18_001930.1	expressed unknown protein	n/a;n/a;n/a
comp24490_c0_seq1.p1	Ec-18_001940.1	Vps52 / Sac2 family protein	NA
comp32873_c0_seq2.p1	Ec-18_001960.1	Rapamycin-insensitive companion of mTOR, N-terminal domain	GO:0005488
comp28448_c0_seq3.p1	Ec-18_001980.1	Clathrin assembly complex, small subunit	GO:0008565;GO:0015031
comp28448_c0_seq4.p1	Ec-18_001990.1	Peptidase S54, rhomboid domain	GO:0004252;GO:0016021
comp31346_c0_seq3.p1	Ec-18_002000.1	DHS-like NAD/FAD-binding domain	GO:0006118;GO:0009055;GO:0050660
comp26811_c0_seq3.p1	Ec-18_002010.1	CCCH-type Zn finger-containing protein	GO:0003676;GO:0008270
comp22365_c0_seq2.p1	Ec-18_002020.1	P-loop containing nucleoside triphosphate hydrolase	n/a;GO:0005524
comp31769_c0_seq7.p2	Ec-18_002030.2	hypothetical protein	n/a;n/a;n/a
comp30932_c0_seq22.p3	Ec-18_002040.1	ARFRP1, ARF-like Ras superfamily GTPase	GO:0005622;GO:0006886;GO:0005525
comp32148_c0_seq3.p1	Ec-18_002060.1	Calycin	n/a;n/a;n/a
comp34430_c0_seq1.p1	Ec-18_002070.1	NAD(P)-binding domain	n/a;GO:0008152;GO:0016491
comp31313_c0_seq4.p1	Ec-18_002080.1	expressed unknown protein	n/a;n/a;n/a
comp31372_c0_seq5.p1	Ec-18_002090.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp28418_c0_seq1.p1	Ec-18_002100.1	expressed unknown protein	n/a;n/a;n/a
comp32049_c0_seq6.p1	Ec-18_002110.2	Hypothetical protein	n/a;n/a;n/a
comp13040_c0_seq1.p1	Ec-18_002130.1	Dihydroxyacetone/glycerone kinase	GO:0004371;GO:0006071
comp12989_c0_seq1.p1	Ec-18_002140.1	Carotenoid oxygenase	n/a;n/a;n/a
comp29444_c0_seq3.p1	Ec-18_002160.1	hypothetical protein	NA
comp57728_c0_seq1.p1	Ec-18_002180.1	hypothetical protein	n/a;n/a;n/a
comp20472_c0_seq1.p1	Ec-18_002190.1	Zinc finger, RING/FYVE/PHD-type	GO:0007031;GO:0005779;GO:0008022;GO:0008270;GO:0006625;GO:0005778
comp13792_c0_seq1.p1	Ec-18_002200.1	Tubulin-tyrosine ligase/Tubulin polyglutamylase	GO:0006464
comp72044_c0_seq1.p2	Ec-18_002240.2	Hypothetical leucine rich repeat calmodulin binding protein	NA
comp27529_c0_seq1.p1	Ec-18_002260.1	similar to bleomycin hydrolase	GO:0006508;GO:0004197
comp32325_c0_seq1.p1	Ec-18_002270.1	alpha tubulin	GO:0003924;GO:0005525;GO:0006184;GO:0043234;GO:0051258
comp13132_c0_seq1.p1	Ec-18_002280.1	Alpha-1,2-glucosyltransferase ALG10-A, family GT59	GO:0004583;GO:0016758;GO:0006488;GO:0016021;GO:0005789
comp22113_c0_seq3.p1	Ec-18_002290.1	MHCK/EF2 kinase	GO:0004674;GO:0005524;GO:0006468
comp21903_c0_seq1.p1	Ec-18_002300.1	hypothetical protein	n/a;n/a;n/a
comp32029_c2_seq1.p1	Ec-18_002310.1	eukaryotic elongation factor-1 B beta	GO:0003746;GO:0005853;GO:0006414
comp30939_c0_seq17.p3	Ec-18_002330.1	NUDIX hydrolase domain-like	GO:0016787
comp21212_c0_seq2.p1	Ec-18_002340.1	DNA/pantothenate metabolism flavoprotein, C-terminal	n/a;n/a;n/a
comp34088_c0_seq1.p1	Ec-18_002350.1	Phospholipid methyltransferase	n/a;n/a;n/a
comp31611_c0_seq6.p1	Ec-18_002360.1	Mannose-P-dolichol utilization defect 1 protein	n/a;n/a;n/a
comp30828_c0_seq6.p1	Ec-18_002380.1	EsV-1-7 domain protein	NA
comp31611_c0_seq6.p2	Ec-18_002390.1	Endonuclease V	GO:0006281;GO:0004519
comp26729_c0_seq2.p1	Ec-18_002400.1	SR RNA splicing protein	GO:0000166
comp33918_c0_seq1.p1	Ec-18_002410.1	Amino acid transporter, transmembrane	n/a;n/a;n/a
comp31752_c1_seq9.p2	Ec-18_002430.1	Major facilitator superfamily domain	n/a;n/a;n/a
comp32157_c0_seq18.p1	Ec-18_002450.1	CBP-type histone acetylase, zinc finger and Bromodomain protein	GO:0005634;GO:0005515;GO:0006355;GO:0004402;GO:0008270;GO:0003712;GO:0016573
comp33508_c0_seq1.p1	Ec-18_002530.1	hypothetical protein	n/a;n/a;n/a
comp34459_c0_seq1.p2	Ec-18_002540.1	Sm-like protein LSm7	GO:0030529;GO:0016071
comp30547_c0_seq6.p1	Ec-18_002550.1	Zinc finger, RING/FYVE/PHD-type	GO:0005515;GO:0008270
comp29374_c0_seq1.p1	Ec-18_002560.1	inner membrane magnesium transporter	GO:0015693;GO:0015095
comp26942_c0_seq2.p1	Ec-18_002570.1	Serine/threonine protein kinase	GO:0004672;GO:0005524;GO:0006468
comp61964_c0_seq1.p1	Ec-18_002580.1	Acyl-CoA-binding domain-containing protein 6	GO:0005515
comp25478_c0_seq3.p1	Ec-18_002590.1	tRNA-dihydrouridine synthase	GO:0050660;GO:0055114;GO:0008033;GO:0017150
comp32675_c2_seq18.p1	Ec-18_002600.1	Homeodomain-like	GO:0003677
comp28274_c0_seq1.p1	Ec-18_002620.1	EsV-1-7 domain protein	GO:0046872;GO:0016813
comp31304_c0_seq8.p1	Ec-18_002630.1	RmlC-like jelly roll fold	n/a;GO:0016021;GO:0015031
comp32024_c0_seq4.p1	Ec-18_002640.1	hypothetical protein	GO:0016813;GO:0046872
comp30145_c0_seq2.p1	Ec-18_002660.1	Anticodon-binding	n/a;n/a;n/a
comp13889_c0_seq2.p1	Ec-18_002680.1	conserved unknown protein	n/a;n/a;n/a
comp20407_c0_seq2.p1	Ec-18_002690.1	isopentenyl-diphosphate delta-isomerase type 1	GO:0008299;GO:0004452;GO:0016787
comp12073_c0_seq1.p1	Ec-18_002710.1	Beta-grasp domain	GO:0009055;GO:0006457;GO:0031072;GO:0051536;GO:0051082
comp28398_c0_seq3.p1	Ec-18_002725.1	hypothetical protein	NA
comp30955_c0_seq2.p1	Ec-18_002730.1	NEFA-interacting nuclear protein NIP30, N-terminal	GO:0003676;n/a
comp21592_c0_seq1.p1	Ec-18_002730.4	NEFA-interacting nuclear protein NIP30, N-terminal	GO:0003676;n/a
comp31294_c0_seq3.p1	Ec-18_002740.1	Nucleic acid-binding, OB-fold	GO:0003677;GO:0005524;GO:0006260;GO:0006270;GO:0008094
comp34086_c0_seq1.p1	Ec-18_002750.1	conserved unknown protein	n/a;n/a;n/a
comp27632_c0_seq1.p1	Ec-18_002750.4	conserved unknown protein	n/a;n/a;n/a
comp21042_c0_seq1.p1	Ec-18_002760.1	glucose-6-phosphate/phosphate translocator	n/a;n/a;n/a
comp33102_c3_seq5.p2	Ec-18_002800.1	Novel Sm-like protein with long N- and C-terminal domains.	NA
comp30245_c0_seq2.p2	Ec-18_002810.1	Ubiquinol-cytochrome c reductase iron-sulfur subunit 1, (Rieske iron-sulfur protein 1) (RISP1)	GO:0008121;GO:0055114
comp30245_c0_seq2.p1	Ec-18_002820.1	Alpha-ketoglutarate-dependent dioxygenase AlkB-like	n/a;n/a;n/a
comp30832_c0_seq3.p1	Ec-18_002830.1	START-like domain	n/a;n/a;n/a
comp32327_c0_seq3.p1	Ec-18_002860.1	Sorbitol dehydrogenase	GO:0008270;GO:0016491;GO:0055114
comp20155_c0_seq3.p1	Ec-18_002880.1	Hypothetical leucine rich repeat protein	GO:0005515
comp20505_c0_seq1.p1	Ec-18_002890.2	Ankyrin repeat	GO:0005515
comp33022_c1_seq1.p1	Ec-18_002900.1	RmlC-like jelly roll fold	n/a;n/a;n/a
comp91579_c0_seq1.p1	Ec-18_002910.1	calmodulin-binding WW domain protein	n/a;n/a;n/a
comp32705_c0_seq5.p1	Ec-18_002930.1	CRAL-TRIO domain	n/a;n/a;n/a
comp12468_c0_seq1.p1	Ec-18_002940.3	RmlC-like jelly roll fold	GO:0005506;GO:0017172;GO:0046439;GO:0055114;n/a
comp20779_c0_seq1.p1	Ec-18_002950.1	EF-hand domain pair	n/a;n/a;n/a
comp34224_c0_seq1.p1	Ec-18_002980.1	BRCT domain	GO:0005622
comp29493_c0_seq2.p1	Ec-18_002990.1	Carbohydrate kinase PfkB	n/a;n/a;n/a
comp32840_c2_seq27.p1	Ec-18_003010.1	SANT/Myb/Homeodomain-like protein	GO:0003677
comp34314_c0_seq1.p1	Ec-18_003050.1	expressed unknown protein	n/a;n/a;n/a
comp12569_c0_seq1.p1	Ec-18_003060.1	DNA-directed RNA polymerase, RBP11-like dimerisation domain	GO:0006351;GO:0046983
comp102397_c0_seq1.p1	Ec-18_003070.1	hypothetical protein	n/a;n/a;n/a
comp31349_c0_seq1.p1	Ec-18_003080.1	Nucleoside phosphatase GDA1/CD39	GO:0016787
comp69096_c0_seq1.p1	Ec-18_003110.1	hypothetical protein	n/a;n/a;n/a
comp34525_c0_seq1.p1	Ec-18_003120.1	Amino acid transporter, transmembrane	n/a;n/a;n/a
comp32847_c0_seq11.p1	Ec-18_003130.1	Hypothetical protein	n/a;n/a;n/a
comp29024_c0_seq2.p1	Ec-18_003140.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270
comp87801_c0_seq1.p2	Ec-18_003160.1	PapD-like	GO:0016020;n/a;GO:0008654;GO:0016780
comp20421_c0_seq1.p1	Ec-18_003170.3	BTB/POZ	GO:0005515
comp27447_c0_seq3.p1	Ec-18_003180.1	Conidiophore development protein HymA	GO:0005488
comp32826_c0_seq5.p1	Ec-18_003230.1	Rab-GTPase-TBC domain	GO:0005097;GO:0032313
comp32326_c0_seq50.p1	Ec-18_003250.1	Ca2+/calmodulin-dependent protein kinase kinase beta and related serine/threonine protein kinases	GO:0003824
comp33552_c0_seq1.p1	Ec-18_003270.1	Inositol 2-dehydrogenase	GO:0003824;GO:0005488;GO:0008152
comp24840_c0_seq1.p2	Ec-18_003280.1	RNA polymerase II accessory factor, Cdc73	n/a;GO:0016593;GO:0016570;GO:0006368
comp24957_c0_seq1.p1	Ec-18_003290.1	conserved unknown protein	n/a;n/a;n/a

comp35303_c0_seq1.p1	Ec-18_003300.1	LPS-induced tumour necrosis factor alpha factor	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006629: LPS-induced tumour necrosis factor alpha factor; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19561_c0_seq1.p1	Ec-18_003320.1	Glutathione S-transferase, C-terminal-like	n/a;GO:0005515	PTHR12782: ; IPR002109: Glutaredoxin; IPR004046: Glutathione S-transferase, C-terminal; IPR010987: Glutathione S-transferase, C-terminal-like; IPR004045: Glutathione S-transferase, N-terminal; IPR012336: Thioredoxin-like fold; SignalP-TM:	NA
comp34920_c0_seq1.p1	Ec-18_003330.1	Alpha-ketoglutarate-dependent dioxygenase AlkB-like	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF51197: ; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; PTHR13069: ; IPR027450: Alpha-ketoglutarate-dependent dioxygenase AlkB-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34880_c0_seq1.p1	Ec-18_003360.1	Heat shock protein 40	GO:0006457;GO:0031072;GO:0051082	PTHR24076: ; IPR008971: HSP40/DnaJ peptide-binding; IPR002939: Chaperone DnaJ, C-terminal; IPR001623: DnaJ domain; IPR018253: DnaJ domain, conserved site; G3DSA:2.60.260.20:	NA
comp24840_c0_seq1.p1	Ec-18_003370.1	Choline transporter-like	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007603: Choline transporter-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp58108_c0_seq1.p1	Ec-18_003390.1	Ankyrin repeat	GO:0005515	IPR020683: Ankyrin repeat-containing domain; Coil: ; IPR002110: Ankyrin repeat	NA
comp34393_c0_seq1.p1	Ec-18_003420.1	pyruvate dehydrogenase	GO:0003824;GO:0008152	PTHR11624: ; IPR005476: Transketolase, C-terminal; IPR009014: Transketolase, C-terminal/Pyruvate-ferredoxin oxidoreductase, domain II; IPR027110: Pyruvate dehydrogenase E1 component subunit beta; IPR029061: Thiamin diphosphate-binding fold; IPR005475: Transketolase-like, pyrimidine-binding domain	KOG0524
comp34425_c0_seq1.p1	Ec-18_003430.1	Domain of unknown function DUF4149	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR025423: Domain of unknown function DUF4149; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR23241: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29803_c0_seq2.p1	Ec-18_003460.1	MutL protein homolog 1	GO:0005524;GO:0006298;GO:0030983	PF13589: Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase; IPR011186: DNA mismatch repair protein Mlh1/HexB; IPR014762: DNA mismatch repair, conserved site; IPR003594: Histidine kinase-like ATPase, C-terminal domain; IPR013507: DNA mismatch repair protein, C-terminal; IPR002099: DNA mismatch repair protein family; IPR020568: Ribosomal protein S5 domain 2-type fold; Coil: ; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup; PTHR10073:	NA
comp24184_c0_seq1.p1	Ec-18_003480.1	Actin family	GO:0005515	IPR027667: Actin-related protein 4; G3DSA:3.30.420.40: ; G3DSA:3.90.640.10: ; IPR004000: Actin family; SSF53067:	NA
comp31434_c0_seq3.p1	Ec-18_003500.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp26714_c0_seq2.p1	Ec-18_003520.1	ATP phosphoribosyltransferase	GO:0003879	IPR018198: ATP phosphoribosyltransferase, conserved site; IPR001348: ATP phosphoribosyltransferase HisG; IPR015867: Nitrogen regulatory protein PII/ATP phosphoribosyltransferase, C-terminal; IPR020621: ATP phosphoribosyltransferase HisG, long form; IPR013820: ATP phosphoribosyltransferase, catalytic domain; IPR013115: Histidine biosynthesis HisG, C-terminal; IPR011322: Nitrogen regulatory PII-like, alpha/beta; G3DSA:3.40.190.10: ; SSF53850:	KOG2831
comp33878_c0_seq1.p1	Ec-18_003530.1	Translation initiation factor SUI1	GO:0006413;GO:0003743	PTHR12789: ; IPR001950: Translation initiation factor SUI1	NA
comp31572_c0_seq5.p1	Ec-18_003620.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30110_c1_seq30.p1	Ec-18_003630.1	Dynein regulatory complex protein 1, C-terminal	n/a;n/a;n/a	PF14772: Sperm tail; IPR029440: Dynein regulatory complex protein 1, C-terminal; Coil: ; PTHR21625:	NA
comp36180_c0_seq1.p1	Ec-18_003640.1	HORMA domain protein	GO:0007067	PTHR11842: ; IPR027097: Mitotic spindle checkpoint protein Mad2; IPR003511: DNA-binding HORMA	KOG3285
comp24815_c0_seq2.p1	Ec-18_003660.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26581_c0_seq1.p1	Ec-18_003680.1	WD40/YVTN repeat-like-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; IPR015943: WD40/YVTN repeat-like-containing domain; IPR027145: Periodic tryptophan protein 2; IPR001680: WD40 repeat	NA
comp26581_c0_seq1.p2	Ec-18_003700.1	expressed unknown protein	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp19403_c0_seq1.p1	Ec-18_003710.1	Major facilitator superfamily	GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24003: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19486_c0_seq1.p1	Ec-18_003720.1	DNA glycosylase	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp28882_c0_seq1.p1	Ec-18_003730.1	GDP dissociation inhibitor	GO:0043087	PTHR11787: ; G3DSA:3.30.519.10: ; G3DSA:3.50.50.60: ; G3DSA:1.10.405.10: ; IPR018203: GDP dissociation inhibitor; SSF51905:	NA
comp28882_c0_seq1.p2	Ec-18_003740.1	Red chlorophyll catabolite reductase	GO:0000166;GO:0004812;GO:0005524;GO:0005737;GO:0006412;GO:0006418;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009439: Red chlorophyll catabolite reductase; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp33969_c0_seq1.p1	Ec-18_003750.1	Hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29226_c0_seq2.p1	Ec-18_003760.1	expressed unknown protein	n/a;n/a;n/a	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp11789_c0_seq1.p1	Ec-18_003770.1	Taxilin family	GO:0019905	IPR026183: Taxilin family; Coil: ; SignalP-TM:	NA
comp28155_c0_seq5.p1	Ec-18_003810.1	CAAX amino terminal protease	GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003675: CAAX amino terminal protease; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp52814_c0_seq1.p1	Ec-18_003820.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0005634;GO:0000981;GO:0006355;GO:0008270	IPR001138: Zn(2)-C6 fungal-type DNA-binding domain	NA
comp16255_c0_seq1.p1	Ec-18_003830.1	PA14	GO:0006520;GO:0007154;GO:0016021	IPR001298: Filamin/ABP280 repeat; IPR014756: Immunoglobulin E-set; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000742: Epidermal growth factor-like domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF56988: ; IPR011658: PA14; IPR003644: Na-Ca exchanger/integrin-beta4; IPR013783: Immunoglobulin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE: Signal peptide region; IPR017868: Filamin/ABP280 repeat-like; IPR013032: EGF-like, conserved site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF141072: ; SignalP-noTM:	NA
comp51185_c0_seq1.p1	Ec-18_003850.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31305_c0_seq1.p1	Ec-18_003860.1	Zinc finger, RING-type	GO:0005515;GO:0008270	IPR001841: Zinc finger, RING-type; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type	NA
comp32682_c0_seq24.p1	Ec-18_003870.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29588_c0_seq4.p1	Ec-18_003880.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26745_c0_seq3.p1	Ec-18_003900.1	NUO10 homolog, NADH dehydrogenase (ubiquinone) subunit 10	GO:0055114;GO:0006120;GO:0051539;GO:0048038;GO:0008137	IPR006137: NADH:ubiquinone oxidoreductase-like, 20kDa subunit; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF56770: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006138: NADH-ubiquinone oxidoreductase, 20 Kd subunit; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11995:	KOG1687
comp29380_c0_seq2.p1	Ec-18_003910.1	NAD(+) kinase	GO:0003951;GO:0008152;GO:0006741;GO:0019674	IPR002504: NAD kinase; SIGNAL_PEPTIDE: Signal peptide region; IPR017437: ATP-NAD kinase, PpnK-type, all-beta; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR017438: Inorganic polyphosphate/ATP-NAD kinase, domain 1; IPR016064: NAD kinase/diacylglycerol kinase-like domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2178
comp32827_c0_seq11.p1	Ec-18_003920.3	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30469_c0_seq4.p1	Ec-18_003950.1	Domain of unknown function DUF4395	GO:0038032	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR025508: Domain of unknown function DUF4395; G3DSA:1.10.167.10: ; IPR016137: RGS domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12372_c0_seq1.p1	Ec-18_003960.1	D-ribose pyranase RbsD/L-fucose mutarotase FucU	GO:0016853;GO:0005996;GO:0048029	IPR007721: D-ribose pyranase RbsD/L-fucose mutarotase FucU; IPR023750: RbsD-like domain; PTHR31690:	NA
comp31117_c0_seq2.p1	Ec-18_003970.1	Putative phospholipase	NA	IPR029058: Alpha/Beta hydrolase fold; PTHR11614: ; IPR022742: Serine aminopeptidase, S33	no relat
comp34621_c0_seq1.p1	Ec-18_003980.1	Helicase	GO:0003677;GO:0016787;GO:0005524;GO:0004386;GO:0003676	IPR006935: Helicase/UvrB domain; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001650: Helicase, C-terminal; PTHR24031:	NA
comp29617_c0_seq2.p1	Ec-18_004000.1	Rhodanese Homology Domain superfamily	NA	IPR001763: Rhodanese-like domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; PTHR18838: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20343_c0_seq1.p1	Ec-18_004020.1	thioredoxin-like protein	GO:0045454;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR005746: Thioredoxin; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp34699_c0_seq1.p1	Ec-18_004030.1	Nucleophile aminohydrolases, N-terminal	GO:0051603;GO:0004298;GO:0005839;GO:0006511	IPR000426: Proteasome alpha-subunit, N-terminal domain; IPR029055: Nucleophile aminohydrolases, N-terminal; IPR001353: Proteasome, subunit alpha/beta; PTHR11599: ; IPR023332: Proteasome A-type subunit	NA
comp25535_c0_seq1.p1	Ec-18_004050.1	Protein of unknown function DUF2997	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR021375: Protein of unknown function DUF2997; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27456_c0_seq1.p1	Ec-18_004060.1	expressed unknown protein	n/a;n/a;n/a	G3DSA:3.80.10.10: ; SSF52047:	NA
comp34834_c0_seq1.p1	Ec-18_004080.1	Glucose/ribitol dehydrogenase	GO:0008152;GO:0016491	PTHR24322: ; PTHR24322:SF376: ; IPR016040: NAD(P)-binding domain; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR	NA
comp29186_c0_seq2.p1	Ec-18_004090.1	GPA3, alpha subunit of a heterotrimeric G protein	GO:0007165;GO:0004871	IPR001019: Guanine nucleotide binding protein (G-protein), alpha subunit; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR011025: G protein alpha subunit, helical insertion	NA
comp31583_c0_seq4.p1	Ec-18_004170.1	Zinc finger, RING-type	GO:0005515;GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30940_c0_seq8.p1	Ec-18_004180.1	Bromodomain	GO:0005515	SSF63748: ; G3DSA:2.30.30.160: ; IPR016177: DNA-binding domain; IPR000313: PWWP domain; Coil: ; IPR001487: Bromodomain; IPR001471: AP2/ERF domain	NA
comp20841_c0_seq2.p1	Ec-18_004190.1	Deflagellation inducible protein,13 kDa	n/a;n/a;n/a	PTHR28661:SF1: ; Coil: ; PD968187: BETA-DEFENSIN ANTIBIOTIC PRECURSOR ANTIMICROBIAL DEFENSIN BETA SIGNAL DEFENSIN BD-32 DEFB-32; PTHR28661:	NA
comp26262_c0_seq1.p1	Ec-18_004200.1	Intraflagellar transport protein 80	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; PTHR24098: ; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily	KOG1524
comp18199_c0_seq2.p1	Ec-18_004200.3	Intraflagellar transport protein 80	GO:0005515	PTHR24098:SF0: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR24098:	KOG1524
comp28132_c0_seq1.p1	Ec-18_004350.2	hypothetical protein	NA	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR001245: Serine-threonine/tyrosine-protein kinase catalytic domain; IPR011009: Protein kinase-like domain; PTHR23257: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31621_c0_seq3.p2	Ec-18_004370.1	Pectin lyase fold/virulence factor	n/a;n/a;n/a	PTHR11319:SF29: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM: ; IPR012334: Pectin lyase fold; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR011050: Pectin lyase fold/virulence factor; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11319: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006626: Parallel beta-helix repeat	NA
comp31873_c0_seq3.p1	Ec-18_004380.1	Pectin lyase fold/virulence factor	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR012334: Pectin lyase fold; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR011050: Pectin lyase fold/virulence factor; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11319: ; IPR006626: Parallel beta-helix repeat; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26800_c0_seq1.p1	Ec-18_004400.1	HNH endonuclease family protein	GO:0003676;GO:0004519	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002711: HNH endonuclease; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR003615: HNH nuclease; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28887_c0_seq2.p2	Ec-18_004430.1	Protein of unknown function DUF4591	n/a;n/a;n/a	IPR027968: Protein of unknown function DUF4591; Coil:	NA
comp28887_c0_seq2.p1	Ec-18_004440.1	Domain of unknown function DUF2439	GO:0005622;GO:0008270	IPR018838: Domain of unknown function DUF2439; IPR001876: Zinc finger, RanBP2-type	NA
comp28542_c0_seq3.p1	Ec-18_004450.1	Longin domain	GO:0006810;GO:0016192;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR010908: Longin domain; IPR001388: Synaptobrevin; SSF58038: ; PTHR21136: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011012: Longin-like domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20028_c0_seq1.p1	Ec-18_004460.1	expressed unknown protein	n/a;n/a;n/a	SignalP-TM:	NA
comp33152_c1_seq11.p1	Ec-18_004480.1	Poly(ADP-ribose) polymerase, catalytic domain	GO:0003950	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR21328: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR012317: Poly(ADP-ribose) polymerase, catalytic domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF56399:	NA
comp31975_c2_seq1.p2	Ec-18_004490.1	putative Translation Initiation Inhibitor	GO:0005351;GO:0006810;GO:0009401	IPR006175: YjgF/YER057c/UK114 family; PF14588: YjgF/chorismate_mutase-like, putative endoribonuclease; IPR013813: Endoribonuclease L-PSP/chorismate mutase-like	KOG2317
comp31975_c2_seq1.p3	Ec-18_004500.1	putative Translation Initiation Inhibitor	GO:0005351;GO:0006810;GO:0009401	IPR006175: YjgF/YER057c/UK114 family; PF14588: YjgF/chorismate_mutase-like, putative endoribonuclease; IPR013813: Endoribonuclease L-PSP/chorismate mutase-like	KOG2317
comp27198_c0_seq2.p1	Ec-18_004510.1	U4/U6-associated splicing factor PRP4	GO:0005524;GO:0006468;GO:0004672	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; IPR018189: Phosphoglucose isomerase, conserved site; Coil: ; PTHR24056:	KOG0670
comp33153_c0_seq10.p1	Ec-18_004520.1	Bromodomain	GO:0005515	PTHR22880: ; IPR018359: Bromodomain, conserved site; IPR027353: NET domain; Coil: ; IPR001487: Bromodomain	NA
comp33153_c0_seq10.p2	Ec-18_004530.1	Glutathione synthase	GO:0005524;GO:0004363;GO:0016874;GO:0006750	IPR016185: Pre-ATP-grasp domain; IPR014709: Glutathione synthase domain; SSF56059: ; IPR005615: Glutathione synthase, eukaryotic; IPR014049: Glutathione synthase, N-terminal, eukaryotic; IPR004887: Glutathione synthase, substrate-binding, eukaryotic; IPR014042: Glutathione synthase, alpha-helical, eukaryotic	KOG0021
comp33081_c0_seq12.p1	Ec-18_004540.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp31975_c2_seq1.p1	Ec-18_004550.1	Ornithine cyclodeaminase	GO:0008473;GO:0006520	IPR023401: Ornithine cyclodeaminase, N-terminal; IPR016040: NAD(P)-binding domain; PTHR13812:SF19: ; PTHR13812: ; SignalP-TM: ; IPR003462: Ornithine cyclodeaminase/mu-crystallin	NA
comp32701_c0_seq2.p1	Ec-18_004570.1	Methionine--tRNA ligase	GO:0000049	IPR012340: Nucleic acid-binding, OB-fold; IPR015413: Methionyl/Leucyl tRNA synthetase; PTHR11946: ; IPR009080: Aminoacyl-tRNA synthetase, class 1a, anticodon-binding; IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; G3DSA:2.170.220.10: ; SSF52374: ; IPR014758: Methionyl-tRNA synthetase; Coil: ; IPR002547: tRNA-binding domain	KOG0436
comp27836_c0_seq1.p1	Ec-18_004610.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp20167_c0_seq2.p1	Ec-18_004620.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28539_c0_seq3.p1	Ec-18_004630.1	200 kDa antigen p200	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PD968187: BETA-DEFENSIN ANTIBIOTIC PRECURSOR ANTIMICROBIAL DEFENSIN BETA SIGNAL DEFENSIN BD-32 DEFB-32; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp31675_c0_seq3.p1	Ec-18_004640.1	SH3 domain	GO:0005515	IPR011511: Variant SH3 domain; IPR018247: EF-Hand 1, calcium-binding site; G3DSA:2.30.30.40: ; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR022099: Protein of unknown function DUF3638; PTHR13367: ; SSF47473: ; IPR022105: Protein of unknown function DUF3645; IPR001452: SH3 domain; PF13833: EF-hand domain pair; IPR009291: Vacuolar protein sorting-associated protein 62; Coil:	NA
comp33220_c0_seq1.p1	Ec-18_004660.1	dynein heavy chain	GO:0007018;GO:0000166;GO:0017111;GO:0003777	IPR004273: Dynein heavy chain domain; PF12774: Hydrolytic ATP binding site of dynein motor region D1; IPR011704: ATPase, dynein-related, AAA domain; PF12781: ATP-binding dynein motor region D5; IPR013602: Dynein heavy chain, domain-2; IPR018522: DNA topoisomerase, type IIA, conserved site; PF12775: P-loop containing dynein motor region D3; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR013594: Dynein heavy chain, domain-1; IPR024317: Dynein heavy chain, P-loop containing D4 domain; IPR003593: AAA+ ATPase domain; IPR024743: Dynein heavy chain, coiled coil stalk; Coil: ; IPR026983: Dynein heavy chain	KOG3595
comp28930_c0_seq3.p1	Ec-18_004680.1	Mpv17/PMP22	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007248: Mpv17/PMP22; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-noTM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30940_c1_seq1.p1	Ec-18_004700.2	CRAL-TRIO domain	n/a;n/a;n/a	PTHR10174: ; IPR001251: CRAL-TRIO lipid binding domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR10174:SF130: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30940_c1_seq1.p2	Ec-18_004710.1	Protein required for ubiquinone (coenzyme Q) biosynthesis and for respiratory growth	n/a;n/a;n/a	IPR004147: UbiB domain; PTHR10566: ; IPR011009: Protein kinase-like domain	KOG1234
comp15206_c0_seq2.p1	Ec-19_000030.1	IMP dehydrogenase/GMP reductase	GO:0003824;GO:0055114;GO:0016491	IPR013785: Aldolase-type TIM barrel; IPR000644: CBS domain; SSF54631: ; SSF51412: ; IPR005990: Inosine-5'-monophosphate dehydrogenase; IPR001093: IMP dehydrogenase/GMP reductase; PTHR11911: ; IPR015875: IMP dehydrogenase / GMP reductase, conserved site	NA
comp31439_c0_seq2.p1	Ec-19_000100.1	Domain of unknown function DUF3668	n/a;n/a;n/a	PTHR21574: ; IPR022136: Domain of unknown function DUF3668; Coil:	NA
comp26144_c0_seq1.p1	Ec-19_000170.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR002885: Pentatricopeptide repeat; PTHR24015:	NA
comp30379_c0_seq4.p2	Ec-19_000180.1	Adenylylsulfate kinase	GO:0000103;GO:0005524;GO:0016301;GO:0004020;GO:0016772	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR002891: Adenylyl-sulfate kinase; PTHR11055: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20225_c0_seq3.p1	Ec-19_000190.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp31137_c0_seq3.p1	Ec-19_000220.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24755_c0_seq2.p1	Ec-19_000300.1	plastid thioredoxin M	GO:0045454	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; IPR017937: Thioredoxin, conserved site; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005746: Thioredoxin; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PR00421: Thioredoxin family signature; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28484_c0_seq1.p1	Ec-19_000320.2	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20807_c0_seq1.p1	Ec-19_000330.1	Armadillo-type fold	GO:0005488	PTHR22895: ; IPR011989: Armadillo-like helical; IPR000225: Armadillo; IPR016024: Armadillo-type fold	NA
comp28659_c0_seq1.p1	Ec-19_000340.1	NADH:flavin oxidoreductase/NADH oxidase, N-terminal	GO:0055114;GO:0010181;GO:0016491	IPR013785: Aldolase-type TIM barrel; PR00368: FAD-dependent pyridine nucleotide reductase signature; SSF51971: ; PTHR22893: ; SSF51395: ; PR00411: Pyridine nucleotide disulphide reductase class-I signature; IPR001155: NADH:flavin oxidoreductase/NADH oxidase, N-terminal; G3DSA:3.50.50.60: ; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	NA
comp30379_c0_seq4.p1	Ec-19_000370.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000073: Alpha/beta hydrolase fold-1; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR11614: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29043_c0_seq1.p1	Ec-19_000390.1	Amine oxidase carotenoid isomerase-like protein	GO:0016491;n/a	PF13450: NAD(P)-binding Rossmann-like domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10668: ; SignalP-noTM: ; G3DSA:3.50.50.60: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF51905:	NA
comp12440_c0_seq1.p1	Ec-19_000410.1	HotDog domain	n/a;n/a;n/a	PTHR12655:SF0: ; IPR029069: HotDog domain; Coil: ; PTHR12655:	NA
comp32960_c0_seq1.p1	Ec-19_000430.1	Exo-1,3-beta-glucanase, family GH5	GO:0005975	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR017853: Glycoside hydrolase superfamily; IPR001547: Glycoside hydrolase, family 5; PTHR31297: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013781: Glycoside hydrolase, catalytic domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12007_c0_seq2.p1	Ec-19_000440.1	Ribonucleoside-diphosphate reductase small chain	GO:0016491;GO:0046914;GO:0055114	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR012348: Ribonucleotide reductase-related; SignalP-noTM: ; IPR000358: Ribonucleotide reductase small subunit; IPR009078: Ferritin-like superfamily; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29227_c0_seq7.p1	Ec-19_000450.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp31627_c2_seq3.p1	Ec-19_000460.1	ATP-dependent Clp protease proteolytic subunit	GO:0004252;GO:0006508;GO:0008462	IPR029045: ClpP/crotonase-like domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR018215: ClpP, active site; IPR001907: ATP-dependent Clp protease proteolytic subunit; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023562: Clp protease proteolytic subunit /Translocation-enhancing protein TepA	KOG0840
comp20062_c0_seq1.p2	Ec-19_000470.1	THO complex subunit 7/Mft1	GO:0006397;GO:0000445	IPR008501: THO complex subunit 7/Mft1; Coil:	NA
comp20062_c0_seq1.p1	Ec-19_000510.1	PapD-like	n/a;GO:0005198;GO:0005789	IPR008962: PapD-like; IPR000535: MSP domain; IPR016763: Vesicle-associated membrane-protein-associated protein	NA
comp32362_c0_seq7.p1	Ec-19_000520.1	C2 domain	GO:0005515	SSF57889: ; IPR002219: Protein kinase C-like, phorbol ester/diacylglycerol-binding domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:3.30.60.20: ; Coil: ; IPR000008: C2 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21465_c0_seq1.p1	Ec-19_000540.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp11904_c0_seq1.p1	Ec-19_000560.1	Protein of unknown function UPF0301	n/a;n/a;n/a	IPR003774: Protein of unknown function UPF0301; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF143456: ; SignalP-noTM: ; G3DSA:3.40.1740.10: ; PTHR31984: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31863_c1_seq3.p2	Ec-19_000570.1	LysM domain	n/a;n/a;n/a	IPR018392: LysM domain	NA
comp27025_c0_seq1.p1	Ec-19_000610.1	Arf3-interacting protein 1, N-terminal domain	n/a;n/a;n/a	IPR012860: Arf3-interacting protein 1, N-terminal domain; PTHR10919: ; PF08616: Stabilization of polarity axis	NA
comp26198_c0_seq1.p2	Ec-19_000620.1	Coatomer protein complex, zeta sub-unit	GO:0006810	SIGNAL_PEPTIDE: Signal peptide region; G3DSA:3.30.450.60: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR022775: AP complex, mu/sigma subunit; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11043:SF0: ; IPR011012: Longin-like domain; PTHR11043: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG3343
comp26198_c0_seq1.p1	Ec-19_000630.1	RME1, RME-1/EHD family ATPase with a C-terminal EH domain	GO:0005509	IPR030381: Dynamin-type guanine nucleotide-binding (G) domain; IPR018247: EF-Hand 1, calcium-binding site; IPR002048: EF-hand domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR011992: EF-hand domain pair; SSF47473: ; IPR022812: Dynamin superfamily; IPR000261: EPS15 homology (EH); PTHR11216: ; PF00350: Dynamin family; PF12763: Cytoskeletal-regulatory complex EF hand	NA
comp20132_c0_seq1.p1	Ec-19_000640.1	Chaperone	GO:0006457;GO:0005524;GO:0051082	IPR017998: Chaperone tailless complex polypeptide 1 (TCP-1); IPR027410: TCP-1-like chaperonin intermediate domain; IPR027409: GroEL-like apical domain; IPR002194: Chaperonin TCP-1, conserved site; IPR002423: Chaperonin Cpn60/TCP-1 family; SSF54849: ; IPR012720: T-complex protein 1, eta subunit; IPR027413: GroEL-like equatorial domain; SSF48592:	NA
comp32514_c0_seq1.p1	Ec-19_000660.1	Domain of unknown function DUF2183	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR019236: Domain of unknown function DUF2183; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32514_c0_seq1.p8	Ec-19_000670.1	Ubiquitin-conjugating enzyme/RWD-like	GO:0019787;GO:0043687;GO:0051246	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; PTHR24067: ; SM00212: Ubiquitin-conjugating enzyme E2, catalytic domain homologues; IPR000608: Ubiquitin-conjugating enzyme E2; IPR023313: Ubiquitin-conjugating enzyme, active site; IPR027230: SUMO-conjugating enzyme Ubc9	NA
comp30974_c0_seq4.p1	Ec-19_000710.1	GroEL-like apical domain	GO:0016307;GO:0046488	IPR027409: GroEL-like apical domain; IPR027483: Phosphatidylinositol-4-phosphate 5-kinase, C-terminal; IPR016034: Phosphatidylinositol-4-phosphate 5-kinase, core, subgroup; IPR027484: Phosphatidylinositol-4-phosphate 5-kinase, N-terminal domain; IPR002423: Chaperonin Cpn60/TCP-1 family; IPR000306: FYVE zinc finger; IPR017455: Zinc finger, FYVE-related; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; SSF56104: ; IPR002498: Phosphatidylinositol-4-phosphate 5-kinase, core	NA
comp32831_c0_seq2.p1	Ec-19_000730.1	Peptide chain release factor class I/class II	GO:0006415;GO:0003747	SSF75620: ; IPR014720: Double-stranded RNA-binding domain; PTHR11075: ; IPR000352: Peptide chain release factor class I/class II	NA
comp24694_c1_seq3.p1	Ec-19_000750.1	Sirtuin family	GO:0070403	IPR003000: Sirtuin family; IPR029035: DHS-like NAD/FAD-binding domain; IPR026590: Sirtuin family, catalytic core domain; IPR026591: Sirtuin family, catalytic core small domain	NA
comp31863_c1_seq3.p1	Ec-19_000760.1	Exocyst complex, component 1/SEC3	n/a;n/a;n/a	PTHR16092: ; IPR019160: Exocyst complex, component 1/SEC3; Coil:	NA
comp26940_c0_seq4.p1	Ec-19_000780.2	Bardet-Biedl syndrome 1	GO:0005515	IPR028784: Bardet-Biedl syndrome 1 protein; IPR017986: WD40-repeat-containing domain; PTHR20870: ; IPR015943: WD40/YVTN repeat-like-containing domain; IPR032728: Bardet-Biedl syndrome 1, N-terminal	NA
comp26662_c0_seq1.p3	Ec-19_000790.1	Sm-like protein LSm6	NA	PTHR11021: ; IPR001163: LSM domain, eukaryotic/archaea-type; G3DSA:2.30.30.100: ; PTHR11021:SF2: ; IPR010920: LSM domain	NA
comp29626_c0_seq3.p1	Ec-19_000810.1	Cation-transporting P-type ATPase, N-terminal	GO:0006754;GO:0006812;GO:0015662;GO:0016020	IPR023298: P-type ATPase, transmembrane domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR008250: P-type ATPase, A domain; SSF81653: ; IPR023214: HAD-like domain; IPR004014: Cation-transporting P-type ATPase, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001757: P-type ATPase; SSF81665: ; IPR006068: Cation-transporting P-type ATPase, C-terminal; IPR018303: P-type ATPase, phosphorylation site; IPR023299: P-type ATPase, cytoplasmic domain N; PTHR24093: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11354_c0_seq1.p1	Ec-19_000840.2	trafficking protein particle complex subunit 2, putative	GO:0005622;GO:0006810;GO:0006888	IPR006722: Trafficking protein particle complex subunit 2; IPR011012: Longin-like domain; G3DSA:3.30.450.70:	NA
comp31606_c0_seq5.p2	Ec-19_000840.3	trafficking protein particle complex subunit 2, putative	GO:0005622;GO:0006810;GO:0006888	IPR027805: Transposase, Helix-turn-helix domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027806: Harbinger transposase-derived nuclease domain; PTHR23080: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR23080:SF75: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29624_c0_seq1.p1	Ec-19_000870.1	Histidine phosphatase superfamily	GO:0003993	IPR029033: Histidine phosphatase superfamily; IPR000560: Histidine phosphatase superfamily, clade-2; PTHR11567:	NA
comp32103_c0_seq40.p1	Ec-19_000890.1	Tetratricopeptide-like helical domain	GO:0005515	PF13424: Tetratricopeptide repeat; PTHR19959: ; IPR011990: Tetratricopeptide-like helical domain; Coil: ; IPR019734: Tetratricopeptide repeat	NA
comp33864_c0_seq1.p1	Ec-19_000900.1	Lysyl-tRNA Synthetase	GO:0006430;GO:0005524;GO:0005737;GO:0000166;GO:0004812;GO:0004824	IPR012340: Nucleic acid-binding, OB-fold; IPR004365: OB-fold nucleic acid binding domain, AA-tRNA synthetase-type; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR006195: Aminoacyl-tRNA synthetase, class II; SSF55681: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004364: Aminoacyl-tRNA synthetase, class II (D/K/N); IPR018149: Lysyl-tRNA synthetase, class II, C-terminal; IPR018150: Aminoacyl-tRNA synthetase, class II (D/K/N)-like; G3DSA:3.30.930.10: ; SignalP-noTM: ; IPR002313: Lysine-tRNA ligase, class II; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1885
comp16354_c0_seq1.p1	Ec-19_000910.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001594: Zinc finger, DHHC-type, palmitoyltransferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22883: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30568_c0_seq3.p1	Ec-19_000920.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR15959: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32568_c1_seq1.p1	Ec-19_000930.1	MFS family transporter: sugar	GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24003: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.1250.20: ; IPR011701: Major facilitator superfamily; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29142_c0_seq1.p1	Ec-19_000960.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0006470	IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C; Coil:	NA
comp32762_c0_seq2.p1	Ec-19_000970.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp20783_c0_seq1.p1	Ec-19_000990.1	Armadillo-type fold	GO:0005488	PTHR23316: ; IPR011989: Armadillo-like helical; IPR000225: Armadillo; IPR016024: Armadillo-type fold	NA
comp32770_c0_seq5.p1	Ec-19_001010.1	Peptidase S54, rhomboid domain	GO:0004252;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR022764: Peptidase S54, rhomboid domain; PTHR22790: ; SSF144091: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31760_c0_seq3.p2	Ec-19_001020.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp28010_c0_seq1.p1	Ec-19_001030.1	Riboflavin synthase-like beta-barrel	GO:0055114;GO:0016491	IPR017927: Ferredoxin reductase-type FAD-binding domain; IPR001094: Flavodoxin; G3DSA:2.40.30.10: ; IPR029039: Flavoprotein-like; IPR008254: Flavodoxin/nitric oxide synthase; SSF52343: ; IPR001433: Oxidoreductase FAD/NAD(P)-binding; G3DSA:3.40.50.80: ; IPR017938: Riboflavin synthase-like beta-barrel; IPR023173: NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3; IPR003097: FAD-binding, type 1; PTHR19384: ; IPR001709: Flavoprotein pyridine nucleotide cytochrome reductase	NA
comp13565_c0_seq1.p2	Ec-19_001050.1	immunophilin	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.10.50.40: ; SSF54534: ; IPR023566: Peptidyl-prolyl cis-trans isomerase, FKBP-type; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12310_c0_seq1.p1	Ec-19_001060.1	SGF29 tudor-like domain	n/a;n/a;n/a	IPR010750: SGF29 tudor-like domain; IPR024610: Inhibitor of growth protein, N-terminal; PTHR21539:	NA
comp11721_c0_seq1.p1	Ec-19_001080.1	Domain of unknown function DUF304	GO:0016491;GO:0055114	PTHR35688: ; IPR005182: Domain of unknown function DUF304	NA
comp32488_c0_seq8.p1	Ec-19_001090.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31667_c3_seq3.p1	Ec-19_001200.1	Zinc finger, FYVE/PHD-type	n/a;n/a;n/a	IPR000306: FYVE zinc finger; IPR001841: Zinc finger, RING-type; IPR017455: Zinc finger, FYVE-related; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR020683: Ankyrin repeat-containing domain; PF13920: Zinc finger, C3HC4 type (RING finger); IPR011011: Zinc finger, FYVE/PHD-type	NA
comp31311_c0_seq4.p1	Ec-19_001220.1	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0036459;GO:0006511	SSF54001: ; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase	NA
comp30825_c0_seq7.p1	Ec-19_001230.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp29989_c0_seq1.p1	Ec-19_001240.1	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR16220:SF0: ; PTHR16220: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp31667_c3_seq7.p1	Ec-19_001280.1	zinc finger protein	GO:0005515;GO:0008270;GO:0046872	IPR001841: Zinc finger, RING-type; cd00162: RING; IPR000306: FYVE zinc finger; SSF57850: ; IPR017455: Zinc finger, FYVE-related; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR020683: Ankyrin repeat-containing domain; PTHR11353:SF84: ; PF13920: Zinc finger, C3HC4 type (RING finger); PTHR11353: ; IPR011011: Zinc finger, FYVE/PHD-type	NA
comp24293_c0_seq2.p1	Ec-19_001310.1	ATP-dependent helicase, C-terminal	GO:0005634;GO:0005524;GO:0006139;GO:0008026;GO:0003676;GO:0016818	PTHR11472: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014013: Helicase, superfamily 1/2, ATP-binding domain, DinG/Rad3-type; IPR001945: Xeroderma pigmentosum group D protein; IPR006554: Helicase-like, DEXD box c2 type; IPR006555: ATP-dependent helicase, C-terminal; IPR010614: DEAD2; IPR002464: DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site; IPR013020: DNA helicase (DNA repair), Rad3 type; IPR010643: Domain of unknown function DUF1227	NA
comp31469_c0_seq4.p2	Ec-19_001330.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:1.10.510.10: ; PTHR24362: ; IPR011009: Protein kinase-like domain	NA
comp30043_c1_seq2.p1	Ec-19_001350.1	Peptidase C48, SUMO/Sentrin/Ubl1	GO:0008234;GO:0006508	PTHR12438: ; IPR003653: Peptidase C48, SUMO/Sentrin/Ubl1; SSF54001: ; Coil: ; G3DSA:3.30.310.130:	NA
comp27311_c0_seq1.p1	Ec-19_001360.1	NADP-dependent oxidoreductase domain	GO:0031177	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001395: Aldo/keto reductase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018170: Aldo/keto reductase, conserved site; IPR020471: Aldo/keto reductase subgroup; SignalP-noTM: ; IPR023210: NADP-dependent oxidoreductase domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32078_c0_seq5.p1	Ec-19_001380.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp74249_c0_seq1.p1	Ec-19_001380.2	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp10926_c0_seq2.p1	Ec-19_001390.1	conserved unknown protein	n/a;n/a;n/a	PF14892: Domain of unknown function (DUF4490)	NA
comp32652_c2_seq6.p1	Ec-19_001400.1	glutamyl-tRNA(Gln) amidotransferase, B subunit	GO:0016874;GO:0016884	IPR003789: Aspartyl/glutamyl-tRNA amidotransferase subunit B-related; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR006075: Aspartyl/Glutamyl-tRNA(Gln) amidotransferase, subunit B/E, catalytic; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR017958: Glutamyl-tRNA(Gln) amidotransferase, subunit B, conserved site; IPR004413: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, B subunit; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017959: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B/E; SignalP-noTM: ; SSF55931: ; IPR018027: Asn/Gln amidotransferase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24705_c1_seq1.p1	Ec-19_001420.1	DENN domain	GO:0004871;n/a	IPR016137: RGS domain; IPR001194: DENN domain	NA
comp34931_c0_seq1.p3	Ec-19_001440.1	conserved unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30967_c0_seq2.p1	Ec-19_001450.1	P-loop containing nucleoside triphosphate hydrolase	GO:0004601;GO:0006118;GO:0006979;GO:0020037	IPR005118: Transcription-repair-coupling factor, C-terminal domain; IPR011545: DEAD/DEAH box helicase domain; IPR003711: CarD-like/TRCF domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SSF143517: ; IPR014001: Helicase superfamily 1/2, ATP-binding domain; PTHR14025: ; IPR001650: Helicase, C-terminal	NA
comp30175_c0_seq2.p1	Ec-19_001480.2	ARC5, dynamin-related protein involved in plastid division	GO:0003924;GO:0005525	IPR030381: Dynamin-type guanine nucleotide-binding (G) domain; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001401: Dynamin, GTPase domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR022812: Dynamin superfamily; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR11566:SF78: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31722_c1_seq3.p1	Ec-19_001500.3	hypothetical protein	n/a;n/a;n/a	IPR032675: Leucine-rich repeat domain, L domain-like; Coil:	NA
comp32337_c0_seq20.p1	Ec-19_001510.1	NADP-thioredoxin reductase C, plastid protein	GO:0055114;GO:0016491	IPR005982: Thioredoxin reductase; PR00368: FAD-dependent pyridine nucleotide reductase signature; PTHR22912: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.50.50.60: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR000103: Pyridine nucleotide-disulphide oxidoreductase, class-II; SIGNAL_PEPTIDE: Signal peptide region; IPR013766: Thioredoxin domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR008255: Pyridine nucleotide-disulphide oxidoreductase, class-II, active site; SignalP-noTM: ; IPR001327: Pyridine nucleotide-disulphide oxidoreductase, NAD-binding domain; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	NA
comp24486_c0_seq6.p1	Ec-19_001560.1	MORN motif	n/a;n/a;n/a	G3DSA:2.20.110.10: ; PTHR23084: ; IPR003409: MORN motif; SSF82185:	NA
comp11742_c0_seq1.p1	Ec-19_001640.1	COX11 homolog, cytochrome c oxidase assembly protein	GO:0005507	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007533: Cytochrome c oxidase assembly protein CtaG/Cox11; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023471: Cytochrome c oxidase assembly protein CtaG/Cox11, domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2540
comp26961_c0_seq3.p1	Ec-19_001650.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp12397_c0_seq1.p1	Ec-19_001660.1	SGNH hydrolase-type esterase domain	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR026057: PC-Esterase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR012419: Cas1p 10 TM acyl transferase domain; PTHR13533: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013830: SGNH hydrolase-type esterase domain	NA
comp32260_c0_seq3.p1	Ec-19_001670.1	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28251_c0_seq1.p1	Ec-19_001690.1	Phosphoribosyl-ATP pyrophosphohydrolase-like	GO:0000105;GO:0004636	SSF141734: ; IPR002496: Phosphoribosyl-AMP cyclohydrolase domain; PTHR21256:SF2: ; PTHR21256:	NA
comp24442_c1_seq2.p1	Ec-19_001705.1	hypothetical protein	GO:0004553;GO:0005975	PTHR10963:SF50: ; PTHR10963: ; IPR013320: Concanavalin A-like lectin/glucanase domain; cd08023: GH16_laminarinase_like; IPR000757: Glycoside hydrolase family 16	NA
comp29734_c0_seq2.p1	Ec-19_001710.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR019410: Nicotinamide N-methyltransferase-like; PTHR14614:	NA
comp25099_c0_seq1.p1	Ec-19_001720.1	NUOI homolog, NADH dehydrogenase (ubiquinone) subunit	GO:0055114;GO:0051536;GO:0016491	IPR010226: NADH-quinone oxidoreductase, chain I; PTHR10849: ; G3DSA:1.10.1060.10: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF54862: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001450: 4Fe-4S binding domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017896: 4Fe-4S ferredoxin-type, iron-sulphur binding domain; IPR017900: 4Fe-4S ferredoxin, iron-sulphur binding, conserved site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG3256
comp30167_c0_seq2.p1	Ec-19_001750.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR000719: Protein kinase domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR011009: Protein kinase-like domain; PTHR24343:	NA
comp20574_c0_seq1.p1	Ec-19_001780.1	mitochondrial pyrimidine nucleotide transporter	GO:0016020;GO:0005488;GO:0006810	PTHR24089: ; IPR002067: Mitochondrial carrier protein; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier	NA
comp18018_c0_seq1.p1	Ec-19_001830.1	Alpha/beta hydrolase fold-1	GO:0008270	IPR000306: FYVE zinc finger; IPR029058: Alpha/Beta hydrolase fold; IPR017455: Zinc finger, FYVE-related; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; IPR000073: Alpha/beta hydrolase fold-1; PTHR10992:	NA
comp27412_c0_seq1.p1	Ec-19_001840.1	TRAM/LAG1/CLN8 homology domain	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006634: TRAM/LAG1/CLN8 homology domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27616_c0_seq2.p1	Ec-19_001850.1	glyceraldehyde 3-phosphate dehydrogenase	GO:0016620;GO:0055114	IPR020831: Glyceraldehyde/Erythrose phosphate dehydrogenase family; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020828: Glyceraldehyde 3-phosphate dehydrogenase, NAD(P) binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR006424: Glyceraldehyde-3-phosphate dehydrogenase, type I; SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; IPR020830: Glyceraldehyde 3-phosphate dehydrogenase, active site; SSF55347: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR020829: Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain; SignalP-noTM: ; G3DSA:3.30.360.10: ; IPR016040: NAD(P)-binding domain	KOG0657
comp32522_c1_seq1.p1	Ec-19_001860.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp28239_c0_seq1.p1	Ec-19_001900.1	Protein phosphatase methylesterase, eukaryotic	GO:0006482;GO:0052689	SSF51995: ; IPR029058: Alpha/Beta hydrolase fold; IPR000073: Alpha/beta hydrolase fold-1; Coil: ; IPR016812: Protein phosphatase methylesterase, eukaryotic	NA
comp31592_c0_seq1.p1	Ec-19_001910.1	CRAL-TRIO domain	n/a;n/a;n/a	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011074: CRAL/TRIO, N-terminal domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001251: CRAL-TRIO domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR23324:	NA
comp26694_c0_seq1.p1	Ec-19_001920.1	Fatty acid desaturase	GO:0020037	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR001199: Cytochrome b5-like heme/steroid binding domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005804: Fatty acid desaturase, type 1; SignalP-noTM: ; IPR012171: Fatty acid desaturase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR19353: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG4232
comp31863_c0_seq10.p1	Ec-19_001930.1	Glycerol-3-phosphate dehydrogenase	GO:0055114;GO:0004367;GO:0009331;GO:0006072	SSF51735: ; IPR013328: 6-phosphogluconate dehydrogenase, domain 2; IPR008927: 6-phosphogluconate dehydrogenase C-terminal domain-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR011128: Glycerol-3-phosphate dehydrogenase, NAD-dependent, N-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR006168: Glycerol-3-phosphate dehydrogenase, NAD-dependent; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; IPR006109: Glycerol-3-phosphate dehydrogenase, NAD-dependent, C-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2711
comp31863_c0_seq8.p2	Ec-19_001940.1	Thioredoxin-like fold	n/a;n/a;n/a	IPR012336: Thioredoxin-like fold	NA
comp31863_c0_seq5.p1	Ec-19_001950.1	Zinc finger, PHD-finger	GO:0005515	IPR019786: Zinc finger, PHD-type, conserved site; IPR001965: Zinc finger, PHD-type; IPR011989: Armadillo-like helical; IPR024986: Sister chromatid cohesion C-terminal domain; PTHR21704: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR016024: Armadillo-type fold; Coil: ; IPR011011: Zinc finger, FYVE/PHD-type; IPR019787: Zinc finger, PHD-finger	NA
comp31730_c0_seq6.p1	Ec-19_002030.1	Hydroxymethylglutaryl-CoA synthase	GO:0008152;GO:0003824	IPR016039: Thiolase-like; IPR013746: Hydroxymethylglutaryl-coenzyme A synthase C-terminal domain; IPR013528: Hydroxymethylglutaryl-coenzyme A synthase, N-terminal; IPR010122: Hydroxymethylglutaryl-CoA synthase, eukaryotic; IPR014030: Beta-ketoacyl synthase, N-terminal; IPR016038: Thiolase-like, subgroup; PTHR11877:	NA
comp32138_c1_seq20.p1	Ec-19_002040.1	Repressor of RNA polymerase III transcription Maf1	GO:0016480	IPR015257: Repressor of RNA polymerase III transcription Maf1	NA
comp18158_c0_seq1.p1	Ec-19_002050.2	Quinoprotein alcohol dehydrogenase-like superfamily	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily	NA
comp25372_c0_seq1.p1	Ec-19_002080.1	RNA polymerase II-associated, Paf1	n/a;GO:0016593;GO:0016570;GO:0006368	IPR007133: RNA polymerase II associated factor Paf1; Coil:	NA
comp27555_c0_seq2.p1	Ec-19_002100.1	Radical SAM, alpha/beta horseshoe	n/a;n/a;n/a	SSF102114: ; IPR023970: Methylthiotransferase/radical SAM-type protein; IPR023404: Radical SAM, alpha/beta horseshoe; IPR002792: TRAM domain	NA
comp32979_c0_seq14.p1	Ec-19_002110.1	acid phosphatase	GO:0003993	PTHR12750:SF9: ; PTHR12750: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029033: Histidine phosphatase superfamily; IPR000560: Histidine phosphatase superfamily, clade-2; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34156_c0_seq1.p1	Ec-19_002140.1	Rab1A, RAB family GTPase	GO:0016020;GO:0007165;GO:0005622;GO:0007264;GO:0005525	IPR002041: Ran GTPase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; IPR020849: Small GTPase superfamily, Ras type; IPR003579: Small GTPase superfamily, Rab type; PS51419: small GTPase Rab1 family profile.; PTHR24073:	NA
comp19747_c0_seq2.p1	Ec-19_002200.1	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp22498_c0_seq1.p1	Ec-19_002210.1	Radical SAM	GO:0003824;GO:0051536	SSF102114: ; PTHR11918:SF43: ; IPR023970: Methylthiotransferase/radical SAM-type protein; IPR020612: Methylthiotransferase, conserved site; SIGNAL_PEPTIDE: Signal peptide region; IPR013848: Methylthiotransferase, N-terminal; IPR007197: Radical SAM; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023404: Radical SAM, alpha/beta horseshoe; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27192_c1_seq4.p1	Ec-19_002220.1	AAA+ ATPase domain	GO:0005524	IPR003959: ATPase, AAA-type, core; IPR003593: AAA+ ATPase domain; IPR003960: ATPase, AAA-type, conserved site; IPR001270: ClpA/B family; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR23077:	NA
comp28754_c0_seq2.p1	Ec-19_002230.1	Fungal lipase-like domain	GO:0006629	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002921: Fungal lipase-like domain; IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR21493: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp89139_c0_seq1.p1	Ec-19_002290.1	Tubby C-terminal-like domain	n/a;n/a;n/a	PTHR16517: ; IPR025659: Tubby C-terminal-like domain; PTHR16517:SF26: ; IPR000007: Tubby, C-terminal	NA
comp32903_c0_seq6.p1	Ec-19_002310.1	hypothetical protein	n/a;n/a;n/a	IPR001478: PDZ domain	NA
comp28754_c0_seq2.p2	Ec-19_002320.1	Nicotinamide N-methyltransferase-like	GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR019410: Nicotinamide N-methyltransferase-like; PTHR14614:	NA
comp34206_c0_seq1.p1	Ec-19_002330.1	Ribosomal protein S11	GO:0003735;GO:0005840;GO:0006412	SSF53137: ; IPR001971: Ribosomal protein S11; IPR018102: Ribosomal S11, conserved site	NA
comp29901_c0_seq2.p1	Ec-19_002340.1	Putative RNA methylase domain	n/a;n/a;n/a	PTHR14911: ; IPR000241: Putative RNA methylase domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR004114: THUMP domain; SSF143437:	NA
comp29901_c0_seq2.p3	Ec-19_002350.1	Fatty acid elongase	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PS01188: ELO family signature.; IPR002076: ELO family; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3071
comp29570_c0_seq7.p1	Ec-19_002360.1	ssDNA-binding transcriptional regulator	GO:0003677;GO:0006355	PTHR13215: ; IPR009044: ssDNA-binding transcriptional regulator; IPR003173: Transcriptional coactivator p15 (PC4); Coil: ; PTHR13215:SF0:	NA
comp31591_c0_seq5.p1	Ec-19_002370.1	RNA binding motif and ELMO/CED-12 domain	GO:0005856;GO:0006909	IPR030731: ELMO domain-containing protein 3; IPR006816: Engulfment/cell motility, ELMO; PTHR12771:	NA
comp24263_c0_seq1.p5	Ec-19_002380.1	GRIM-19	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009346: GRIM-19; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24263_c0_seq1.p1	Ec-19_002390.1	Tubby, C-terminal	n/a;n/a;n/a	PTHR16517: ; IPR025659: Tubby C-terminal-like domain; PTHR16517:SF24: ; IPR000007: Tubby, C-terminal	NA
comp34105_c0_seq1.p1	Ec-19_002400.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp27789_c0_seq1.p1	Ec-19_002410.1	Protein of unknown function DUF3752	NA	Coil: ; IPR022226: Protein of unknown function DUF3752	NA
comp28957_c0_seq2.p1	Ec-19_002430.1	expressed unknown protein	GO:0003677;n/a	PTHR10641: ; IPR001005: SANT/Myb domain; cd00167: SANT; IPR009057: Homeodomain-like; PTHR10641:SF221: ; IPR017930: Myb domain	NA
comp33000_c0_seq8.p1	Ec-19_002440.1	40S ribosomal protein S17	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR001210: Ribosomal protein S17e; IPR018273: Ribosomal protein S17e, conserved site	NA
comp28661_c0_seq1.p1	Ec-19_002450.1	WD40-repeat-containing domain	GO:0005634;GO:0003676;GO:0005515	PF10433: Mono-functional DNA-alkylating methyl methanesulfonate N-term; PTHR10644: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR004871: Cleavage/polyadenylation specificity factor, A subunit, C-terminal	KOG1897
comp29066_c0_seq6.p2	Ec-19_002470.1	Integral membrane protein TerC, riboswitch-linked	GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR005496: Integral membrane protein TerC; IPR022369: Integral membrane protein TerC, riboswitch-linked; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR30238: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29066_c0_seq6.p1	Ec-19_002480.1	G protein-coupled receptor kinase G protein-coupled receptor kinase 2	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; PTHR24355: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000961: AGC-kinase, C-terminal; IPR000719: Protein kinase domain; IPR016137: RGS domain; PTHR24355:SF18: ; G3DSA:1.10.510.10:	KOG0986
comp29428_c2_seq2.p1	Ec-19_002500.1	Mef1, mitochondrial translation elongation factor EF-G	GO:0003924;GO:0005525	IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:2.40.30.10: ; IPR000795: Transcription factor, GTP-binding domain; IPR005517: Translation elongation factor EFG/EF2, domain IV; G3DSA:3.30.70.870: ; IPR005225: Small GTP-binding protein domain; IPR000640: Translation elongation factor EFG, V domain; IPR004161: Translation elongation factor EFTu/EF1A, domain 2; PTHR23115: ; IPR031157: Tr-type G domain, conserved site; IPR020568: Ribosomal protein S5 domain 2-type fold; IPR004540: Translation elongation factor EFG/EF2; PF00009: Elongation factor Tu GTP binding domain; IPR009022: Elongation factor G, III-V domain; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup; IPR009000: Translation protein, beta-barrel domain	NA
comp21715_c0_seq3.p1	Ec-19_002520.1	Protein of unknown function DUF544	n/a;n/a;n/a	IPR007518: Protein of unknown function DUF544	NA
comp21715_c0_seq3.p2	Ec-19_002530.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32730_c1_seq5.p1	Ec-19_002580.1	Glyoxalase/fosfomycin resistance/dioxygenase domain	n/a;n/a;n/a	PTHR10374: ; IPR029068: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR004360: Glyoxalase/fosfomycin resistance/dioxygenase domain	NA
comp30763_c0_seq3.p1	Ec-19_002600.1	DENN domain	n/a;n/a;n/a	SSF48452: ; SSF50729: ; IPR001194: DENN domain; IPR011990: Tetratricopeptide-like helical domain; IPR011993: Pleckstrin homology-like domain; IPR001849: Pleckstrin homology domain	NA
comp26222_c0_seq1.p1	Ec-19_002600.3	DENN domain	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain	NA
comp27741_c0_seq1.p1	Ec-19_002610.1	ADF-H/Gelsolin-like domain	GO:0005525;GO:0005874;GO:0007017	SSF55753: ; IPR007122: Villin/Gelsolin; IPR029006: ADF-H/Gelsolin-like domain	NA
comp17989_c0_seq1.p1	Ec-19_002620.1	EGF-like domain, extracellular	n/a;n/a;n/a	PTHR24035: ; SIGNAL_PEPTIDE: Signal peptide region; IPR000742: Epidermal growth factor-like domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013032: EGF-like, conserved site; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR013111: EGF-like domain, extracellular; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; G3DSA:2.170.300.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30736_c0_seq9.p2	Ec-19_002640.1	Putative subunit of the Anaphase Promoting Complex	n/a;n/a;n/a	PTHR12936: ; IPR004939: Anaphase-promoting complex, subunit 10/DOC domain; IPR016901: Anaphase-promoting complex, subunit 10; IPR008979: Galactose-binding domain-like	KOG3437
comp30736_c0_seq9.p1	Ec-19_002650.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28331_c0_seq2.p1	Ec-19_002660.1	HotDog domain	n/a;n/a;n/a	IPR006683: Thioesterase superfamily; IPR029069: HotDog domain	NA
comp27537_c0_seq3.p1	Ec-19_002680.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;GO:0008152;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR10108: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013216: Methyltransferase type 11	NA
comp27200_c0_seq2.p1	Ec-19_002690.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp35036_c0_seq1.p1	Ec-19_002700.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp27658_c0_seq1.p1	Ec-19_002710.1	TFIIH subunit Tfb4/p34	GO:0006355;GO:0006289;GO:0000439	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004600: TFIIH subunit Tfb4/p34; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp35148_c0_seq1.p1	Ec-19_002720.1	Flavine reductase	GO:0003824;GO:0005488;GO:0008152	SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR15020: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; PF13460: NADH(P)-binding; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1203
comp33952_c0_seq1.p1	Ec-19_002730.1	NUDIX hydrolase domain	GO:0016787	SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; PTHR13994: ; IPR020084: NUDIX hydrolase, conserved site; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003293: Nudix hydrolase 6-like; IPR015797: NUDIX hydrolase domain-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020476: NUDIX hydrolase; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR000086: NUDIX hydrolase domain	NA
comp31280_c0_seq6.p1	Ec-19_002740.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp31514_c0_seq3.p1	Ec-19_002750.1	Gibberellin 2-beta-dioxygenase	GO:0016491;n/a	IPR002283: Isopenicillin N synthase; IPR005123: Oxoglutarate/iron-dependent dioxygenase; SSF51197: ; IPR027443: Isopenicillin N synthase-like; PTHR10209: ; IPR026992: Non-haem dioxygenase N-terminal domain	KOG0143
comp33245_c3_seq1.p1	Ec-19_002770.1	Cation/H+ exchanger	GO:0006812;GO:0015299;GO:0016021;GO:0055085	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PTHR16254: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR16254:SF14: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006153: Cation/H+ exchanger; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26588_c0_seq2.p1	Ec-19_002790.1	Phosphorylated CTD interacting factor 1, WW domain	n/a;n/a;n/a	IPR022035: Phosphorylated CTD interacting factor 1, WW domain; PTHR21727: ; Coil:	NA
comp12448_c0_seq2.p1	Ec-19_002800.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp20179_c0_seq1.p1	Ec-19_002850.1	Plastid lipid-associated protein/fibrillin conserved domain	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; PTHR31906: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR006843: Plastid lipid-associated protein/fibrillin conserved domain	NA
comp29582_c0_seq2.p2	Ec-19_002860.1	Basic-leucine zipper domain	GO:0003700;GO:0006355;GO:0043565	NA	NA
comp22945_c0_seq3.p1	Ec-19_002870.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32970_c0_seq4.p1	Ec-19_002880.1	Mitochondrial substrate/solute carrier	GO:0005488;GO:0006810;GO:0016020	PTHR24089: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27003_c0_seq3.p1	Ec-19_002890.1	acyltransferase	NA	PTHR13906: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR004299: Membrane bound O-acyl transferase, MBOAT; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR13906:SF4: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2704
comp31280_c0_seq2.p1	Ec-19_002920.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp16260_c0_seq1.p1	Ec-19_002930.1	phosphoenolpyruvate carboxykinase (ATP)	GO:0005524;GO:0006094;GO:0004611;GO:0004612;GO:0017076	SSF53795: ; IPR015994: Phosphoenolpyruvate carboxykinase (ATP), conserved site; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR008210: Phosphoenolpyruvate carboxykinase, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001272: Phosphoenolpyruvate carboxykinase, ATP-utilising; IPR013035: Phosphoenolpyruvate carboxykinase, C-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR30031:	NA
comp20083_c0_seq3.p1	Ec-19_002950.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003677;GO:0003682;GO:0005524	cd00009: AAA; IPR011991: Winged helix-turn-helix DNA-binding domain; IPR003959: ATPase, AAA-type, core; IPR027417: P-loop containing nucleoside triphosphate hydrolase; mobidb-lite: consensus disorder prediction; G3DSA:3.40.50.300: ; IPR003593: AAA+ ATPase domain; PTHR10763:SF31: ; PTHR10763: ; G3DSA:1.10.8.60: ; cd04370: BAH; IPR001025: Bromo adjacent homology (BAH) domain	NA
comp32646_c0_seq1.p1	Ec-19_002960.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; PTHR21228: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp33922_c0_seq1.p1	Ec-19_002970.1	m-AAA protease subunit, Afg3/Yta10-like protein	GO:0004222;GO:0005524;GO:0008270;GO:0016021	PTHR23076: ; IPR003959: ATPase, AAA-type, core; IPR003960: ATPase, AAA-type, conserved site; IPR000642: Peptidase M41; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SSF140990: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005936: Peptidase, FtsH; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; G3DSA:1.10.8.60: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0731
comp34977_c0_seq1.p1	Ec-19_002980.1	conserved unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32813_c0_seq2.p1	Ec-19_003010.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp33217_c0_seq39.p1	Ec-19_003020.1	hypothetical protein	GO:0006096;GO:0051287;GO:0004365	NA	NA
comp25143_c0_seq4.p1	Ec-19_003030.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp24890_c0_seq2.p1	Ec-19_003090.1	Autophagy-related protein 9	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR007241: Autophagy-related protein 9; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29074_c1_seq1.p1	Ec-19_003100.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp35873_c0_seq1.p1	Ec-19_003110.1	conserved unknown protein	n/a;n/a;n/a	IPR023214: HAD-like domain	NA
comp28751_c0_seq1.p1	Ec-19_003130.1	Integrator complex subunit 2	GO:0032039	IPR029321: Integrator complex subunit 2	NA
comp20788_c0_seq1.p1	Ec-19_003140.1	ENTH/VHS	n/a;n/a;n/a	NA	NA
comp21318_c0_seq3.p1	Ec-27_006700.1	Mannuronan C-5-epimerase	NA	PF13229: Right handed beta helix region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012334: Pectin lyase fold; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR011050: Pectin lyase fold/virulence factor; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR006626: Parallel beta-helix repeat	NA
comp26722_c0_seq1.p1	Ec-19_003170.1	Endoplasmic reticulum oxidoreductin 1	GO:0005783;GO:0055114;GO:0016671;GO:0003756	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007266: Endoplasmic reticulum oxidoreductin 1; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF110019: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12381_c0_seq1.p1	Ec-19_003190.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33681_c0_seq1.p1	Ec-19_003200.1	TAFII28-like protein	GO:0005634;GO:0046982;GO:0006367	IPR006809: TAFII28-like protein; IPR009072: Histone-fold	NA
comp26764_c0_seq1.p1	Ec-19_003210.1	conserved unknown protein	n/a;n/a;n/a	SSF52047: ; IPR032675: Leucine-rich repeat domain, L domain-like	NA
comp24484_c0_seq1.p1	Ec-19_003220.1	Endoribonuclease YbeY	GO:0004222;GO:0006364	IPR023091: Metalloprotease catalytic domain, predicted; SSF55486: ; PTHR22881: ; IPR002036: Endoribonuclease YbeY	NA
comp32177_c2_seq1.p1	Ec-19_003230.1	Acetyl-CoA carboxylase, partial	GO:0003989;GO:0005524;GO:0006633	IPR011762: Acetyl-coenzyme A carboxyltransferase, N-terminal; IPR029045: ClpP/crotonase-like domain; PTHR18866: ; IPR000022: Carboxyl transferase; IPR011763: Acetyl-coenzyme A carboxyltransferase, C-terminal; IPR013537: Acetyl-CoA carboxylase, central domain	KOG0368
comp62519_c0_seq1.p1	Ec-19_003250.1	Malate/L-lactate dehydrogenase	GO:0008152;GO:0055114;GO:0016491	IPR003767: Malate/L-lactate dehydrogenase; G3DSA:3.30.1370.60:	NA
comp23774_c0_seq2.p1	Ec-19_003270.1	Zinc/iron permease	GO:0016020;GO:0055085;GO:0046873;GO:0030001	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003689: Zinc/iron permease; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31725_c0_seq2.p1	Ec-19_003280.1	WD40-repeat-containing domain	GO:0005515	IPR001810: F-box domain; PTHR22844: ; G3DSA:1.20.1280.50: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp32940_c0_seq17.p1	Ec-19_003290.1	Tubulin-tyrosine ligase/Tubulin polyglutamylase	GO:0006464	SSF56059: ; IPR004344: Tubulin-tyrosine ligase/Tubulin polyglutamylase; IPR027746: Probable tubulin-tyrosine ligase; PTHR12241:	NA
comp26857_c0_seq2.p1	Ec-19_003310.1	C2 domain	GO:0005515	IPR001202: WW domain; IPR000008: C2 domain; G3DSA:2.20.70.10:	NA
comp27865_c0_seq2.p1	Ec-19_003320.1	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR005135: Endonuclease/exonuclease/phosphatase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR12121: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32648_c3_seq2.p1	Ec-19_003350.3	hypothetical protein	n/a;n/a;n/a	NA	NA
comp74344_c0_seq1.p2	Ec-19_003360.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp32779_c0_seq15.p1	Ec-19_003390.2	expressed unknown protein	n/a;n/a;n/a	IPR003228: Transcription initiation factor TFIID; IPR009072: Histone-fold; Coil: ; PTHR12264:	NA
comp30338_c0_seq2.p1	Ec-19_003410.1	Ubiquitin-related domain	n/a;n/a;n/a	IPR029071: Ubiquitin-related domain; IPR018997: PUB domain; IPR006567: PUG domain; IPR021569: UBX domain containing protein TUG/UBX4; PTHR23153: ; SSF143503:	NA
comp31648_c0_seq1.p1	Ec-19_003430.2	WW domain	GO:0005515	IPR000306: FYVE zinc finger; IPR017455: Zinc finger, FYVE-related; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011989: Armadillo-like helical; IPR001202: WW domain; PTHR11353: ; IPR016024: Armadillo-type fold; IPR011011: Zinc finger, FYVE/PHD-type; G3DSA:2.20.70.10:	NA
comp24655_c0_seq1.p1	Ec-19_003440.1	Phosphatidylinositol-glycan biosynthesis class S protein	GO:0016255;GO:0042765	IPR019540: Phosphatidylinositol-glycan biosynthesis class S protein; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28357_c0_seq1.p1	Ec-19_003460.2	Cullin repeat-like-containing domain	n/a;n/a;n/a	IPR011991: Winged helix-turn-helix DNA-binding domain; G3DSA:1.20.1310.10: ; IPR016158: Cullin homology; IPR016159: Cullin repeat-like-containing domain; IPR019559: Cullin protein, neddylation domain; PTHR11932: ; IPR001373: Cullin, N-terminal; IPR016157: Cullin, conserved site; PTHR11932:SF23: ; G3DSA:4.10.1030.10:	NA
comp26495_c0_seq2.p1	Ec-19_003470.1	nitroreductase-like protein	GO:0006118;GO:0016491	IPR000415: Nitroreductase-like; SIGNAL_PEPTIDE: Signal peptide region; PTHR23026: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR029479: Nitroreductase	NA
comp33058_c0_seq2.p1	Ec-19_003500.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp30491_c0_seq4.p2	Ec-19_003510.1	ARL8, ARF-like Ras superfamily GTPase	GO:0005525	IPR024156: Small GTPase superfamily, ARF type; PTHR11711: ; IPR005225: Small GTP-binding protein domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR006687: Small GTPase superfamily, SAR1-type; IPR006689: Small GTPase superfamily, ARF/SAR type	NA
comp30491_c0_seq7.p1	Ec-19_003520.1	expressed unknown protein	n/a;n/a;n/a	PTHR21392: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005636: DTW; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31851_c1_seq1.p1	Ec-19_003530.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA

comp12806_c0_seq1.p1	Ec-19_003560.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp20789_c0_seq2.p1	Ec-19_003570.1	BCP1 family	n/a;n/a;n/a	Coil: ; IPR025602: BCP1 family	NA
comp31435_c0_seq2.p1	Ec-19_003580.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp22290_c0_seq3.p1	Ec-19_003590.2	translesion synthesis DNA polymerase eta splice variant	GO:0003684;GO:0006281	PTHR11076:SF11: ; SSF56672: ; IPR017961: DNA polymerase, Y-family, little finger domain; G3DSA:3.30.70.270: ; G3DSA:1.10.150.20: ; IPR001126: UmuC domain; PTHR11076:	NA
comp29245_c0_seq1.p1	Ec-19_003600.1	Pleckstrin homology-like domain	n/a;n/a;n/a	SSF50729: ; PR01228: Eggshell protein signature; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001849: Pleckstrin homology domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011993: Pleckstrin homology-like domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28893_c2_seq1.p1	Ec-19_003610.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; Coil: ; IPR019734: Tetratricopeptide repeat	NA
comp27585_c0_seq1.p1	Ec-19_003700.1	DEAD box helicase	n/a;n/a;n/a	PTHR13710:SF76: ; PTHR13710: ; IPR011545: DEAD/DEAH box helicase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR010666: Zinc finger, GRF-type; SSF68906: ; IPR003034: SAP domain; IPR004589: DNA helicase, ATP-dependent, RecQ type; IPR014001: Helicase superfamily 1/2, ATP-binding domain; Coil: ; IPR001650: Helicase, C-terminal	KOG0351
comp32526_c0_seq43.p2	Ec-19_003710.1	Major intrinsic protein	GO:0016020;GO:0006810;GO:0005215	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR023271: Aquaporin-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR022357: Major intrinsic protein, conserved site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000425: Major intrinsic protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29860_c0_seq2.p1	Ec-19_003720.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33866_c0_seq1.p1	Ec-19_003730.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp29158_c0_seq2.p1	Ec-19_003750.1	Ran binding domain	GO:0046907;GO:0005643	IPR000156: Ran binding domain; SSF50729: ; IPR011993: Pleckstrin homology-like domain; PTHR23138: ; IPR015007: Nuclear pore complex, NUP2/50/61	NA
comp20966_c0_seq1.p1	Ec-19_003760.1	WD40 repeat	GO:0005515	IPR015155: PLAA family ubiquitin binding, PFU; IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR020472: G-protein beta WD-40 repeat; PTHR19849: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR013535: PUL	NA
comp21105_c0_seq1.p1	Ec-19_003780.1	Ankyrin repeat	GO:0005515	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR002110: Ankyrin repeat	NA
comp31547_c0_seq1.p1	Ec-19_003790.1	Nucleolar pre-ribosomal-associated protein 1, N-terminal	GO:0005515;GO:0005524;GO:0005737;GO:0006457;GO:0044267	PTHR13500: ; IPR032436: Nucleolar pre-ribosomal-associated protein 1, C-terminal domain; IPR021714: Nucleolar pre-ribosomal-associated protein 1, N-terminal	NA
comp12876_c0_seq1.p1	Ec-19_003820.2	PDZ domain	GO:0005515	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PTHR22939: ; IPR001478: PDZ domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR008915: Peptidase M50; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22939:SF97: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31756_c2_seq3.p1	Ec-19_003830.1	Armadillo-type fold	GO:0005488	PTHR10997: ; IPR001494: Importin-beta, N-terminal domain; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold	NA
comp31435_c0_seq4.p1	Ec-19_003840.1	BRCT domain	GO:0005622	PTHR12221: ; Coil: ; IPR010613: Pescadillo; IPR001357: BRCT domain	NA
comp33808_c0_seq1.p1	Ec-19_003850.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020	PTHR24089: ; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier	NA
comp22215_c0_seq1.p1	Ec-19_003860.1	Domain of unknown function DUF399	GO:0005215;GO:0006810;GO:0016020;GO:0055085	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR007314: Domain of unknown function DUF399; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SSF159501: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31329_c0_seq3.p1	Ec-19_003950.1	putative respiratory burst oxidase homolog	GO:0055114;GO:0016491	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:2.40.30.10: ; PTHR11972: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013121: Ferric reductase, NAD binding; G3DSA:3.40.50.80: ; IPR013112: FAD-binding 8; IPR017938: Riboflavin synthase-like beta-barrel; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0039
comp34935_c0_seq1.p1	Ec-19_003980.1	Domain of unknown function DUF1995	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR018962: Domain of unknown function DUF1995; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp34877_c0_seq1.p1	Ec-19_004050.1	Monothiol glutaredoxin-related	n/a;n/a;n/a	IPR002109: Glutaredoxin; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR004480: Monothiol glutaredoxin-related; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28519_c0_seq1.p1	Ec-19_004060.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33581_c0_seq1.p1	Ec-19_004070.1	ARL1, ARF-like Ras superfamily GTPase	GO:0005525	PTHR11711: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR006687: Small GTPase superfamily, SAR1-type; IPR006689: Small GTPase superfamily, ARF/SAR type; IPR024156: Small GTPase superfamily, ARF type; IPR005225: Small GTP-binding protein domain; IPR003579: Small GTPase superfamily, Rab type; Coil:	NA
comp30137_c0_seq1.p1	Ec-19_004100.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp20398_c0_seq1.p1	Ec-19_004120.2	Poly(ADP-ribose) polymerase, catalytic domain	GO:0003950	PTHR21328:SF2: ; PTHR21328: ; IPR012317: Poly(ADP-ribose) polymerase, catalytic domain; SSF56399:	NA
comp31198_c0_seq2.p1	Ec-19_004150.1	Nitrate high affinity transporter	GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24003: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004737: Nitrate transporter; IPR011701: Major facilitator superfamily; G3DSA:1.20.1250.20: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32331_c2_seq10.p1	Ec-19_004190.1	SET domain protein	GO:0005515	NA	NA
comp27966_c0_seq2.p1	Ec-19_004220.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp30674_c0_seq2.p1	Ec-19_004230.1	Heat shock protein 40	GO:0006457;GO:0031072;GO:0051082	IPR008971: HSP40/DnaJ peptide-binding; IPR002939: Chaperone DnaJ, C-terminal; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001623: DnaJ domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR018253: DnaJ domain, conserved site; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR24076: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:2.60.260.20:	NA
comp21332_c0_seq2.p1	Ec-19_004240.1	Light harvesting complex protein	GO:0009765;GO:0016020	SIGNAL_PEPTIDE: Signal peptide region; IPR022796: Chlorophyll A-B binding protein; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023329: Chlorophyll a/b binding protein domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001344: Chlorophyll A-B binding protein, plant; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28220_c0_seq2.p2	Ec-19_004250.1	Hypothetical leucine rich repeat protein	GO:0005515	PTHR10588: ; SSF52075: ; G3DSA:3.80.10.10: ; IPR003591: Leucine-rich repeat, typical subtype; IPR001611: Leucine-rich repeat; Coil:	NA
comp21570_c0_seq2.p2	Ec-19_004270.2	Leo1-like protein	n/a;n/a;n/a	PTHR23146:SF0: ; PTHR23146: ; IPR007149: Leo1-like protein	NA
comp29298_c0_seq2.p1	Ec-19_004280.1	RME1L3, RME1-like GTPase/ATPase without a C-terminal EH domain	GO:0003924;GO:0005525	IPR030381: Dynamin-type guanine nucleotide-binding (G) domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR022812: Dynamin superfamily; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11216: ; Coil: ; PF00350: Dynamin family; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27682_c0_seq3.p1	Ec-19_004290.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PTHR24362: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	NA
comp31709_c0_seq1.p1	Ec-19_004300.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28893_c1_seq1.p2	Ec-19_004310.1	Alpha-D-phosphohexomutase, alpha/beta/alpha domain II	GO:0016868;GO:0005975	IPR016066: Alpha-D-phosphohexomutase, conserved site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR016055: Alpha-D-phosphohexomutase, alpha/beta/alpha I/II/III; PTHR22573: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005845: Alpha-D-phosphohexomutase, alpha/beta/alpha domain II; IPR005844: Alpha-D-phosphohexomutase, alpha/beta/alpha domain I; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31395_c0_seq17.p1	Ec-19_004400.1	MORN motif	n/a;n/a;n/a	IPR005113: uDENN domain; IPR001194: DENN domain; G3DSA:2.20.110.10: ; IPR005112: dDENN domain; IPR003409: MORN motif; SSF82185: ; PTHR12296: ; IPR023341: MABP domain	NA
comp19470_c0_seq1.p1	Ec-19_004410.1	Regulator of chromosome condensation, RCC1	GO:0005515	PTHR22870: ; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II; IPR000408: Regulator of chromosome condensation, RCC1; IPR013069: BTB/POZ; IPR011333: BTB/POZ fold; IPR000210: BTB/POZ-like; G3DSA:3.30.710.10:	NA
comp35220_c0_seq1.p1	Ec-19_004520.1	Electron donor (NADH / NADPH)-dependent reductase	GO:0055114;GO:0045454;GO:0016491	IPR012999: Pyridine nucleotide-disulphide oxidoreductase, class I, active site; PR00368: FAD-dependent pyridine nucleotide reductase signature; IPR004099: Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain; PTHR22912: ; PR00411: Pyridine nucleotide disulphide reductase class-I signature; IPR006338: Thioredoxin/glutathione reductase selenoprotein; IPR016156: FAD/NAD-linked reductase, dimerisation domain; IPR001327: Pyridine nucleotide-disulphide oxidoreductase, NAD-binding domain; G3DSA:3.50.50.60: ; PIRSF000350: ; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	KOG4716
comp19991_c1_seq1.p1	Ec-19_004530.2	WD40-repeat-containing domain	GO:0005515	IPR003882: Pistil-specific extensin-like protein; PTHR22847: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; IPR020472: G-protein beta WD-40 repeat	NA
comp12425_c0_seq1.p1	Ec-19_004540.1	Uncharacterised conserved protein UCP010045, transmembrane eukaryotic	GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002809: Protein of unknown function DUF106, transmembrane; IPR005568: Uncharacterised conserved protein UCP010045, transmembrane eukaryotic; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12227_c0_seq1.p1	Ec-19_004560.1	Bifunctional Aldehyde Dehydrogenase/Phosphoglucomutase	GO:0008152;GO:0055114;GO:0016868;GO:0005975;GO:0016491	IPR005843: Alpha-D-phosphohexomutase, C-terminal; IPR029510: Aldehyde dehydrogenase, glutamic acid active site; IPR016162: Aldehyde dehydrogenase N-terminal domain; IPR016055: Alpha-D-phosphohexomutase, alpha/beta/alpha I/II/III; PTHR11699: ; IPR016163: Aldehyde dehydrogenase, C-terminal; IPR005846: Alpha-D-phosphohexomutase, alpha/beta/alpha domain III; IPR016161: Aldehyde/histidinol dehydrogenase; IPR015590: Aldehyde dehydrogenase domain; IPR016160: Aldehyde dehydrogenase, cysteine active site	KOG2454
comp31220_c0_seq4.p1	Ec-19_004570.1	RGS domain	GO:0038032	IPR016137: RGS domain; IPR000950: Globin-like; G3DSA:1.10.167.10: ; PTHR22924: ; IPR007607: Protein of unknown function DUF583; IPR009050: Globin-like; IPR012292: Globin/Protoglobin	NA
comp31161_c0_seq1.p1	Ec-19_004600.4	WD40/YVTN repeat-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR32215: ; Coil: ; SSF82171:	NA
comp21134_c0_seq1.p1	Ec-19_004610.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR019410: Nicotinamide N-methyltransferase-like; PTHR14614:	NA
comp21570_c0_seq2.p1	Ec-19_004630.1	Acetyl-CoA acetyltransferase subunit, putative mitochondrial precursor Acetyl-CoA acetyltransferase,	GO:0008152;GO:0005824;GO:0016747	IPR002155: Thiolase; IPR020616: Thiolase, N-terminal; IPR020617: Thiolase, C-terminal; PTHR18919: ; IPR016039: Thiolase-like; IPR016038: Thiolase-like, subgroup; IPR020615: Thiolase, acyl-enzyme intermediate active site	KOG1392
comp28759_c0_seq2.p1	Ec-19_004640.1	Nucleotidyltransferase, predicted	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018775: Nucleotidyltransferase, predicted; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp26215_c0_seq1.p1	Ec-19_004650.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp32095_c0_seq4.p4	Ec-19_004690.2	Tetratricopeptide-like helical domain	GO:0005515	IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; Coil: ; IPR019734: Tetratricopeptide repeat	NA
comp32458_c0_seq17.p1	Ec-19_004720.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp32358_c0_seq4.p1	Ec-19_004730.1	hypothetical protein	GO:0003725;GO:0005622	IPR014720: Double-stranded RNA-binding domain; SSF54768: ; Coil:	NA
comp12433_c0_seq2.p1	Ec-19_004740.1	Phosphatidylinositol N-acetylglucosaminyltransferase subunit C	GO:0006506;GO:0017176;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR009450: Phosphatidylinositol N-acetylglucosaminyltransferase subunit C; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp47898_c0_seq1.p1	Ec-19_004760.2	Domain of unknown function DUF547	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21567_c0_seq1.p3	Ec-19_004780.1	Ria1, cytoplasmic GTPase involved in biogenesis of the 60S ribosome	n/a;n/a;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:2.40.30.10: ; IPR000795: Transcription factor, GTP-binding domain; G3DSA:3.30.70.870: ; IPR005225: Small GTP-binding protein domain; PTHR23115: ; IPR000640: Translation elongation factor EFG, V domain; IPR020568: Ribosomal protein S5 domain 2-type fold; PF00009: Elongation factor Tu GTP binding domain; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup; IPR009022: Elongation factor G, III-V domain; G3DSA:3.90.1430.10: ; IPR009000: Translation protein, beta-barrel domain	NA
comp28091_c0_seq1.p1	Ec-19_004790.1	Chromosome segregation protein Spc25	n/a;n/a;n/a	PTHR14281: ; IPR013255: Chromosome segregation protein Spc25; Coil:	NA
comp31785_c0_seq4.p1	Ec-19_004820.1	conserved C2H2 zinc finger protein	GO:0005622;GO:0008270;n/a	IPR015880: Zinc finger, C2H2-like; PTHR13182: ; IPR003604: Zinc finger, U1-type; SIGNAL_PEPTIDE: Signal peptide region; PF12756: C2H2 type zinc-finger (2 copies); SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013087: Zinc finger C2H2-type/integrase DNA-binding domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007087: Zinc finger, C2H2; IPR022755: Zinc finger, double-stranded RNA binding; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF57667:	KOG2785
comp28498_c0_seq1.p1	Ec-19_004890.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32916_c0_seq1.p1	Ec-19_004900.1	EGF-like calcium-binding domain	GO:0005509	G3DSA:2.10.25.10: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001881: EGF-like calcium-binding domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000152: EGF-type aspartate/asparagine hydroxylation site; IPR018097: EGF-like calcium-binding, conserved site; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023413: Green fluorescent protein-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32678_c0_seq7.p1	Ec-19_004920.1	Tetratricopeptide-like helical domain	GO:0005515	PF13424: Tetratricopeptide repeat; SSF48452: ; SSF57850: ; PTHR19959: ; IPR001841: Zinc finger, RING-type; IPR011990: Tetratricopeptide-like helical domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; PF13374: Tetratricopeptide repeat	NA
comp31785_c0_seq4.p2	Ec-19_004940.1	Protein of unknown function UPF0568	n/a;n/a;n/a	Coil: ; IPR019265: Protein of unknown function UPF0568	NA
comp33497_c1_seq4.p1	Ec-19_004980.1	SWAP/Surp	GO:0006396;GO:0003723;GO:0003676	IPR000061: SWAP/Surp; IPR000467: G-patch domain; Coil: ; PTHR23340:	NA
comp32002_c0_seq6.p1	Ec-19_004990.1	UDP-glucose/GDP-mannose dehydrogenase, N-terminal	GO:0016616;GO:0051287;GO:0055114	IPR001732: UDP-glucose/GDP-mannose dehydrogenase, N-terminal; IPR008927: 6-phosphogluconate dehydrogenase C-terminal domain-like; IPR013328: 6-phosphogluconate dehydrogenase, domain 2; SSF51735: ; IPR016040: NAD(P)-binding domain; IPR014026: UDP-glucose/GDP-mannose dehydrogenase, dimerisation; IPR017476: UDP-glucose/GDP-mannose dehydrogenase	NA
comp24608_c0_seq1.p1	Ec-19_005000.1	Pex19 protein	GO:0005777	IPR006708: Pex19 protein	NA
comp31847_c1_seq1.p1	Ec-19_005030.1	C2 domain	GO:0005515	IPR000008: C2 domain	NA
comp31757_c0_seq3.p1	Ec-19_005040.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp31757_c0_seq2.p1	Ec-19_005050.1	Protein of unknown function DUF3661, vacuolar transmembrane	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR022127: Protein of unknown function DUF3661, vacuolar transmembrane; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR31735: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31757_c0_seq3.p2	Ec-19_005050.2	Protein of unknown function DUF3661, vacuolar transmembrane	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR022127: Store-operated calcium entry regulator STIMATE; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR31735: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33727_c0_seq1.p1	Ec-19_005060.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp34646_c0_seq1.p1	Ec-19_005090.1	Proton-dependent oligopeptide transporter family	GO:0016020;GO:0006810;GO:0005215	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020846: Major facilitator superfamily domain; IPR018456: PTR2 family proton/oligopeptide symporter, conserved site; IPR000109: Proton-dependent oligopeptide transporter family; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11654:SF64: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32963_c1_seq18.p1	Ec-19_005080.1	Ribonuclease H-like domain	GO:0003676	IPR012337: Ribonuclease H-like domain; PTHR23272:	NA
comp31731_c0_seq1.p1	Ec-19_005100.1	SET domain protein	GO:0005515;GO:0008270	IPR001214: SET domain; G3DSA:2.170.270.10: ; IPR001965: Zinc finger, PHD-type; PF13831: PHD-finger; SSF82199: ; PF13832: PHD-zinc-finger like domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR13793: ; IPR011011: Zinc finger, FYVE/PHD-type; IPR019787: Zinc finger, PHD-finger; Coil:	NA
comp30103_c0_seq2.p1	Ec-19_005130.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp34262_c0_seq1.p1	Ec-19_005140.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33748_c0_seq1.p1	Ec-19_005150.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005634;GO:0030163;GO:0005737;GO:0016787	PTHR23073: ; IPR003593: AAA+ ATPase domain; IPR003959: ATPase, AAA-type, core; IPR003960: ATPase, AAA-type, conserved site; G3DSA:1.10.8.60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR005937: 26S proteasome subunit P45	NA
comp21456_c0_seq2.p1	Ec-19_005210.1	tropinone reductase, putative / tropine dehydrogenase, putative	GO:0008152;GO:0016491	SSF51735: ; IPR020904: Short-chain dehydrogenase/reductase, conserved site; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR24310: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013968: Polyketide synthase, ketoreductase domain	NA
comp24948_c0_seq1.p1	Ec-19_005230.1	G-patch domain	GO:0003676	SSF54928: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; IPR000467: G-patch domain; IPR003954: RNA recognition motif domain, eukaryote; PTHR13288: ; Coil:	NA
comp32764_c5_seq12.p1	Ec-19_005240.1	Sulfotransferase	GO:0008146;GO:0016021	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR005331: Sulfotransferase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30015_c0_seq1.p1	Ec-19_005250.1	Trehalose 6-phosphate synthase, family GT20 / Trehalose 6-phosphate phosphatase	GO:0003824;GO:0005992	SSF53756: ; IPR013784: Carbohydrate-binding-like fold; IPR002044: Carbohydrate binding module family 20; IPR023214: HAD-like domain; G3DSA:3.40.50.2000: ; PTHR10788:SF17: ; IPR013783: Immunoglobulin-like fold; IPR001830: Glycosyl transferase, family 20; Coil: ; PTHR10788: ; IPR003337: Trehalose-phosphatase	KOG1050
comp25092_c0_seq2.p2	Ec-19_005260.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp25092_c0_seq1.p1	Ec-19_005270.3	EamA domain	GO:0016020;GO:0016021	SSF103481: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004853: Sugar phosphate transporter domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11132: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32520_c2_seq14.p1	Ec-19_005290.1	hydroxyacyl-Coenzyme A dehydrogenase	GO:0055114;GO:0070403;GO:0006631;GO:0003857	PTHR23309: ; IPR013328: 6-phosphogluconate dehydrogenase, domain 2; SSF51735: ; IPR008927: 6-phosphogluconate dehydrogenase C-terminal domain-like; IPR016040: NAD(P)-binding domain; IPR006176: 3-hydroxyacyl-CoA dehydrogenase, NAD binding; IPR006108: 3-hydroxyacyl-CoA dehydrogenase, C-terminal; IPR022694: 3-hydroxyacyl-CoA dehydrogenase	KOG2304
comp24446_c0_seq2.p1	Ec-19_005300.1	conserved unknown protein	GO:0004190;GO:0006508	NA	NA
comp21431_c0_seq1.p1	Ec-19_005310.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24242_c0_seq2.p1	Ec-19_005320.1	Triose-phosphate transporter domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004853: Sugar phosphate transporter domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11132: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11132:SF32:	NA
comp25138_c0_seq2.p1	Ec-19_005330.1	expressed unknown protein	n/a;n/a;n/a	PTHR15157: ; PTHR15157:SF5: ; Coil:	NA
comp34284_c0_seq1.p1	Ec-19_005360.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp32933_c1_seq1.p1	Ec-19_005370.1	expressed unknown protein	GO:0005840;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR038826: 30S ribosomal protein	NA
comp21333_c0_seq1.p1	Ec-19_005380.1	conserved unknown protein	NA	IPR007991: RNA polymerase I specific transcription initiation factor RRN3; Coil:	NA
comp28156_c0_seq2.p1	Ec-19_005390.1	coproporphyrinogen oxidase (aerobic), putative chloroplast precursor	GO:0055114;GO:0006779;GO:0004109	IPR001260: Coproporphyrinogen III oxidase, aerobic; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018375: Coproporphyrinogen III oxidase, conserved site; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp14247_c0_seq1.p1	Ec-19_005440.1	Aspartyl-tRNA Synthetase	GO:0000166;GO:0004812;GO:0005524;GO:0006418	IPR004523: Aspartyl-tRNA synthetase, archaeal-type; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000738: WHEP-TRS; SignalP-TM: ; IPR006195: Aminoacyl-tRNA synthetase, class II; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004364: Aminoacyl-tRNA synthetase, class II (D/K/N); IPR009068: S15/NS1, RNA-binding; G3DSA:3.30.930.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR020719: RNA 3'-terminal phosphate cyclase-like, conserved site; IPR012340: Nucleic acid-binding, OB-fold; IPR004365: OB-fold nucleic acid binding domain, AA-tRNA synthetase-type; SIGNAL_PEPTIDE: Signal peptide region; IPR002312: Aspartyl/Asparaginyl-tRNA synthetase, class IIb; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF55681: ; IPR018150: Aminoacyl-tRNA synthetase, class II (D/K/N)-like; SignalP-noTM:	KOG0556
comp32076_c1_seq2.p1	Ec-19_005450.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0016887	IPR003439: ABC transporter-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR026082: ABC transporter A, ABCA; PF12698: ABC-2 family transporter protein; IPR017871: ABC transporter, conserved site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27468_c0_seq1.p1	Ec-20_000010.1	TRANSCRIPTION INITIATION FACTOR TFIID	NA	PTHR15137: ; SSF63737:	NA
comp21263_c0_seq1.p1	Ec-20_000050.2	STAS domain	GO:0008271;GO:0008272;GO:0016020;GO:0055085	IPR011547: SLC26A/SulP transporter domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002645: STAS domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001902: SLC26A/SulP transporter; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp22476_c0_seq1.p1	Ec-20_000060.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp12611_c1_seq6.p1	Ec-20_000070.1	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	GO:0046872;GO:0010309;GO:0005886;GO:0055114	IPR004313: Acireductone dioxygenase ARD family; IPR011051: RmlC-like cupin domain; IPR027496: 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase, eukaryotes; IPR014710: RmlC-like jelly roll fold	NA
comp12426_c1_seq2.p1	Ec-20_000080.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp19507_c0_seq1.p1	Ec-20_000110.2	Beta-lactamase-like	n/a;n/a;n/a	PTHR12553: ; IPR001279: Metallo-beta-lactamase; PTHR12553:SF7:	NA
comp27812_c0_seq1.p1	Ec-20_000120.1	putative ABC transporter Nda	GO:0005524;GO:0006355;GO:0005622;GO:0008134;GO:0016887	PTHR11384: ; IPR003439: ABC transporter-like; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:1.20.1560.10: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR025662: Sigma-54 interaction domain, ATP-binding site 1; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011527: ABC transporter type 1, transmembrane domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR017871: ABC transporter, conserved site; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; SignalP-noTM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32141_c0_seq2.p2	Ec-20_000160.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24169_c0_seq3.p1	Ec-20_000180.1	Adipose-regulatory protein, Seipin	n/a;n/a;n/a	IPR009617: Seipin family; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PTHR21212:SF0: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF81995: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR21212: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29084_c0_seq1.p1	Ec-20_000200.2	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32273_c0_seq3.p1	Ec-20_000230.1	xanthine dehydrogenase	GO:0009055;GO:0006118;GO:0055114;GO:0016491	IPR016208: Aldehyde oxidase/xanthine dehydrogenase; G3DSA:3.30.390.50: ; PTHR11908: ; IPR001041: 2Fe-2S ferredoxin-type domain; IPR002346: Molybdopterin dehydrogenase, FAD-binding; IPR014307: Xanthine dehydrogenase, small subunit; IPR012675: Beta-grasp domain; IPR002888: [2Fe-2S]-binding; IPR016167: FAD-binding, type 2, subdomain 1; IPR016166: FAD-binding, type 2; IPR005107: CO dehydrogenase flavoprotein, C-terminal; IPR006058: 2Fe-2S ferredoxin, iron-sulphur binding site; IPR016169: CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2; IPR000674: Aldehyde oxidase/xanthine dehydrogenase, a/b hammerhead; IPR008274: Aldehyde oxidase/xanthine dehydrogenase, molybdopterin binding	NA
comp23470_c0_seq1.p1	Ec-20_000240.1	Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	GO:0006457	SSF54534: ; G3DSA:3.10.50.40: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001179: Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29413_c0_seq1.p1	Ec-20_000250.1	C2 domain	GO:0005515	PTHR10774: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000008: C2 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28582_c0_seq1.p1	Ec-20_000260.1	expressed unknown protein	n/a;n/a;n/a	SSF50729: ; IPR001849: Pleckstrin homology domain	NA
comp32705_c0_seq14.p1	Ec-20_000270.1	SH3 domain	GO:0005515	IPR001452: SH3 domain; G3DSA:2.30.30.40:	NA
comp30261_c0_seq9.p1	Ec-20_000280.2	conserved unknown protein	n/a;n/a;n/a	SSF51197: ; IPR008775: Phytanoyl-CoA dioxygenase; G3DSA:2.60.120.620:	NA
comp19416_c0_seq1.p1	Ec-20_000330.1	TBP1P domain containing protein	n/a;n/a;n/a	Coil: ; IPR010776: Tat binding protein 1-interacting	KOG4603
comp27641_c0_seq2.p1	Ec-20_000370.1	conserved unknown protein	NA	NA	NA
comp24605_c0_seq1.p1	Ec-20_000380.1	Ankyrin repeat	GO:0005515	IPR020683: Ankyrin repeat-containing domain; IPR002110: Ankyrin repeat; PTHR24188:	NA
comp21048_c0_seq1.p1	Ec-20_000390.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	SSF54928: ; IPR000504: RNA recognition motif domain; PF14259: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain); IPR012677: Nucleotide-binding alpha-beta plait domain; Coil: ; PTHR23139:	NA
comp21135_c0_seq4.p1	Ec-20_000400.1	Hypothetical protein	n/a;n/a;n/a	IPR001841: Zinc finger, RING-type; Coil:	NA
comp16162_c0_seq2.p1	Ec-20_000410.1	U2 snRNP protein Rds3p	n/a;n/a;n/a	IPR005345: PHF5-like	NA
comp14199_c0_seq2.p1	Ec-20_000420.1	Plastid protein-export protein secB, putative	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp12800_c0_seq1.p1	Ec-20_000460.1	HAD-like domain	n/a;n/a;n/a	IPR023214: HAD-like domain	NA
comp30813_c0_seq3.p1	Ec-20_000470.1	Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase	GO:0016787	IPR029052: Metallo-dependent phosphatase-like; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; IPR006186: Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase; PTHR11668:	KOG0374
comp29545_c0_seq1.p1	Ec-20_000490.1	Cupin superfamily protein	n/a;n/a;n/a	NA	NA
comp12980_c0_seq1.p1	Ec-20_000510.1	Protein of unknown function DUF4602	n/a;n/a;n/a	IPR027973: Protein of unknown function DUF4602; Coil:	NA
comp30637_c0_seq1.p1	Ec-20_000520.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001650: Helicase, C-terminal; PTHR24031:	KOG0330
comp32463_c3_seq2.p1	Ec-20_000540.1	Protein kinase domain	GO:0005524;GO:0006468;GO:0004672	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR020636: Calcium/calmodulin-dependent/calcium-dependent protein kinase; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain	NA
comp30496_c0_seq1.p1	Ec-20_000560.1	Protein of unknown function DUF1757	n/a;n/a;n/a	IPR013869: Protein of unknown function DUF1757	NA
comp11758_c0_seq1.p1	Ec-20_000570.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp35000_c0_seq1.p1	Ec-20_000580.1	Winged helix-turn-helix DNA-binding domain	n/a;n/a;n/a	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR000717: Proteasome component (PCI) domain; PTHR10758:	NA
comp28166_c0_seq3.p1	Ec-20_000590.1	dynein heavy chain	GO:0007018;GO:0003777	IPR004273: Dynein heavy chain domain; PF12774: Hydrolytic ATP binding site of dynein motor region D1; IPR011704: ATPase, dynein-related, AAA domain; PF12781: ATP-binding dynein motor region D5; IPR013602: Dynein heavy chain, domain-2; PF12775: P-loop containing dynein motor region D3; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR026979: Dynein heavy chain 7, axonemal; IPR024317: Dynein heavy chain, P-loop containing D4 domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003593: AAA+ ATPase domain; IPR024743: Dynein heavy chain, coiled coil stalk; Coil: ; IPR026983: Dynein heavy chain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3595
comp29161_c0_seq5.p2	Ec-20_000600.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29161_c0_seq8.p1	Ec-20_000610.1	Conserved C2H2 zinc finger protein	n/a;GO:0005622;GO:0046872;GO:0008270	IPR015880: Zinc finger, C2H2-like; IPR003656: Zinc finger, BED-type; PTHR23215: ; IPR007087: Zinc finger, C2H2	KOG2893
comp12529_c0_seq1.p1	Ec-20_000620.1	Cleavage/polyadenylation specificity factor, A subunit, C-terminal	GO:0005634;GO:0003676	PF10433: Mono-functional DNA-alkylating methyl methanesulfonate N-term; PTHR10644: ; Coil: ; IPR004871: Cleavage/polyadenylation specificity factor, A subunit, C-terminal	NA
comp30721_c0_seq1.p1	Ec-20_000630.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31474_c1_seq11.p1	Ec-20_000640.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	PTHR24012: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; PTHR24012:SF489:	NA
comp31474_c1_seq11.p2	Ec-20_000650.1	nitrite transporter NAR1	GO:0016020;GO:0005215;GO:0006810	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR023271: Aquaporin-like; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000292: Formate/nitrite transporter; PTHR30520: ; SignalP-noTM: ; IPR024002: Formate/nitrite transporter, conserved site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31474_c1_seq12.p1	Ec-20_000660.1	endonuclease III/similar to 8-oxoguanine DNA glycosylase isoform 1b	GO:0006284	PTHR10242:SF2: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; G3DSA:3.30.310.40: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR023170: Helix-turn-helix, base-excision DNA repair, C-terminal; IPR011257: DNA glycosylase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR10242: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF55945: ; IPR003265: HhH-GPD domain; IPR012904: 8-oxoguanine DNA glycosylase, N-terminal	NA
comp12682_c0_seq1.p1	Ec-20_000670.1	CaaX prenyl protease Ste24	GO:0007186;GO:0001584;GO:0016020;GO:0004222;GO:0007601;GO:0006508;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PTHR10120: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; G3DSA:3.30.2010.10: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027057: CAAX prenyl protease 1; IPR001915: Peptidase M48; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33209_c1_seq1.p1	Ec-20_000680.1	Pleckstrin homology-like domain	n/a;n/a;n/a	SSF50729: ; IPR011993: Pleckstrin homology-like domain; PTHR22902: ; IPR001849: Pleckstrin homology domain	NA
comp33209_c1_seq3.p1	Ec-20_000690.2	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0006511;GO:0036459	IPR018200: Ubiquitin specific protease, conserved site; SSF54001: ; IPR028889: Ubiquitin specific protease domain; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase; Coil: ; PTHR24006:	NA
comp31765_c0_seq9.p3	Ec-20_000700.1	Pseudouridine synthase, RsuA/RluB/C/D/E/F	GO:0003723;GO:0001522;GO:0009451;GO:0009982	IPR020103: Pseudouridine synthase, catalytic domain; IPR006145: Pseudouridine synthase, RsuA/RluB/C/D/E/F; IPR006224: Pseudouridine synthase, RluC/RluD, conserved site; PTHR10436:	NA
comp31765_c0_seq9.p1	Ec-20_000710.1	AAA+ ATPase domain	GO:0005634;GO:0030163;GO:0005737;GO:0016787	IPR003959: ATPase, AAA-type, core; IPR003960: ATPase, AAA-type, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR005937: 26S proteasome subunit P45; PTHR23073: ; IPR003593: AAA+ ATPase domain; G3DSA:1.10.8.60: ; Coil:	NA
comp31765_c0_seq9.p2	Ec-20_000720.1	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid	GO:0003824	PTHR11774: ; IPR008930: Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid; IPR001330: Prenyltransferase/squalene oxidase; PF13249: Prenyltransferase-like	NA
comp31208_c0_seq3.p1	Ec-20_000760.1	MORN motif	n/a;n/a;n/a	G3DSA:2.20.110.10: ; PTHR23084: ; IPR003409: MORN motif; SSF82185:	NA
comp28746_c0_seq1.p1	Ec-20_000780.1	Mtg2, mitochondrial Obg/CgtA-like GTPase	GO:0000287;GO:0003924;GO:0005525	IPR006169: GTP1/OBG domain; IPR031167: OBG-type guanine nucleotide-binding (G) domain; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR11702: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR014100: GTP-binding protein Obg/CgtA; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005225: Small GTP-binding protein domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006073: GTP binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24456_c0_seq4.p1	Ec-20_000790.1	SAC3/GANP/Nin1/mts3/eIF-3 p25	n/a;n/a;n/a	PTHR12436: ; PTHR12436:SF4: ; IPR005062: SAC3/GANP/THP3	NA
comp28852_c0_seq6.p1	Ec-20_000810.1	DNA repair and recombination protein Rad51A	GO:0003677;GO:0005524;GO:0006259;GO:0003690;GO:0003697;GO:0000150;GO:0008094;GO:0000724;GO:1990426	IPR020588: DNA recombination and repair protein RecA-like, ATP-binding domain; IPR010995: DNA repair Rad51/transcription factor NusA, alpha-helical; IPR016467: DNA recombination and repair protein, RecA-like; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR011941: DNA recombination/repair protein Rad51; PF14520: Helix-hairpin-helix domain; PTHR22942: ; IPR003593: AAA+ ATPase domain; G3DSA:1.10.150.20: ; IPR020587: DNA recombination and repair protein RecA, monomer-monomer interface; IPR013632: DNA recombination and repair protein Rad51, C-terminal	KOG1433
comp28852_c0_seq2.p1	Ec-20_000820.1	DNA repair protein rad10	GO:0003684;GO:0004519;GO:0005634;GO:0006281	G3DSA:1.10.150.20: ; IPR011335: Restriction endonuclease type II-like; IPR004579: DNA repair protein rad10; PTHR12749: ; IPR010994: RuvA domain 2-like	NA
comp24749_c0_seq1.p1	Ec-20_000830.1	Mannose-6-phosphate isomerase	n/a;GO:0004476	G3DSA:1.10.441.10: ; IPR016305: Mannose-6-phosphate isomerase; IPR011051: RmlC-like cupin domain; IPR001250: Mannose-6-phosphate isomerase, type I; IPR014710: RmlC-like jelly roll fold; IPR018050: Phosphomannose isomerase, type I, conserved site	KOG2757
comp20212_c0_seq2.p1	Ec-20_000840.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp27290_c0_seq2.p1	Ec-20_000860.1	Nucleic acid-binding, OB-fold	GO:0003677;GO:0006355	IPR019844: Cold-shock conserved site; IPR012340: Nucleic acid-binding, OB-fold; PTHR12913:SF1: ; IPR001374: R3H domain; PTHR12913: ; IPR011129: Cold shock protein; Coil: ; IPR002059: Cold-shock protein, DNA-binding	NA
comp29015_c0_seq2.p1	Ec-20_000850.3	expressed unknown protein	n/a;n/a;n/a	SSF52047: ; IPR032675: Leucine-rich repeat domain, L domain-like; PTHR24006:	NA
comp27354_c1_seq2.p1	Ec-20_000890.1	Alanyl-tRNA Synthetase	GO:0003676;GO:0004813;GO:0005524;GO:0005737;GO:0006412;GO:0006419	IPR018163: Threonyl/alanyl tRNA synthetase, class II-like, putative editing domain; IPR002318: Alanine-tRNA ligase, class IIc; IPR023033: Alanine-tRNA ligase, eukaryota/bacteria; IPR018162: Alanine-tRNA ligase, class IIc, anti-codon-binding domain; PTHR11777: ; IPR018165: Alanyl-tRNA synthetase, class IIc, core domain; IPR018164: Alanyl-tRNA synthetase, class IIc, N-terminal; IPR012947: Threonyl/alanyl tRNA synthetase, SAD; SSF55681: ; G3DSA:3.30.930.10: ; Coil: ; IPR009000: Translation protein, beta-barrel domain	KOG0188
comp12235_c1_seq8.p1	Ec-20_000900.1	Pleckstrin homology domain	n/a;n/a;n/a	SSF50729: ; IPR011993: Pleckstrin homology-like domain; IPR001609: Myosin head, motor domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; PTHR13140: ; IPR001849: Pleckstrin homology domain	NA
comp27354_c0_seq1.p1	Ec-20_000910.1	CTP synthase	n/a;n/a;n/a	IPR004468: CTP synthase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR017456: CTP synthase, N-terminal; IPR017926: Glutamine amidotransferase; IPR029062: Class I glutamine amidotransferase-like	NA
comp33821_c0_seq1.p1	Ec-20_000920.1	Trigger factor, ribosome-binding, bacterial	GO:0006457;GO:0015031	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR008881: Trigger factor, ribosome-binding, bacterial; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32199_c0_seq4.p1	Ec-20_000940.1	Serine-threonine/tyrosine-protein kinase catalytic domain	GO:0004672;GO:0006468	PTHR23257: ; IPR000719: Protein kinase domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR001245: Serine-threonine/tyrosine-protein kinase catalytic domain; PTHR23257:SF446: ; IPR011009: Protein kinase-like domain	NA
comp19899_c0_seq2.p1	Ec-20_000950.1	Radical SAM	GO:0003824;GO:0051536	SSF102114: ; IPR013785: Aldolase-type TIM barrel; SIGNAL_PEPTIDE: Signal peptide region; IPR007197: Radical SAM; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR024521: Domain of unknown function DUF3641; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR11228: ; IPR026351: Radical SAM/Cys-rich domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32025_c0_seq6.p2	Ec-20_000990.1	putative kinesin	n/a;n/a;n/a	Coil:	NA
comp29046_c0_seq1.p1	Ec-20_001020.2	Sulfatase-modifying factor 2 precursor	GO:0005488	PTHR23150:SF23: ; IPR005532: Sulfatase-modifying factor enzyme; IPR016187: C-type lectin fold; PTHR23150:	NA
comp31820_c0_seq1.p1	Ec-20_001030.1	NADH dehydrogenase (ubiquinone)	n/a;n/a;n/a	PTHR12964:	KOG3426
comp20828_c0_seq1.p1	Ec-20_001040.1	CAP domain	n/a;n/a;n/a	PTHR15654: ; Coil: ; IPR025254: Domain of unknown function DUF4201; IPR014044: CAP domain	NA
comp20990_c0_seq1.p1	Ec-20_001080.2	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp12789_c0_seq1.p1	Ec-20_001090.1	Protein of unknown function DUF1754, eukaryotic	n/a;n/a;n/a	IPR013865: Protein of unknown function DUF1754, eukaryotic	NA
comp34527_c0_seq1.p1	Ec-20_001100.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR12791: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000727: Target SNARE coiled-coil domain; G3DSA:1.20.5.110: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF58038: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3385
comp26979_c0_seq1.p1	Ec-20_001110.1	Serine/threonine-protein kinase SRPK1, putative	GO:0006468;GO:0004674;GO:0004672	PTHR24055: ; IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	NA
comp10927_c0_seq1.p1	Ec-20_001120.1	myosin heavy chain, putative	n/a;n/a;n/a	IPR016030: Adenosylcobalamin biosynthesis, ATP:cob(I)alamin adenosyltransferase-like; Coil:	NA
comp30518_c0_seq2.p1	Ec-20_001130.1	conserved unknown protein	n/a;n/a;n/a	PTHR31199: ; Coil:	NA
comp31387_c0_seq14.p1	Ec-20_001140.1	carnitine/acylcarnitine carrier protein	GO:0005215;GO:0005743;GO:0006810;GO:0055085	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR24089: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0758
comp31895_c2_seq2.p2	Ec-20_001170.1	expressed unknown protein	GO:0003677;n/a	NA	NA
comp33157_c2_seq1.p1	Ec-20_001180.1	MRG domain	n/a;n/a;n/a	Coil: ; IPR026541: MRG domain	NA
comp32031_c1_seq3.p1	Ec-20_001190.1	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	GO:0005215;GO:0005576;GO:0006810	IPR000408: Regulator of chromosome condensation, RCC1; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR006970: PT repeat; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR22870: ; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22870:SF201: ; PF13540: Regulator of chromosome condensation (RCC1) repeat; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29880_c0_seq2.p2	Ec-20_001210.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29880_c0_seq6.p1	Ec-20_001220.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12365_c0_seq1.p1	Ec-20_001250.1	GTR2, Ras superfamily GTPase	GO:0005525;GO:0005634;GO:0005737	IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR11259:SF2: ; IPR006762: Gtr1/RagA G protein	NA
comp33117_c3_seq2.p1	Ec-20_001270.1	conserved unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF101447: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp22711_c0_seq2.p1	Ec-20_001280.1	Aldehyde Dehydrogenase	GO:0008152;GO:0016491;GO:0055114	IPR016161: Aldehyde/histidinol dehydrogenase; IPR015590: Aldehyde dehydrogenase domain; IPR016162: Aldehyde dehydrogenase N-terminal domain; IPR016160: Aldehyde dehydrogenase, cysteine active site; PTHR11699: ; IPR016163: Aldehyde dehydrogenase, C-terminal; PTHR11699:SF148:	KOG2451
comp34728_c0_seq1.p1	Ec-20_001290.1	EsV-1-7 domain protein	NA	NA	NA
comp32271_c0_seq1.p1	Ec-20_001300.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp26206_c0_seq1.p1	Ec-20_001320.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29459_c0_seq3.p1	Ec-20_001350.1	MORN motif precursor	n/a;n/a;n/a	G3DSA:2.20.110.10: ; PTHR23084: ; IPR003409: MORN motif; SSF82185:	NA
comp28123_c0_seq2.p1	Ec-20_001360.1	Mitochondrial transcription termination factor	GO:0006355;GO:0003690;GO:0005739	Coil: ; IPR003690: Mitochondrial transcription termination factor; PTHR13068:	NA
comp25871_c0_seq1.p1	Ec-20_001370.4	Peptidase M16, C-terminal domain	GO:0003824;GO:0046872	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR007863: Peptidase M16, C-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011765: Peptidase M16, N-terminal; IPR011249: Metalloenzyme, LuxS/M16 peptidase-like; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001431: Peptidase M16, zinc-binding site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11851: ; PTHR11851:SF151: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31469_c0_seq17.p1	Ec-20_001390.1	branched chain amino acid aminotransferase	GO:0003824;GO:0004084;GO:0008152;GO:0009081	IPR001544: Aminotransferase, class IV; IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:3.30.470.10: ; G3DSA:3.20.10.10:	KOG0975
comp31388_c0_seq2.p1	Ec-20_001420.1	Rab2B, RAB family GTPase	GO:0016020;GO:0007165;GO:0007264;GO:0005525;GO:0015031	IPR002041: Ran GTPase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; IPR003579: Small GTPase superfamily, Rab type; IPR020849: Small GTPase superfamily, Ras type; PS51419: small GTPase Rab1 family profile.; PTHR24073:	NA
comp32495_c1_seq2.p3	Ec-20_001430.1	Uncharacterised conserved protein UCP014543	n/a;n/a;n/a	IPR016621: Uncharacterised conserved protein UCP014543	NA
comp32495_c1_seq2.p1	Ec-20_001440.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp31695_c0_seq7.p1	Ec-20_001460.1	Regulator of chromosome condensation, RCC1	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR22870: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II; IPR000408: Regulator of chromosome condensation, RCC1; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF13540: Regulator of chromosome condensation (RCC1) repeat; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29536_c0_seq5.p1	Ec-20_001490.1	Kae1/YgjD family	GO:0004222;GO:0006508;n/a	IPR017860: Peptidase M22, conserved site; SIGNAL_PEPTIDE: Signal peptide region; PTHR11735: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR022450: tRNA N6-adenosine threonylcarbamoyltransferase, TsaD; IPR000905: Gcp-like domain; IPR017861: Kae1/TsaD family; SSF53067: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.30.420.40: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27072_c0_seq2.p2	Ec-20_001500.1	Cyclin-like	n/a;GO:0019901;GO:0000079	IPR013763: Cyclin-like; PTHR15615: ; IPR013922: Cyclin PHO80-like	NA
comp31624_c2_seq5.p1	Ec-20_001520.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp44611_c0_seq1.p1	Ec-20_001540.1	Protein kinase domain containing protein	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil: ; PTHR24056:	NA
comp32145_c4_seq1.p1	Ec-20_001560.1	SANT/Myb domain	GO:0003682	PTHR10641: ; IPR001005: SANT/Myb domain; IPR009057: Homeodomain-like; Coil: ; IPR017930: Myb domain; IPR017877: Myb-like domain	NA
comp14876_c0_seq1.p1	Ec-20_001590.2	Ribonuclease CAF1	GO:0005634	PTHR10797:SF0: ; IPR006941: Ribonuclease CAF1; PTHR10797: ; IPR012337: Ribonuclease H-like domain	NA
comp30030_c0_seq2.p1	Ec-20_001610.1	ABC transporter family protein	GO:0005524;GO:0016887	IPR003593: AAA+ ATPase domain; IPR003439: ABC transporter-like; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR12847:	NA
comp30030_c0_seq1.p1	Ec-20_001620.1	Protein of unknown function DUF819	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR008537: Protein of unknown function DUF819; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20531_c0_seq1.p1	Ec-20_001630.1	Aspartic peptidase domain	GO:0004190;GO:0006508	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR021109: Aspartic peptidase domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp46195_c0_seq1.p1	Ec-20_001660.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp33644_c0_seq1.p1	Ec-20_001680.1	Protein of unknown function DUF2419	n/a;n/a;n/a	IPR019438: Protein of unknown function DUF2419	NA
comp31417_c0_seq8.p1	Ec-20_001690.1	HAD-like domain	GO:0005524;GO:0006754;GO:0015662;GO:0016020;GO:0016021;GO:0030001	IPR006121: Heavy metal-associated domain, HMA; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023299: P-type ATPase, cytoplasmic domain N; IPR008250: P-type ATPase, A domain; PTHR24093: ; SSF81653: ; IPR023214: HAD-like domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:3.30.70.100: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027256: P-type ATPase, subfamily IB; IPR001757: P-type ATPase; SSF81665: ; IPR018303: P-type ATPase, phosphorylation site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33209_c2_seq6.p1	Ec-20_001700.1	Sulfotransferase	GO:0008146;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018011: Carbohydrate sulfotransferase-related; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR005331: Sulfotransferase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	NA
comp26852_c1_seq2.p1	Ec-20_001720.1	Indole 2,3-Dioxygenase	GO:0020037	IPR000898: Indoleamine 2,3-dioxygenase; SSF140959:	NA
comp24163_c0_seq2.p1	Ec-20_001730.1	Mitotic checkpoint protein	n/a;GO:0007094	SSF75704: ; IPR008672: Spindle assembly checkpoint component Mad1; Coil:	NA
comp34779_c0_seq1.p1	Ec-20_001740.1	CBF1-interacting co-repressor CIR, N-terminal domain	GO:0003676;GO:0008270;n/a	PTHR24016: ; IPR019339: CBF1-interacting co-repressor CIR, N-terminal domain; Coil:	NA
comp25284_c0_seq1.p1	Ec-20_001750.2	T-complex 11	n/a;n/a;n/a	IPR008862: T-complex 11; PTHR12832:SF11:	NA
comp29362_c0_seq1.p1	Ec-20_001760.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0006470	IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C	NA
comp20475_c0_seq2.p1	Ec-20_001780.1	similar polyubiquitin	GO:0006464;GO:0005515	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR019956: Ubiquitin; PTHR10666: ; G3DSA:3.10.20.90: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029071: Ubiquitin-related domain; SignalP-noTM: ; IPR000626: Ubiquitin-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31651_c0_seq5.p3	Ec-20_001790.1	RAC, RHO family GTPase	GO:0016020;GO:0007165;GO:0007264;GO:0005525	IPR002041: Ran GTPase; PTHR24072: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR005225: Small GTP-binding protein domain; IPR001806: Small GTPase superfamily; IPR003579: Small GTPase superfamily, Rab type; IPR020849: Small GTPase superfamily, Ras type	NA
comp31651_c0_seq3.p1	Ec-20_001800.1	Isopenicillin N synthase-like	n/a;n/a;n/a	PTHR12366: ; IPR007803: Arginine/Asparagine/Proline hydroxylase; SSF51197: ; IPR027443: Isopenicillin N synthase-like	NA
comp27228_c0_seq1.p1	Ec-20_001810.1	Protein of unknown function DUF1365	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR010775: Protein of unknown function DUF1365; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp22014_c0_seq1.p2	Ec-20_001820.1	EF-hand domain pair	n/a;n/a;n/a	IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; Coil: ; SSF47473: ; IPR004018: RPEL repeat	NA
comp30077_c1_seq4.p1	Ec-20_001820.2	EF-hand domain pair	n/a;n/a;n/a	IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; Coil: ; IPR004018: RPEL repeat	NA
comp24982_c0_seq1.p1	Ec-20_001840.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29206_c0_seq2.p1	Ec-20_001900.1	Ribosomal L11 methyltransferase, PrmA	GO:0005737;GO:0006479;GO:0008276	PF06325: Ribosomal protein L11 methyltransferase (PrmA); IPR011990: Tetratricopeptide-like helical domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; G3DSA:2.70.160.11: ; IPR025799: Protein arginine N-methyltransferase; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; PTHR11006:SF60:	NA
comp29277_c1_seq1.p1	Ec-20_001920.1	Ankyrin repeat domain-containing protein 13	n/a;n/a;n/a	IPR020683: Ankyrin repeat-containing domain; IPR021832: Ankyrin repeat domain-containing protein 13; IPR002110: Ankyrin repeat	NA
comp29277_c0_seq1.p1	Ec-20_001920.2	Ankyrin repeat domain-containing protein 13	n/a;n/a;n/a	NA	NA
comp26888_c0_seq1.p1	Ec-20_001950.1	Peptidase M24, structural domain	GO:0004177;GO:0004239;GO:0006508;GO:0008235	PTHR10804:SF82: ; IPR000994: Peptidase M24; PTHR10804: ; IPR002467: Peptidase M24A, methionine aminopeptidase, subfamily 1; IPR001714: Peptidase M24, methionine aminopeptidase	NA
comp31526_c1_seq2.p1	Ec-20_001940.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp20011_c0_seq2.p1	Ec-20_001950.1	putative Glutathione S-transferase	n/a;n/a;n/a	NA	NA
comp20011_c0_seq1.p1	Ec-20_001960.1	Glutathione S-transferase	GO:0005515	NA	NA
comp26806_c0_seq1.p1	Ec-20_001970.1	Regulator of chromosome condensation, RCC1	n/a;n/a;n/a	PTHR22870: ; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II; IPR028641: Protein RCC2; IPR000408: Regulator of chromosome condensation, RCC1; Coil:	NA
comp27076_c0_seq1.p1	Ec-20_001990.1	Ribosomal protein L7/L12, C-terminal/adaptor protein ClpS-like	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; IPR014719: Ribosomal protein L7/L12, C-terminal/adaptor protein ClpS-like; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003769: Adaptor protein ClpS, core; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25607_c0_seq2.p1	Ec-20_002000.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp27076_c0_seq1.p2	Ec-20_002010.1	Endoribonuclease L-PSP/chorismate mutase-like	n/a;n/a;n/a	IPR006175: YjgF/YER057c/UK114 family; IPR006785: Peroxisome membrane anchor protein Pex14p, N-terminal; IPR013813: Endoribonuclease L-PSP/chorismate mutase-like	NA
comp24903_c0_seq1.p1	Ec-20_002020.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32784_c0_seq1.p1	Ec-20_002030.1	hypothetical protein	n/a;GO:0005515	Coil: ; IPR000048: IQ motif, EF-hand binding site	NA
comp20441_c0_seq1.p1	Ec-20_002040.1	haloacid dehalogenase-like hydrolase	GO:0003824;GO:0008152	PTHR12725: ; IPR023214: HAD-like domain	NA
comp30705_c0_seq2.p1	Ec-20_002060.1	selenoprotein O homolog, but not a selenoprotein itself	NA	IPR003846: Uncharacterised protein family UPF0061; PTHR12153:	NA
comp31022_c0_seq2.p1	Ec-20_002070.1	hypothetical protein	GO:0004252;GO:0004289;GO:0006508	Coil:	NA
comp19796_c0_seq1.p1	Ec-20_002080.1	Serine/threonine protein kinase	GO:0004672;GO:0005524;GO:0006468	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; Coil: ; PTHR24361: ; IPR011009: Protein kinase-like domain	KOG0201
comp30580_c0_seq2.p1	Ec-20_002090.2	oligopeptidase A	GO:0004222;GO:0006508;GO:0008237;GO:0008270	PTHR11804:SF49: ; PTHR11804: ; IPR024077: Neurolysin/Thimet oligopeptidase, domain 2; IPR001567: Peptidase M3A/M3B; IPR024079: Metallopeptidase, catalytic domain; SSF55486: ; Coil:	NA
comp27557_c1_seq1.p1	Ec-20_002110.2	WD40 repeat	GO:0005515	IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR22838: ; PTHR22838:SF0:	NA
comp12939_c0_seq2.p1	Ec-20_002120.1	chp-1 / RAR1 homologue	n/a;n/a;n/a	PTHR12621: ; IPR007051: Cysteine/histidine-rich domain	KOG1667
comp27337_c0_seq2.p1	Ec-20_002130.1	NAD(P)-binding domain	GO:0006608;GO:0016564	SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; PTHR14194: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PF13460: NAD(P)H-binding	NA
comp29592_c0_seq4.p1	Ec-20_002140.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	GO:0006810;GO:0016192;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR010908: Longin domain; IPR001388: Synaptobrevin; SSF58038: ; SignalP-TM: ; PTHR21136: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR011012: Longin-like domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0862
comp27391_c0_seq1.p1	Ec-20_002150.1	Snu114, GTPase of the U5 snRNP particle	n/a;n/a;n/a	IPR000795: Transcription factor, GTP-binding domain; G3DSA:2.40.30.10: ; IPR005517: Translation elongation factor EFG/EF2, domain IV; IPR005225: Small GTP-binding protein domain; IPR004161: Translation elongation factor EFTu/EF1A, domain 2; IPR020568: Ribosomal protein S5 domain 2-type fold; PF00009: Elongation factor Tu GTP binding domain; G3DSA:3.90.1430.10: ; IPR009000: Translation protein, beta-barrel domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR031950: 116 kDa U5 small nuclear ribonucleoprotein component, N-terminal; G3DSA:3.30.70.870: ; IPR000640: Translation elongation factor EFG, V domain; PTHR23115: ; PTHR23115:SF5: ; IPR009022: Elongation factor G, III-V domain; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup	NA
comp31997_c0_seq1.p1	Ec-20_002160.1	Presenilin/signal peptide peptidase	GO:0004190;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR006639: Presenilin/signal peptide peptidase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR007369: Peptidase A22B, signal peptide peptidase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31752_c1_seq16.p1	Ec-20_002170.1	Thioredoxin-like fold	n/a;n/a;n/a	PTHR15871: ; IPR012336: Thioredoxin-like fold	NA
comp29531_c0_seq1.p1	Ec-20_002180.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	SSF54928: ; PTHR24012: ; IPR000504: RNA recognition motif domain; PF14259: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain); IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp42335_c0_seq1.p1	Ec-20_002190.1	Beta-adaptin appendage, C-terminal subdomain	GO:0030131;GO:0016192;GO:0006886	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015151: Beta-adaptin appendage, C-terminal subdomain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30580_c0_seq2.p2	Ec-20_002200.3	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp19969_c0_seq1.p1	Ec-20_002230.1	TCP-1-like chaperonin intermediate domain	GO:0006457;GO:0005524;GO:0051082	IPR017998: Chaperone tailless complex polypeptide 1 (TCP-1); IPR027410: TCP-1-like chaperonin intermediate domain; IPR027409: GroEL-like apical domain; IPR002194: Chaperonin TCP-1, conserved site; IPR002423: Chaperonin Cpn60/TCP-1 family; IPR012716: T-complex protein 1, beta subunit; SSF54849: ; IPR027413: GroEL-like equatorial domain; SSF48592: ; Coil:	NA
comp31934_c0_seq1.p1	Ec-20_002250.1	Carotenoid oxygenase	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR004294: Carotenoid oxygenase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30717_c0_seq7.p1	Ec-20_002280.1	Protein-tyrosine phosphatase-like	GO:0005515	IPR029021: Protein-tyrosine phosphatase-like; IPR016130: Protein-tyrosine phosphatase, active site; IPR030564: Myotubularin family; IPR010569: Myotubularin-like phosphatase domain; IPR000008: C2 domain	NA
comp30494_c1_seq1.p1	Ec-20_002290.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp28017_c0_seq1.p1	Ec-20_002310.1	Soluble NSF Attachment Protein (SNAP) Receptor (SNARE)	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR21230: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:1.20.5.110: ; SSF58038: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25097_c0_seq2.p1	Ec-20_002320.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28104_c1_seq1.p1	Ec-20_002330.1	CAP Gly-rich domain	n/a;GO:0019970;GO:0045502;GO:0005869	IPR000938: CAP Gly-rich domain; Coil: ; IPR027663: Dynactin subunit 1; PTHR18916:	NA
comp12613_c0_seq1.p1	Ec-20_002340.1	Mitochondrial carrier protein, putative	GO:0016020;GO:0005468;GO:0006810	PTHR24089: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023395: Mitochondrial carrier domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR018108: Mitochondrial substrate/solute carrier	NA
comp33018_c0_seq1.p1	Ec-20_002350.1	Tubulin/FtsZ, 2-layer sandwich domain	GO:0003924;GO:0005525;GO:0006184;GO:0043234;GO:0051258	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000158: Cell division protein FtsZ; PTHR30314: ; IPR003008: Tubulin/FtsZ, GTPase domain; IPR008280: Tubulin/FtsZ, C-terminal; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR024757: Cell division protein FtsZ, C-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR30314:SF3: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR018316: Tubulin/FtsZ, 2-layer sandwich domain	NA
comp31905_c0_seq4.p1	Ec-20_002360.1	expressed unknown protein	GO:0006801;GO:0046872	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27523_c0_seq1.p1	Ec-20_002410.2	mitogen-activated protein kinase	GO:0004672;GO:0005524;GO:0006468	PTHR24055: ; IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR001849: Pleckstrin homology domain; PTHR24055:SF10: ; IPR003527: Mitogen-activated protein (MAP) kinase, conserved site; IPR000719: Protein kinase domain; IPR011993: PH domain-like; G3DSA:1.10.510.10:	NA
comp31347_c0_seq1.p1	Ec-20_002420.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp31347_c0_seq9.p1	Ec-20_002430.1	Bromodomain	GO:0005515	PTHR22880: ; IPR027353: NET domain; IPR001487: Bromodomain	NA
comp30045_c0_seq3.p1	Ec-20_002440.1	RuvA domain 2-like	GO:0003677;GO:0006281;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PF12836: Helix-hairpin-helix motif; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.10.150.280: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR010994: RuvA domain 2-like	NA
comp25249_c0_seq1.p1	Ec-20_002450.1	Eukaryotic translation initiation factor 3 subunit J	GO:0005737;GO:0003743;GO:0005852	IPR013906: Eukaryotic translation initiation factor 3 subunit J; Coil:	NA
comp21589_c0_seq1.p1	Ec-20_002460.1	SET domain protein	GO:0005515	NA	NA
comp24652_c0_seq1.p1	Ec-20_002470.1	Histidine phosphatase superfamily, clade-2	GO:0003993	IPR029033: Histidine phosphatase superfamily; IPR000560: Histidine phosphatase superfamily, clade-2; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31972_c0_seq1.p2	Ec-20_002490.1	Selenoprotein SelK/SelG	n/a;n/a;n/a	PTHR16875: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR024491: Selenoprotein SelK/SelG; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31938_c0_seq5.p1	Ec-20_002520.1	acetyl-CoA carboxylase	GO:0003824;GO:0005909;GO:0004075;GO:0005524;GO:0006633;GO:0016874;GO:0046872	PTHR18866:SF6: ; IPR029045: ClpP/crotonase-like domain; IPR000022: Carboxyl transferase; IPR005481: Biotin carboxylase-like, N-terminal domain; IPR016185: Pre-ATP-grasp domain; IPR005482: Biotin carboxylase, C-terminal; IPR011761: ATP-grasp fold; PTHR18866: ; IPR005479: Carbamoyl phosphate synthetase large subunit-like, ATP-binding domain; SSF56059: ; IPR013815: ATP-grasp fold, subdomain 1; IPR013537: Acetyl-CoA carboxylase, central domain; IPR001882: Biotin-binding site; IPR011816: ATP-grasp fold, subdomain 2; IPR011763: Acetyl-coenzyme A carboxyltransferase, C-terminal; IPR011054: Rudiment single hybrid motif	KOG0368
comp21543_c0_seq1.p1	Ec-20_002530.1	Monogalactosyldiacylglycerol synthase, family GT28	GO:0009247;GO:0016758	PTHR21015: ; SSF53756: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; G3DSA:3.40.50.2000: ; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009695: Diacylglycerol glucosyltransferase, N-terminal; IPR007235: Glycosyl transferase, family 28, C-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	[illegible]
comp31631_c0_seq5.p1	Ec-20_002560.1	mitogen-activated protein kinase, putative	GO:0005524;GO:0006468;GO:0004672	PTHR24055: ; IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR003527: Mitogen-activated protein (MAP) kinase, conserved site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10:	NA
comp21513_c0_seq2.p1	Ec-20_002600.1	Transketolase-like, pyrimidine-binding domain	n/a;n/a;n/a	PTHR11624: ; IPR005478: Transketolase, bacterial-like; IPR005474: Transketolase, N-terminal; IPR005476: Transketolase, C-terminal; IPR009014: Transketolase, C-terminal/Pyruvate-ferredoxin oxidoreductase, domain II; IPR029061: Thiamin diphosphate-binding fold; IPR005475: Transketolase-like, pyrimidine-binding domain	NA
comp32296_c0_seq13.p1	Ec-20_002650.1	Heat shock protein 70 - likely pseudogene	NA	PTHR19375: ; PTHR19375:SF173: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF53067: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.30.420.40: ; G3DSA:3.90.640.10: ; IPR013126: Heat shock protein 70 family; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32970_c0_seq1.p1	Ec-20_002660.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28273_c0_seq4.p1	Ec-20_002670.1	Uncharacterised protein family Ycf19	GO:0016020	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR003425: Uncharacterised protein family Ycf19	NA
comp33954_c0_seq1.p1	Ec-20_002680.2	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26850_c0_seq5.p1	Ec-20_002710.1	C-type lectin	GO:0005488	NA	NA
comp28116_c0_seq1.p1	Ec-20_002710.2	C-type lectin	GO:0005488	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12627_c0_seq1.p1	Ec-20_002720.1	Lamin Tail Domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001322: Lamin Tail Domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31372_c0_seq1.p1	Ec-20_002740.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp26018_c0_seq1.p1	Ec-20_002750.1	hypothetical protein	n/a;n/a;n/a	SignalP-TM:	NA

comp26487_c0_seq4.p1	Ec-20_002760.1	expressed unknown protein	n/a;n/a;n/a
comp23779_c0_seq1.p1	Ec-20_002770.1	PC-Esterase	GO:0004601;GO:0006118;GO:0006979;GO:0020037
comp32165_c1_seq7.p1	Ec-20_002790.1	Bromodomain	GO:0005515
comp30159_c0_seq2.p1	Ec-20_002800.1	Similar to 1-Aminocyclopropane-1-Carboxylate Deaminase	GO:0003824;GO:0008152;GO:0030170
comp33082_c1_seq1.p1	Ec-20_002810.2	Glycosyltransferase, family GT34	GO:0016021;GO:0016758
comp30587_c0_seq2.p2	Ec-20_002820.1	Protein of unknown function DUF1415	n/a;n/a;n/a
comp29814_c0_seq4.p3	Ec-20_002830.1	expressed unknown protein	n/a;n/a;n/a
comp19395_c0_seq1.p1	Ec-20_002870.1	Protein phosphatase inhibitor 2 (IPP-2)	GO:0004864;GO:0043666;GO:0009966
comp24660_c0_seq3.p1	Ec-20_002880.1	Protein of unknown function DUF1295	n/a;n/a;n/a
comp30582_c1_seq6.p1	Ec-20_002960.1	Protein-tyrosine phosphatase-like	n/a;n/a;n/a
comp34582_c0_seq1.p1	Ec-20_002980.1	YihA3, YihA/EngB-like GTPase	GO:0005525;GO:0005622
comp31524_c1_seq2.p1	Ec-20_002990.3	Tubby, C-terminal	n/a;n/a;n/a
comp24718_c0_seq1.p1	Ec-20_003010.1	conserved unknown protein	n/a;n/a;n/a
comp31642_c1_seq16.p1	Ec-20_003020.1	Protein kinase-like domain	GO:0016772
comp12799_c0_seq1.p1	Ec-20_003070.1	Similar to G-protein coupled receptors	GO:0016021
comp27694_c0_seq2.p1	Ec-20_003080.1	Beta-lactamase-like	GO:0016787
comp32286_c1_seq3.p1	Ec-20_003100.2	Pectin lyase fold	n/a;n/a;n/a
comp32966_c0_seq2.p1	Ec-20_003150.1	Enoyl-CoA hydratase/isomerase family protein	GO:0008152;GO:0003824
comp24120_c0_seq1.p1	Ec-20_003170.1	conserved unknown protein	GO:0006952;GO:0009607
comp32901_c0_seq1.p1	Ec-20_003180.3	RGS domain	GO:0038032
comp28098_c0_seq4.p1	Ec-20_003190.1	RGS domain	GO:0038032
comp24505_c1_seq2.p1	Ec-20_003200.2	carotenoid isomerase-like protein	GO:0009055;GO:0016117;GO:0016491;GO:0016705;GO:0050660
comp19412_c0_seq1.p1	Ec-20_003220.1	Armadillo-like helical	GO:0005488
comp29544_c1_seq2.p1	Ec-20_003230.1	Nog1, nucleolar GTPase	GO:0005525
comp21218_c0_seq1.p1	Ec-20_003280.1	Light harvesting complex protein	GO:0009765;GO:0016020
comp32231_c0_seq20.p1	Ec-20_003310.1	Mlo-related protein	GO:0006952;GO:0016021
comp30344_c0_seq3.p1	Ec-20_003330.1	Zinc finger, CCCH-type	GO:0046872
comp19718_c0_seq2.p1	Ec-20_003340.2	ATP-grasp fold, subdomain 2	GO:0005524
comp19963_c0_seq1.p1	Ec-20_003350.1	Mpv17/PMP22	GO:0016021
comp12212_c0_seq1.p1	Ec-20_003380.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a
comp28316_c0_seq4.p1	Ec-20_003410.2	expressed unknown protein	n/a;n/a;n/a
comp41320_c0_seq1.p1	Ec-20_003420.1	Pseudouridine synthase, RsuA/RluB/C/D/E/F	GO:0001522;GO:0003723;GO:0009451;GO:0009982
comp33691_c0_seq1.p1	Ec-20_003430.2	Heat shock protein 40 like protein	GO:0031072
comp11927_c0_seq1.p1	Ec-20_003450.1	Tetratricopeptide-like helical domain	GO:0005515
comp31713_c0_seq3.p1	Ec-20_003460.1	Tetratricopeptide-like helical domain	GO:0005515
comp33287_c1_seq1.p1	Ec-20_003470.1	P-loop containing nucleoside triphosphate hydrolase	GO:0016787
comp21004_c0_seq1.p1	Ec-20_003490.1	signal peptide peptidase	n/a;GO:0008233;GO:0006508
comp29050_c0_seq1.p2	Ec-20_003500.1	Glucose/ribitol dehydrogenase	GO:0008152;GO:0016491
comp27190_c0_seq1.p1	Ec-20_003510.1	Uncharacterised domain UPF0066	n/a;n/a;n/a
comp37618_c0_seq1.p1	Ec-20_003520.1	mRNA decapping complex protein	GO:0016787
comp30609_c0_seq5.p1	Ec-20_003540.1	ABC transporter periplasmic binding domain	GO:0005488
comp29059_c0_seq6.p2	Ec-20_003550.1	similar to putative mitochondrial rna splicing protein OR magnesium ion transporter Mrs2	GO:0016020;GO:0055085;GO:0046873;GO:0030001;GO:0015693;GO:0015095
comp29059_c0_seq6.p1	Ec-20_003560.1	Histidine phosphatase superfamily	GO:0003993
comp26209_c0_seq1.p2	Ec-20_003590.1	DPB3 class protein with histone-like transcription factor (NF-YC subunit) domain	GO:0046982;GO:0043565;GO:0005622
comp26518_c0_seq1.p1	Ec-20_003620.1	Lipoxygenase	GO:0046872
comp30003_c0_seq2.p1	Ec-20_003650.1	hypothetical protein	n/a;n/a;n/a
comp27630_c0_seq1.p1	Ec-20_003670.1	hypothetical protein	n/a;n/a;n/a
comp32248_c4_seq1.p1	Ec-20_003690.4	Similar to dedicator of cytokinesis	GO:0005622;GO:0008270
comp20704_c0_seq2.p1	Ec-20_003720.1	Glycosyltransferase, family GT8	GO:0016757;GO:0016758;GO:0016051
comp30811_c0_seq4.p1	Ec-20_003750.3	Transmembrane Fragile-X-F-associated protein	n/a;n/a;n/a
comp20722_c0_seq3.p1	Ec-20_003760.2	expressed unknown protein	n/a;n/a;n/a
comp24280_c0_seq1.p1	Ec-20_003770.1	Heat shock protein 70	n/a;n/a;n/a
comp12256_c0_seq1.p1	Ec-20_003790.1	Aldehyde Dehydrogenase	GO:0016620;GO:0008152;GO:0055114;GO:0016491
comp12312_c0_seq1.p1	Ec-20_003810.1	Major facilitator superfamily	GO:0055085;GO:0016021
comp34140_c0_seq1.p1	Ec-20_003830.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0005634;GO:0000981;GO:0006355;GO:0008270
comp27472_c0_seq2.p1	Ec-20_003840.4	conserved unknown protein	NA
comp32029_c1_seq9.p1	Ec-20_003870.1	Similar to tubulin, gamma complex associated protein 2	GO:0005815;GO:0000922;GO:0000226
comp34574_c0_seq1.p1	Ec-20_003890.1	Proteasome assembly chaperone 2	n/a;n/a;n/a
comp27119_c0_seq1.p1	Ec-20_003900.1	Protochlorophyllide reductase, putative chloroplast precursor	GO:0008152;0016630;GO:0016491
comp27119_c0_seq1.p2	Ec-20_003910.1	conserved unknown protein	n/a;n/a;n/a
comp12427_c0_seq1.p1	Ec-20_003920.1	Glutaredoxin	n/a;n/a;n/a
comp27601_c0_seq3.p1	Ec-20_003930.1	Thioredoxin-like fold	n/a;n/a;n/a
comp27601_c0_seq3.p3	Ec-20_003940.1	expressed unknown protein	n/a;n/a;n/a
comp63287_c0_seq1.p1	Ec-20_003950.1	WD40 repeat	GO:0005515
comp24429_c0_seq2.p1	Ec-20_003960.1	Alpha/Beta hydrolase fold	GO:0016787
comp26756_c0_seq3.p1	Ec-20_003970.1	Actin family	GO:0005515
comp26756_c0_seq3.p2	Ec-20_003980.1	trehalose-6-phosphate phosphatase, fragment (C-terminal end)	GO:0003824;GO:0005992
comp26976_c0_seq1.p1	Ec-20_004010.1	hypothetical protein	n/a;n/a;n/a
comp24429_c0_seq3.p1	Ec-20_004020.1	Mpv17/PMP22	GO:0016021
comp19714_c0_seq1.p1	Ec-20_004030.1	Cytochrome c oxidase biogenesis protein Cmc1-like	n/a;n/a;n/a
comp21279_c0_seq2.p1	Ec-20_004040.1	GBP5, guanylate-binding protein (divergent)	GO:0003924;GO:0005525
comp18970_c0_seq1.p1	Ec-20_004060.1	Peptide chain release factor class I/class II	GO:0006415;GO:0003747
comp22563_c0_seq1.p1	Ec-20_004090.1	Tetratricopeptide-like helical domain	GO:0005515
comp30551_c0_seq3.p1	Ec-20_004110.1	hypothetical protein	n/a;n/a;n/a
comp30377_c0_seq9.p1	Ec-20_004140.1	Vacuolar protein sorting protein 11, C-terminal	GO:0005488;GO:0016192;GO:0006886
comp66916_c0_seq1.p1	Ec-20_004160.2	TPR repeat and glycosyl transferase domain containing protein	NA
comp34612_c0_seq1.p1	Ec-20_004170.1	eukaryotic initiation factor 2A	GO:0005515
comp25256_c0_seq1.p1	Ec-20_004180.1	RNase L inhibitor-like protein	GO:0005524;GO:0016887
comp25466_c0_seq1.p1	Ec-20_004190.1	Ribosomal protein L6, alpha-beta domain	GO:0005840;GO:0005622;GO:0006412;GO:0003735;GO:0019843
comp32840_c7_seq1.p1	Ec-20_004200.1	SART-1 protein	n/a;GO:0000398
comp33028_c0_seq2.p1	Ec-20_004210.1	Uncharacterised domain, di-copper centre	n/a;n/a;n/a
comp32579_c0_seq41.p1	Ec-20_004220.1	DTW	n/a;n/a;n/a
comp31840_c0_seq1.p1	Ec-20_004230.1	cytochrome P450	GO:0005506;GO:0016705;GO:0020037;GO:0055114
comp28554_c0_seq1.p1	Ec-20_004250.1	Kelch-type beta propeller	GO:0005515
comp28698_c0_seq2.p1	Ec-20_004260.1	Zinc finger, RING/FYVE/PHD-type	GO:0005515;GO:0008270
comp25549_c0_seq3.p1	Ec-20_004280.1	Nucleotide-diphospho-sugar transferases	n/a;n/a;n/a
comp27464_c0_seq3.p1	Ec-20_004310.1	conserved unknown protein	NA
comp27464_c0_seq1.p1	Ec-20_004320.1	conserved unknown protein	NA
comp32391_c1_seq62.p1	Ec-20_004330.5	Hypothetical protein	n/a;n/a;n/a
comp29696_c0_seq4.p1	Ec-20_004340.1	Proline-rich protein PRCC	n/a;n/a;n/a
comp27428_c0_seq2.p1	Ec-20_004350.1	NIN-like transcription factor	n/a;n/a;n/a
comp33190_c0_seq1.p1	Ec-20_004390.3	expressed unknown protein	n/a;n/a;n/a
comp33028_c0_seq3.p1	Ec-20_004410.1	Tyrosinase copper-binding domain	GO:0008152;GO:0016491
comp21419_c0_seq1.p1	Ec-20_004460.1	Tetratricopeptide-like helical domain	GO:0005515
comp21419_c0_seq1.p3	Ec-20_004470.1	expressed unknown protein	n/a;n/a;n/a
comp12642_c0_seq1.p1	Ec-20_004480.1	Cell division protein FtsZ	GO:0005525;GO:0005737
comp32897_c0_seq1.p1	Ec-20_004500.1	conserved unknown protein	n/a;n/a;n/a
comp33088_c0_seq23.p1	Ec-20_004510.1	Ankyrin repeat-containing domain	GO:0005515
comp20061_c0_seq1.p1	Ec-20_004520.1	expressed unknown protein	n/a;n/a;n/a
comp27436_c0_seq2.p1	Ec-20_004540.1	Metallopeptidase, catalytic domain	GO:0008237
comp12671_c1_seq1.p1	Ec-20_004550.1	SUN domain-containing protein 1	GO:0034993;GO:0005639
comp24899_c0_seq1.p1	Ec-20_004560.1	Ubiquitin-like	GO:0005515
comp27654_c0_seq1.p2	Ec-20_004580.1	EsV-1-7 domain protein, putative copper transporter	GO:0046872;GO:0030001
comp32261_c0_seq2.p1	Ec-20_004610.1	YgfZ/GcvT conserved site	GO:0004047;GO:0005737;GO:0006546
comp27112_c0_seq1.p1	Ec-20_004620.1	casein kinase II alpha subunit	GO:0004672;GO:0005524;GO:0006468
comp64086_c0_seq1.p1	Ec-20_004630.1	WD repeat protein	GO:0005515
comp24447_c0_seq1.p1	Ec-20_004640.1	Zinc finger, RING/FYVE/PHD-type	n/a;GO:0003677;GO:0006281
comp28296_c0_seq3.p1	Ec-20_004660.1	WD40 repeat	GO:0005515
comp33515_c0_seq1.p1	Ec-20_004670.1	ROK	n/a;n/a;n/a
comp27107_c0_seq2.p1	Ec-20_004680.3	CASP, C-terminal	GO:0006891;GO:0030173
comp22737_c0_seq1.p1	Ec-20_004690.1	CDC2-like protein kinase	GO:0006468;GO:0004672
comp29566_c0_seq5.p1	Ec-20_004720.1	Protein of unknown function DUF1168	n/a;n/a;n/a
comp32269_c3_seq24.p1	Ec-20_004740.1	Myosin light chain kinase (MLCK)	GO:0004672;GO:0005524;GO:0006468
comp7355_c0_seq1.p1	Ec-20_004750.1	WD40 repeat	GO:0005515
comp13051_c0_seq1.p1	Ec-20_004760.1	Thioredoxin-like fold	GO:0016209;GO:0016491;n/a
comp31077_c0_seq1.p1	Ec-20_004770.1	Kinase phosphorylation domain	n/a;n/a;n/a
comp32062_c0_seq8.p1	Ec-20_004780.1	haloacid dehalogenase (HAD) superfamily protein	NA
comp23592_c0_seq2.p1	Ec-20_004790.1	Hypothetical protein	n/a;n/a;n/a
comp12490_c0_seq1.p1	Ec-20_004800.1	Beta-glucosidase, family GH3	NA
comp31381_c0_seq1.p1	Ec-20_004810.1	T-complex protein 10, C-terminal domain	GO:0003824;GO:0008152
comp30943_c0_seq1.p1	Ec-20_004860.1	violaxanthin de-epoxidase-related protein of unknown function	GO:0009055;GO:0051536
comp28534_c0_seq2.p1	Ec-20_004880.1	Phosphorylated CTD interacting factor 1, WW domain	n/a;n/a;n/a
comp21449_c0_seq1.p1	Ec-20_004890.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp29606_c0_seq7.p1	Ec-20_004900.1	WW domain	GO:0005515
comp30570_c0_seq3.p1	Ec-20_004910.1	Basic-leucine zipper and PAS domains	GO:0007165;GO:0006355;GO:0043565;GO:0004871;GO:0003700
comp29606_c0_seq1.p1	Ec-20_004920.1	Elongator protein 3/MiaB/NifB	GO:0003824;GO:0051536
comp24412_c0_seq1.p1	Ec-20_004930.1	hypothetical protein	n/a;n/a;n/a
comp24412_c0_seq2.p1	Ec-20_004940.1	expressed unknown protein	n/a;n/a;n/a
comp24451_c0_seq1.p1	Ec-20_004950.1	P-loop containing nucleoside triphosphate hydrolase	GO:0004798;GO:0005524;GO:0006233;GO:0006235
comp20349_c0_seq1.p1	Ec-20_004960.1	putative, spindle assembly abnormal protein 6	n/a;n/a;n/a
comp32717_c0_seq3.p1	Ec-20_004970.1	conserved unknown protein	GO:0000786;GO:0003677;GO:0006334;n/a
comp28411_c0_seq4.p1	Ec-20_004980.2	Cellulose synthase (UDP-forming), family GT2	NA
comp28411_c0_seq1.p1	Ec-20_004990.1	Cellulose synthase (UDP-forming), family GT2	NA
comp27082_c0_seq1.p1	Ec-20_005010.1	Fatty acid desaturase	GO:0055114;GO:0016491;GO:0006629
comp32256_c0_seq2.p1	Ec-20_005020.1	Glycerol:H+ symporter	NA
comp32445_c0_seq2.p1	Ec-20_005030.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0006470
comp29902_c0_seq3.p2	Ec-20_005040.1	Protein of unknown function UPF0301	n/a;n/a;n/a
comp30274_c0_seq2.p1	Ec-20_005050.1	Transcription termination factor	GO:0006355;GO:0005739;GO:0003690
comp29115_c0_seq4.p1	Ec-20_005070.1	expressed unknown protein	n/a;n/a;n/a
comp24105_c0_seq2.p1	Ec-20_005080.1	SGNH hydrolase-type esterase domain	n/a;n/a;n/a
comp32621_c0_seq4.p1	Ec-21_000047.1	hypothetical protein	NA
comp28806_c0_seq1.p1	Ec-21_000110.1	hypothetical protein	n/a;n/a;n/a
comp29706_c1_seq1.p1	Ec-21_000200.1	Oxa1-like homolog, mitochondrial inner membrane insertase	GO:0016021;GO:0051205
comp11733_c0_seq2.p1	Ec-21_000210.1	U1 zinc finger protein	GO:0003676;GO:0005622;GO:0008270
comp20887_c0_seq1.p1	Ec-21_000240.1	conserved unknown protein	GO:0043564;GO:0005634;GO:0003677;GO:0004003;GO:0005958;GO:0042162;GO:0003684;GO:0006303;GO:0000723
comp34788_c0_seq1.p1	Ec-21_000250.1	Glyceraldehyde 3-phosphate dehydrogenase; alternative name: imm downregulated 12	GO:0016620;GO:0008152;GO:0003824;GO:0005488;GO:0055114
comp34721_c0_seq1.p1	Ec-21_000260.1	conserved unknown protein	n/a;n/a;n/a
comp30656_c0_seq5.p1	Ec-21_000270.2	Peptidase C48, SUMO/Sentrin/Ubl1	GO:0006508;GO:0008234
comp12894_c0_seq2.p1	Ec-21_000280.1	Rubredoxin-type fold	GO:0006118;GO:0009055;GO:0046872
comp51236_c0_seq1.p1	Ec-21_000290.1	Hypothetical leucine rich repeat protein	GO:0005515
comp30237_c0_seq3.p1	Ec-21_000330.1	TFIIEalpha/SarR/Rpc3 HTH domain	GO:0003677;GO:0003899;GO:0006350
comp30237_c0_seq2.p1	Ec-21_000340.1	RNA polymerase III subunit RPC82-related, helix-turn-helix	n/a;n/a;n/a
comp26221_c0_seq1.p1	Ec-21_000350.1	Major facilitator superfamily	GO:0055085;GO:0016021
comp30288_c0_seq2.p1	Ec-21_000360.1	hypothetical protein	n/a;n/a;n/a
comp31473_c0_seq1.p1	Ec-21_000370.1	Glycosyl transferase, family 3	GO:0008152;GO:0016757
comp30841_c0_seq2.p1	Ec-21_000530.6	Zn(2)-C6 fungal-type DNA-binding domain	GO:0000981;GO:0005634;GO:0006355;GO:0008270
comp28653_c0_seq2.p1	Ec-21_000790.1	hypothetical protein	n/a;n/a;n/a
comp30334_c1_seq1.p1	Ec-21_000810.1	hypothetical protein	n/a;n/a;n/a
comp30699_c0_seq1.p1	Ec-21_000820.3	Armadillo-like helical	GO:0005488
comp32991_c0_seq2.p2	Ec-21_000830.1	Hypothetical protein	n/a;n/a;n/a
comp19592_c0_seq1.p1	Ec-21_000850.1	expressed unknown protein	n/a;n/a;n/a
comp29682_c0_seq6.p1	Ec-21_000870.1	Protein kinase 2	GO:0005524;GO:0006468;GO:0004672
comp29234_c0_seq1.p1	Ec-21_000890.1	conserved unknown protein	n/a;n/a;n/a
comp24532_c0_seq1.p1	Ec-21_000900.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777
comp28128_c0_seq4.p1	Ec-21_000920.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0005634;GO:0000981;GO:0006355;GO:0008270
comp32719_c0_seq8.p1	Ec-21_000930.1	Zn(2)-C6 fungal-type DNA-binding domain	GO:0005634;GO:0000981;GO:0006355;GO:0008270
comp32534_c1_seq4.p1	Ec-21_000950.3	von Willebrand factor, type D domain	n/a;n/a;n/a
comp20960_c0_seq1.p1	Ec-21_000990.1	tocopherol phytyltransferase	GO:0004659;GO:0016021
comp20903_c0_seq2.p1	Ec-21_001000.1	Lectin domain	GO:0016020
comp27109_c0_seq1.p1	Ec-21_001010.1	eukaryotic translation initiation factor 2B family protein / eIF-2B family protein	GO:0044237
comp32329_c1_seq20.p1	Ec-21_001080.1	Alpha/beta hydrolase fold-1	n/a;n/a;n/a
comp12005_c0_seq1.p1	Ec-21_001090.1	Inositol monophosphatase	GO:0046854
comp27563_c0_seq2.p1	Ec-21_001100.1	Pentatricopeptide repeat	GO:0003995;GO:0006118;GO:0055114
comp27567_c0_seq2.p1	Ec-21_001110.1	Protein of unknown function DUF1183, TMEM66	n/a;n/a;n/a
comp32167_c0_seq1.p1	Ec-21_001120.1	Contains domains for prephenate dehydrogenase and nucleoside-diphosphate-sugar epimerases	GO:0003824;GO:0005488;GO:0008152
comp31671_c0_seq1.p1	Ec-21_001130.1	Hypothetical protein	n/a;n/a;n/a
comp31477_c0_seq8.p5	Ec-21_001150.1	NADH dehydrogenase (ubiquinone)	GO:0016651;GO:0022904;GO:0005743
comp31477_c0_seq8.p1	Ec-21_001160.1	EGF-like domain, extracellular	n/a;n/a;n/a
comp25184_c0_seq1.p1	Ec-21_001170.1	CUL4-RING ubiquitin ligase complex component	NA
comp32126_c0_seq1.p1	Ec-21_001180.1	RmlC-like jelly roll fold	n/a;n/a;n/a
comp30074_c0_seq5.p1	Ec-21_001200.1	SAP domain	GO:0000166
comp30673_c0_seq1.p1	Ec-21_001250.3	WD40 repeat	GO:0005515
comp12366_c0_seq1.p1	Ec-21_001300.1	Major facilitator superfamily domain	n/a;n/a;n/a
comp27263_c1_seq2.p1	Ec-21_001310.1	aluminium resistance family protein	NA
comp30034_c0_seq9.p1	Ec-21_001360.1	Pectin lyase fold	n/a;n/a;n/a
comp31903_c0_seq3.p1	Ec-21_001390.5	Protein kinase-like domain	GO:0016772
comp31903_c0_seq3.p2	Ec-21_001400.2	conserved unknown protein	n/a;n/a;n/a
comp32524_c1_seq1.p1	Ec-21_001440.1	Diphosphomevalonate decarboxylase	NA
comp25165_c0_seq1.p1	Ec-21_001450.1	hypothetical protein	NA
comp31019_c0_seq1.p1	Ec-21_001460.1	WW domain	GO:0005515
comp28979_c0_seq2.p1	Ec-21_001480.1	GDP-fucose protein O-fucosyltransferase	n/a;n/a;n/a
comp30980_c0_seq2.p1	Ec-21_001530.1	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a
comp24689_c0_seq1.p1	Ec-21_001560.1	HSP20-like chaperone	n/a;n/a;n/a
comp29952_c0_seq8.p1	Ec-21_001570.1	conserved unknown protein	n/a;n/a;n/a
comp29952_c0_seq4.p2	Ec-21_001580.1	hypothetical protein	n/a;n/a;n/a
comp22127_c1_seq2.p1	Ec-21_001590.1	Cytochrome P450	GO:0020037;GO:0005506;GO:0055114;GO:0016705
comp24684_c0_seq1.p1	Ec-21_001600.1	Jumonji domain protein	n/a;n/a;n/a
comp24562_c0_seq1.p1	Ec-21_001610.1	Oxa1 or Cox18/Oxa2 homolog, mitochondrial integral inner membrane protein	GO:0016021;GO:0051205
comp24116_c0_seq1.p1	Ec-21_001630.1	Protein kinase-like domain	GO:0006468;GO:0004672;GO:0016772
comp34205_c0_seq1.p1	Ec-21_001640.2	START-like domain	n/a;n/a;n/a
comp31295_c0_seq10.p1	Ec-21_001650.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468
comp31950_c0_seq3.p2	Ec-21_001660.1	expressed unknown protein	n/a;GO:0042325;GO:0005737
comp21149_c0_seq1.p1	Ec-21_001670.1	expressed unknown protein	n/a;n/a;n/a
comp20412_c0_seq1.p1	Ec-21_001680.1	Cactin, C-terminal	GO:0005515
comp32022_c0_seq3.p1	Ec-21_001690.1	Kinesin motor domain	GO:0003777;GO:0005524;GO:0007018;GO:0008017
comp20948_c0_seq2.p1	Ec-21_001700.1	protein tyrosine phosphatase	GO:0008138;GO:0006470
comp12106_c0_seq1.p1	Ec-21_001720.1	Histone deacetylase domain protein	n/a;n/a;n/a
comp29032_c0_seq4.p1	Ec-21_001760.3	eukaryotic translation initiation factor 2B delta subunit	GO:0044237
comp29032_c0_seq3.p1	Ec-21_001770.1	EF-hand domain pair	GO:0005509
comp12156_c0_seq1.p1	Ec-21_001790.1	Sedoheptulose-bisphosphatase	GO:0042578;GO:0005975;GO:0042132
comp13867_c0_seq2.p1	Ec-21_001800.1	cyclic pyranopterin monophosphate synthase	GO:0003824;GO:0046872;GO:0051539
comp26438_c0_seq2.p1	Ec-21_001810.1	glutamyl-tRNA(Gln) and/or aspartyl-tRNA(Asn) amidotransferase, C subunit	GO:0006450
comp24303_c0_seq4.p1	Ec-21_001820.1	Dynein assembly factor 3, C-terminal domain	n/a;n/a;n/a
comp29281_c0_seq4.p1	Ec-21_001830.1	Mitochondrial transcription termination factor	GO:0003690;GO:0005739;GO:0006355
comp28621_c0_seq4.p2	Ec-21_001840.1	iron-sulfur cluster assembly protein, similar to nifU	GO:0005506;GO:0051536;GO:0016226
comp28621_c0_seq4.p1	Ec-21_001860.1	FAD-binding, type 2, subdomain 1	GO:0008762;GO:0050660;GO:0003824;GO:0055114;GO:0016491
comp11857_c0_seq1.p1	Ec-21_001870.1	HSP20-like chaperone	n/a;n/a;n/a
comp28544_c0_seq6.p1	Ec-21_001880.1	Mitochondrial carrier domain	n/a;n/a;n/a
comp13120_c0_seq1.p1	Ec-21_001890.1	conserved unknown protein	n/a;n/a;n/a
comp32858_c1_seq1.p1	Ec-21_001900.1	Cobalamin (vitamin B12)-dependent enzyme, catalytic subdomain	GO:0008152;GO:0016866;GO:0031419
comp32858_c1_seq1.p2	Ec-21_001910.1	50S ribosomal protein L19	GO:0005840;GO:0005622;GO:0006412;GO:0003735
comp31705_c0_seq1.p1	Ec-21_001920.1	Protein-tyrosine phosphatase-like	n/a;n/a;n/a
comp34107_c0_seq1.p1	Ec-21_001960.1	SMAD/FHA domain	GO:0005515
comp26383_c0_seq2.p1	Ec-21_001970.1	Protein of unknown function DUF1517	n/a;n/a;n/a
comp34186_c0_seq1.p1	Ec-21_001980.1	Chaperonin Cpn60/TCP-1	GO:0006457;GO:0005524;GO:0044267;GO:0051082
comp29049_c0_seq2.p1	Ec-21_002030.1	Cytidyltransferase-like domain	GO:0003824;GO:0009058
comp35573_c0_seq1.p1	Ec-21_002040.1	Ribosomal protein L25/L23	GO:0005840;GO:0006412;GO:0003735
comp32381_c0_seq1.p1	Ec-21_002070.1	Protein of unknown function DUF4419	n/a;n/a;n/a
comp27425_c0_seq2.p1	Ec-21_002080.1	Carboxypeptidase, regulatory domain	GO:0030246
comp30449_c0_seq4.p1	Ec-21_002090.1	TLDc domain	n/a;n/a;n/a
comp28469_c0_seq4.p1	Ec-21_002290.1	Hypothetical protein	n/a;n/a;n/a
comp12520_c0_seq1.p1	Ec-21_002310.1	Oxoglutarate dehydrogenase, N-terminal part	GO:0008152;GO:0006520;GO:0016624
comp30753_c0_seq5.p1	Ec-21_002350.1	Hypothetical leucine rich repeat protein	GO:0005515
comp24806_c0_seq4.p1	Ec-21_002360.1	expressed unknown protein	n/a;n/a;n/a
comp33036_c0_seq9.p1	Ec-21_002370.1	expressed unknown protein	n/a;n/a;n/a
comp31399_c0_seq1.p1	Ec-21_002410.4	Adaptor protein ClpS, core	GO:0030163
comp26750_c0_seq3.p1	Ec-21_002520.1	retinitis pigmentosa 2 (X-linked recessive)	GO:0000902
comp25214_c0_seq1.p1	Ec-21_002560.1	MBipA, mitochondrial GTPase BipA/TypA	GO:0005525
comp28997_c0_seq2.p1	Ec-21_002580.1	conserved unknown protein	NA
comp30623_c0_seq7.p1	Ec-21_002600.1	Transglutaminase-like	n/a;n/a;n/a
comp30623_c0_seq7.p2	Ec-21_002610.1	Cell cycle checkpoint, Hus1	GO:0006281;GO:0000077;GO:0030896;GO:0005730
comp23892_c0_seq2.p1	Ec-21_002620.1	Dpy-30 motif	n/a;n/a;n/a
comp33772_c0_seq1.p1	Ec-21_002680.1	conserved unknown protein	n/a;n/a;n/a
comp27121_c0_seq3.p1	Ec-21_002700.1	tesmin-like, animal TCX proteins are associated with development of both male and female reproductiv	n/a;n/a;n/a
comp21130_c0_seq3.p1	Ec-21_002710.1	Dynactin subunit 4	GO:0005869
comp32214_c1_seq11.p1	Ec-21_002720.1	hypothetical protein	n/a;n/a;n/a
comp27061_c0_seq1.p1	Ec-21_002730.1	Nicotinamide N-methyltransferase-like	n/a;n/a;n/a
comp28236_c0_seq1.p1	Ec-21_002740.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003676;GO:0005524;GO:0008026
comp32214_c1_seq3.p1	Ec-21_002780.1	expressed unknown protein	n/a;n/a;n/a
comp29397_c0_seq5.p1	Ec-21_002790.1	WD40/YVTN repeat-like-containing domain	GO:0005515
comp29397_c0_seq5.p2	Ec-21_002800.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp30088_c0_seq4.p1	Ec-21_002810.2	Chromatin assembly factor 1 subunit A	n/a;n/a;n/a
comp12315_c0_seq1.p1	Ec-21_002820.1	conserved unknown protein	n/a;n/a;n/a
comp25421_c0_seq1.p1	Ec-21_002830.1	Tetratricopeptide-like helical domain	GO:0005515
comp12877_c0_seq1.p1	Ec-21_002850.1	hypothetical protein	n/a;n/a;n/a
comp19635_c0_seq1.p1	Ec-21_002860.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a
comp31315_c0_seq5.p1	Ec-21_002880.2	expressed unknown protein	n/a;n/a;n/a
comp31315_c0_seq5.p2	Ec-21_002890.1	HAD-like domain	n/a;n/a;n/a
comp29302_c0_seq1.p1	Ec-21_002900.1	expressed unknown protein	n/a;n/a;n/a
comp30651_c0_seq1.p1	Ec-21_002910.1	conserved unknown protein	n/a;n/a;n/a
comp33526_c0_seq1.p1	Ec-21_002920.1	ATP-cone	GO:0004748;GO:0005515;GO:0005971;GO:0006260;GO:0055114
comp27397_c0_seq1.p1	Ec-21_002930.1	Calcineurin-like phosphoesterase domain, apaH type	GO:0016787
comp30567_c0_seq1.p1	Ec-21_002940.1	Bile acid:sodium symporter/arsenical resistance protein Acr3	GO:0016020
comp30250_c0_seq3.p1	Ec-21_002990.1	EEF1A1, eukaryotic translation elongation factor 1 alpha	GO:0003746;GO:0005525;GO:0005737;GO:0006414
comp32474_c1_seq1.p1	Ec-21_003020.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008168;GO:0003676;GO:0032259
comp19804_c0_seq1.p5	Ec-21_003030.1	expressed unknown protein	n/a;n/a;n/a
comp29880_c0_seq2.p1	Ec-21_003040.1	expressed unknown protein	n/a;n/a;n/a
comp16918_c0_seq1.p1	Ec-21_003070.1	DM13 domain	n/a;n/a;n/a
comp44797_c0_seq1.p1	Ec-21_003080.2	hypothetical protein	n/a;n/a;n/a
comp31896_c0_seq1.p1	Ec-21_003100.1	NUDIX hydrolase domain-like	GO:0016787
comp29087_c0_seq8.p1	Ec-21_003110.2	hypothetical protein	n/a;n/a;n/a
comp12208_c0_seq1.p1	Ec-21_003120.1	Patatin/Phospholipase A2-related	GO:0006629

comp26924_c0_seq2.p1	Ec-21_003170.1	Conserved oligomeric Golgi complex subunit 6	GO:0006891;GO:0017119	PF06419: Conserved oligomeric complex COG6; IPR010490: Conserved oligomeric Golgi complex subunit 6	NA
comp34566_c0_seq1.p1	Ec-21_003190.1	U2 small nuclear ribonucleoprotein A	GO:0005515	IPR003603: U2A'/phosphoprotein 32 family A, C-terminal; G3DSA:3.80.10.10: ; SSF52058: ; IPR001611: Leucine-rich repeat; PTHR10552: ; PF14580: Leucine-rich repeat; SSF68906: ; IPR003034: SAP domain	NA
comp33600_c0_seq1.p1	Ec-21_003210.1	Cytochrome b561 domain	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR004877: Cytochrome b561 domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR15422: ; IPR006593: Cytochrome b561/ferric reductase transmembrane; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32628_c0_seq3.p1	Ec-21_003220.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp14969_c0_seq2.p1	Ec-21_003230.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777	IPR027640: Kinesin-like protein; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR001752: Kinesin motor domain	NA
comp20188_c0_seq2.p1	Ec-21_003240.1	1-acyl-sn-glycerol-3-phosphate acyltransferase	GO:0016746;GO:0008152;GO:0008415	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10434: ; IPR002123: Phospholipid/glycerol acyltransferase; G3DSA:3.40.1130.10: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF69593: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2848
comp12159_c0_seq1.p2	Ec-21_003250.1	Heat shock protein DnaJ, cysteine-rich domain	GO:0031072;GO:0051082	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001305: Heat shock protein DnaJ, cysteine-rich domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12159_c0_seq1.p1	Ec-21_003260.1	Cytochrome b561/ferric reductase transmembrane	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR004877: Cytochrome b561 domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006593: Cytochrome b561/ferric reductase transmembrane; PTHR10106: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29662_c0_seq1.p1	Ec-21_003270.1	Phosphotyrosine protein phosphatase I superfamily	GO:0004721;GO:0005634;GO:0006397;n/a	IPR006811: RNA polymerase II subunit A	NA
comp29634_c0_seq2.p1	Ec-21_003280.1	mono-or diacylglycerol acyltransferase type 2	GO:0016747	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007130: Diacylglycerol acyltransferase; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0831
comp20303_c0_seq3.p2	Ec-21_003290.1	Ribosomal protein L10/L12	GO:0003735;GO:0005622;GO:0005840;GO:0006414	PF00428: 60s Acidic ribosomal protein; PTHR21141:	NA
comp25155_c0_seq2.p1	Ec-21_003320.1	Nicotinamide nucleotide transhydrogenase	GO:0006118;GO:0008746;GO:0008750;GO:0015992;GO:0016021;GO:0016491;GO:0050661;GO:0055114	IPR007698: Alanine dehydrogenase/pyridine nucleotide transhydrogenase, NAD(H)-binding domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR024605: NAD(P) transhydrogenase, alpha subunit, C-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10160:SF19: ; IPR007886: Alanine dehydrogenase/pyridine nucleotide transhydrogenase, N-terminal; cd05304: Rubrum_tdh; IPR012136: NADP transhydrogenase, beta subunit; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR026255: NAD(P) transhydrogenase, alpha subunit; G3DSA:3.40.50.1770: ; IPR029035: DHS-like NAD/FAD-binding domain; IPR016040: NAD(P)-binding domain; SSF52283: ; IPR023753: FAD/NAD(P)-binding domain; PTHR10160: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29634_c0_seq2.p2	Ec-21_003340.1	nitrite transporter NAR1	GO:0016020;GO:0005215;GO:0006810	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR023271: Aquaporin-like; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000292: Formate/nitrite transporter; SignalP-noTM: ; PTHR30520: ; IPR024002: Formate/nitrite transporter, conserved site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29324_c0_seq4.p2	Ec-21_003370.1	Thioredoxin-like fold	n/a;n/a;n/a	IPR001853: DSBA-like thioredoxin domain; PTHR13887: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33624_c0_seq1.p1	Ec-21_003380.1	Glutaredoxin	GO:0009055;GO:0015035;GO:0045454	IPR002109: Glutaredoxin; SIGNAL_PEPTIDE: Signal peptide region; PTHR10168: ; IPR014025: Glutaredoxin subgroup; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR011767: Glutaredoxin active site; IPR011899: Glutaredoxin, eukaryotic/virial; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1752
comp20617_c0_seq1.p1	Ec-21_003400.1	NUOE homolog, NADH dehydrogenase (ubiquinone) subunit	NA	IPR002023: NADH-quinone oxidoreductase subunit E-like; PTHR10371: ; PF01257: Thioredoxin-like [2Fe-2S] ferredoxin; IPR012336: Thioredoxin-like fold; SignalP-TM:	KOG3196
comp21613_c0_seq1.p1	Ec-21_003420.1	Helicase superfamily 1/2, ATP-binding domain	n/a;n/a;n/a	IPR016135: Ubiquitin-conjugating enzyme/RWD-like; IPR007502: Helicase-associated domain; IPR011545: DEAD/DEAH box helicase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR18934: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29324_c0_seq4.p1	Ec-21_003430.1	OLA1, Obg-like ATPase 1 (YchF-related GTPase)	GO:0005525	IPR031167: OBG-type guanine nucleotide-binding (G) domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR23305: ; IPR012675: Beta-grasp domain; IPR012676: TGS-like; IPR013029: Domain of unknown function DUF933; IPR006073: GTP binding domain; IPR004396: Ribosome-binding ATPase YchF/Obg-like ATPase 1; IPR023192: TGS-like domain	NA
comp24748_c0_seq1.p1	Ec-21_003440.1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	GO:0004719;GO:0006464	IPR000682: Protein-L-isoaspartate(D-aspartate) O-methyltransferase; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase	NA
comp30998_c1_seq2.p1	Ec-21_003460.1	NUDIX hydrolase domain-like	GO:0016787	IPR015797: NUDIX hydrolase domain-like; IPR020084: NUDIX hydrolase, conserved site; IPR000086: NUDIX hydrolase domain	NA
comp29611_c0_seq3.p1	Ec-21_003470.1	SDH1, succinate dehydrogenase subunit 1	GO:0009055;GO:0055114;GO:0016491	PTHR11632: ; IPR027477: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain; IPR015939: Fumarate reductase/succinate dehydrogenase flavoprotein-like, C-terminal; SignalP-TM: ; IPR003953: FAD binding domain; G3DSA:3.50.50.60: ; Coil: ; G3DSA:4.10.80.40: ; SSF51905:	KOG2403
comp33714_c0_seq1.p3	Ec-21_003480.1	Ribosomal protein S26e	GO:0005840;GO:0005622;GO:0006412;GO:0003735	IPR000892: Ribosomal protein S26e	NA
comp31300_c0_seq1.p1	Ec-21_003490.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp1866_c0_seq1.p2	Ec-21_003510.1	C2 domain	GO:0005515	IPR018247: EF-Hand 1, calcium-binding site; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR021656: RPGR-interacting protein 1, first C2 domain; IPR031139: RPGRIP1 family; IPR000048: IQ motif, EF-hand binding site; IPR031133: Protein fantom, invertebrates; IPR001751: S100/Calbindin-D9k, conserved site; Coil: ; IPR000008: C2 domain	NA
comp19393_c0_seq1.p1	Ec-21_003520.1	N-acetyl-gamma-glutamyl-phosphate reductase, C-terminal part	GO:0006526;GO:0055114;GO:0003942	IPR012280: Semialdehyde dehydrogenase, dimerisation domain; SSF51735: ; IPR000534: Semialdehyde dehydrogenase, NAD-binding; PTHR32338: ; G3DSA:3.30.360.10: ; IPR016040: NAD(P)-binding domain; IPR000706: N-acetyl-gamma-glutamyl-phosphate reductase, type 1; SSF55347:	KOG4354
comp19393_c0_seq1.p3	Ec-21_003530.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp25570_c0_seq4.p1	Ec-21_003540.1	PDZ domain	GO:0005515	NA	NA
comp31005_c0_seq12.p1	Ec-21_003560.1	Purple acid phosphatase-like, N-terminal	GO:0046872;GO:0003993	NA	NA
comp31357_c0_seq15.p1	Ec-21_003570.2	EF-hand domain pair	GO:0005509	IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; Coil:	NA
comp20699_c0_seq1.p2	Ec-21_003580.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp25716_c0_seq3.p1	Ec-21_003590.1	Vitamin K epoxide reductase	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR012932: Vitamin K epoxide reductase; SignalP-noTM: ; PTHR14519: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19291_c0_seq2.p1	Ec-21_003610.1	Glutamate ammonia ligase	GO:0004356;GO:0006542;GO:0006807	IPR008146: Glutamine synthetase, catalytic domain; IPR027302: Glutamine synthetase, N-terminal conserved site; IPR008147: Glutamine synthetase, beta-Grasp; PTHR20852: ; SSF55931: ; IPR014746: Glutamine synthetase/guanido kinase, catalytic domain; IPR027303: Glutamine synthetase, glycine-rich site	KOG0683
comp11796_c0_seq1.p1	Ec-21_003620.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001594: Zinc finger, DHHC-type, palmitoyltransferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22883: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26130_c0_seq2.p2	Ec-21_003630.1	Ribosome biogenesis protein Nop16	n/a;n/a;n/a	NA	NA
comp28750_c0_seq2.p1	Ec-21_003640.1	hypothetical protein	GO:0005515;n/a	IPR015943: WD40/YVTN repeat-like-containing domain; mobidb-lite: consensus disorder prediction	NA
comp31994_c0_seq1.p1	Ec-21_003670.1	Solute carrier family 35 member SLC35F1/F2/F6	GO:0006810;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF103481: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR13146: ; IPR009262: Solute carrier family 35 member SLC35F1/F2/F6; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30697_c0_seq1.p1	Ec-21_003680.1	Serine/threonine protein kinase, possibly NIMA-like	GO:0006468;GO:0004672	IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PTHR24361: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	KOG0589
comp11806_c0_seq1.p1	Ec-21_003690.1	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR22847: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; IPR020472: G-protein beta WD-40 repeat	NA
comp29379_c1_seq1.p1	Ec-21_003710.1	Hypothetical leucine rich repeat protein	GO:0005515	PTHR27000:SF291: ; G3DSA:3.30.200.20: ; IPR032675: Leucine-rich repeat domain, L domain-like; IPR011009: Protein kinase-like domain; PTHR27000: ; IPR003591: Leucine-rich repeat, typical subtype; G3DSA:1.10.510.10: ; Coil:	NA
comp32323_c0_seq4.p1	Ec-21_003720.1	Ankyrin repeat	GO:0005515	IPR020683: Ankyrin repeat-containing domain; IPR002110: Ankyrin repeat; PTHR24123:	NA
comp34213_c0_seq1.p1	Ec-21_003730.1	ornithine aminotransferase	GO:0003824;GO:0008483;GO:0030170	IPR015424: Pyridoxal phosphate-dependent transferase; IPR010164: Ornithine aminotransferase; IPR005814: Aminotransferase class-III; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2	KOG1402
comp12320_c0_seq1.p1	Ec-21_003740.1	Cysteine desulfurase	GO:0008152;GO:0003824	IPR015424: Pyridoxal phosphate-dependent transferase; PTHR11601: ; IPR000192: Aminotransferase class V domain; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2; SignalP-TM:	KOG1549
comp26130_c0_seq2.p1	Ec-21_003750.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp13106_c0_seq1.p1	Ec-21_003770.1	Von Willebrand factor type A (vWA) domain	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10166: ; G3DSA:3.30.450.20: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002035: von Willebrand factor, type A	NA
comp12430_c0_seq1.p1	Ec-21_003780.1	Importin subunit alpha	GO:0005634;GO:0008565;GO:0005737;GO:0005488;GO:0006606	PTHR23316: ; IPR002652: Importin-alpha, importin-beta-binding domain; IPR011989: Armadillo-like helical; IPR024931: Importin subunit alpha; IPR000225: Armadillo; IPR016024: Armadillo-type fold	NA
comp27373_c0_seq1.p1	Ec-21_003820.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31935_c0_seq2.p1	Ec-21_003890.1	Alpha-ketoglutarate-dependent dioxygenase FTO, catalytic domain	n/a;n/a;n/a	IPR024366: Alpha-ketoglutarate-dependent dioxygenase FTO, C-terminal; PTHR31291:SF2: ; IPR032868: Alpha-ketoglutarate-dependent dioxygenase FTO; IPR024367: Alpha-ketoglutarate-dependent dioxygenase FTO, catalytic domain; SignalP-TM:	NA
comp31935_c0_seq3.p1	Ec-21_003900.1	MPBQ/MSBQ transferase	GO:0008152;GO:0010189;GO:0008168;GO:0051741;GO:0032259	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; PTHR10108: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR025714: Methyltransferase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR025774: SAM-dependent methyltransferase gamma-tocopherol (gTMT)-type; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1269
comp31624_c2_seq7.p2	Ec-21_004030.1	Sphingomyelin synthase-like domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR21290: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR025749: Sphingomyelin synthase-like domain; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27824_c0_seq1.p1	Ec-21_004040.1	Dynactin subunit 6	GO:0005869	IPR027777: Dynactin subunit 6; IPR011004: Trimeric LpxA-like; G3DSA:2.160.10.10:	NA
comp28321_c0_seq4.p1	Ec-21_004060.1	Hypothetical leucine rich repeat protein	NA	PTHR24106: ; SSF52047: ; IPR032675: Leucine-rich repeat domain, L domain-like; IPR003590: Leucine-rich repeat, ribonuclease inhibitor subtype	NA
comp9637_c0_seq1.p1	Ec-21_004090.1	Armadillo-like helical	GO:0005488	PTHR23315: ; IPR011989: Armadillo-like helical; IPR000225: Armadillo; IPR016024: Armadillo-type fold; Coil:	NA
comp32030_c1_seq28.p1	Ec-21_004100.2	Alpha/Beta hydrolase fold	GO:0003824;GO:0004806;GO:0006629	IPR002921: Fungal lipase-like domain; IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR21493: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31533_c0_seq2.p1	Ec-21_004110.1	Transmembrane amino acid transporter protein	GO:0005525;GO:0005874;GO:0007017	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013057: Amino acid transporter, transmembrane domain; PTHR22950: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27252_c0_seq1.p1	Ec-21_004130.3	hypothetical protein	GO:0005737;GO:0016788;GO:0019478;n/a	IPR023509: D-Tyr tRNAtyr deacylase-like domain; IPR003732: D-aminoacyl-tRNA deacylase DTD	NA
comp24231_c0_seq1.p1	Ec-21_004180.1	Malonyl-CoA decarboxylase	GO:0050080;GO:0006633	IPR007956: Malonyl-CoA decarboxylase	NA
comp26593_c0_seq3.p3	Ec-21_004200.1	Histone-fold	GO:0046982	IPR029003: Kinetochore component CENP-S; IPR009072: Histone-fold; PTHR22980:	NA
comp70884_c0_seq1.p1	Ec-21_004220.1	Light harvesting complex protein	GO:0006096;GO:0004618	IPR001576: Phosphoglycerate kinase; PF14646: MYCBP-associated protein family; IPR015901: Phosphoglycerate kinase, C-terminal; Coil:	NA
comp11804_c0_seq1.p1	Ec-21_004240.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp1830_c0_seq1.p1	Ec-21_004270.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp30579_c0_seq2.p1	Ec-21_004280.2	Tetratricopeptide-like helical domain	GO:0005515	IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; Coil:	NA
comp56348_c0_seq1.p1	Ec-21_004300.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp26593_c0_seq3.p1	Ec-21_004360.1	Hydroxymethylglutaryl-CoA synthase	GO:0008299;GO:0004421;GO:0008152;GO:0003824	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR016038: Thiolase-like, subgroup; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR013746: Hydroxymethylglutaryl-coenzyme A synthase C-terminal domain; IPR016039: Thiolase-like; IPR013528: Hydroxymethylglutaryl-coenzyme A synthase, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR010122: Hydroxymethylglutaryl-CoA synthase, eukaryotic; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11877:	NA
comp21586_c0_seq3.p1	Ec-21_004370.1	glycerol kinase	GO:0016773;GO:0005975	PTHR10196: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR018485: Carbohydrate kinase, FGGY, C-terminal; SSF53067: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR005999: Glycerol kinase; IPR018483: Carbohydrate kinase, FGGY, conserved site; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.30.420.40: ; IPR018484: Carbohydrate kinase, FGGY, N-terminal; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2517
comp33214_c0_seq30.p1	Ec-21_004390.1	Thioredoxin-like fold	n/a;n/a;n/a	IPR023196: Phosducin N-terminal domain; IPR024253: Phosducin, thioredoxin-like domain; PTHR21148: ; IPR012336: Thioredoxin-like fold	NA
comp33227_c0_seq3.p1	Ec-21_004410.1	hypothetical protein	GO:0005515;GO:0000042	IPR000237: GRIP; Coil:	NA
comp32075_c0_seq18.p1	Ec-21_004430.1	Armadillo-like helical	GO:0005488	PTHR22983: ; IPR017441: Protein kinase, ATP binding site; IPR011989: Armadillo-like helical; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR000225: Armadillo; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; PTHR22983:SF6: ; PF13646: HEAT repeats; IPR016024: Armadillo-type fold; Coil:	NA
comp32075_c0_seq4.p1	Ec-21_004440.1	Mitochondrial transcription termination factor	GO:0006355;GO:0003690;GO:0005739	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE: Signal peptide region; PTHR11061: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR003690: Mitochondrial transcription termination factor; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PF13659: Methyltransferase domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25755_c0_seq1.p1	Ec-21_004450.1	Dimeric alpha-beta barrel	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR005545: YCII-related; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.30.70.1060: ; IPR011008: Dimeric alpha-beta barrel; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31650_c0_seq17.p1	Ec-21_004480.3	DEAD2	GO:0003677;GO:0004003;GO:0005524	PTHR11472: ; PTHR11472:SF6: ; IPR010614: DEAD2; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014013: Helicase superfamily 1/2, ATP-binding domain, DinG/Rad3-type; IPR014001: Helicase superfamily 1/2, ATP-binding domain; Coil: ; IPR006554: Helicase-like, DEXD box c2 type; IPR006555: ATP-dependent helicase, C-terminal	NA
comp10234_c0_seq1.p1	Ec-21_004480.4	DEAD2	GO:0003677;GO:0004003;GO:0005524	PTHR11472: ; PTHR11472:SF6: ; IPR010614: DEAD2; IPR014013: Helicase superfamily 1/2, ATP-binding domain, DinG/Rad3-type; Coil: ; IPR006555: ATP-dependent helicase, C-terminal	NA
comp32505_c0_seq1.p1	Ec-21_004490.1	Cupin-like and F-box-like domain protein	n/a;n/a;n/a	NA	NA
comp11775_c0_seq1.p1	Ec-21_004510.2	FCH domain	n/a;n/a;n/a	SSF103657: ; Coil:	NA
comp34136_c0_seq1.p1	Ec-21_004510.3	FCH domain	n/a;n/a;n/a	SSF103657: ; IPR031160: F-BAR domain; IPR001060: FCH domain; Coil:	NA
comp26068_c0_seq4.p1	Ec-21_004520.1	KIAA1430 homologue	n/a;n/a;n/a	Coil: ; IPR029488: KIAA1430 homologue	NA
comp26740_c0_seq1.p1	Ec-21_004530.1	EamA domain	GO:0016020;GO:0016021;GO:0022857	SSF103481: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000620: EamA domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR030184: WAT1-related protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp11872_c0_seq1.p1	Ec-21_004560.1	Nurf-55	GO:0005515	IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; PTHR22850: ; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp27746_c0_seq3.p1	Ec-21_004610.1	ABC transporter-like	GO:0005524;GO:0016887	PTHR19211: ; IPR003593: AAA+ ATPase domain; IPR003439: ABC transporter-like; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR017871: ABC transporter, conserved site	NA
comp29688_c0_seq3.p1	Ec-21_004630.1	calcium/calmodulin-dependent protein kinase IV	GO:0004672;GO:0005524;GO:0006468	IPR000595: Cyclic nucleotide-binding domain; PTHR24349: ; G3DSA:3.30.200.20: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; IPR011992: EF-hand domain pair; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR000719: Protein kinase domain; IPR018490: Cyclic nucleotide-binding-like; G3DSA:1.10.510.10: ; IPR014710: RmlC-like jelly roll fold	NA
comp64115_c0_seq1.p1	Ec-21_004670.1	Sterile alpha motif, type 1	GO:0003676	G3DSA:3.40.140.10: ; IPR013761: Sterile alpha motif/pointed domain; IPR001660: Sterile alpha motif domain; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; SSF47473: ; IPR021129: Sterile alpha motif, type 1; PTHR11644: ; IPR002125: Cytidine and deoxycytidylate deaminases, zinc-binding; IPR016193: Cytidine deaminase-like; IPR014002: Agenet domain, plant type; IPR005824: KOW; IPR002999: Tudor domain	NA
comp11818_c0_seq1.p3	Ec-21_004680.1	Hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31076_c0_seq2.p1	Ec-21_004690.1	ENTH/VHS	n/a;n/a;n/a	IPR002014: VHS; IPR018205: VHS subgroup; IPR008942: ENTH/VHS; SSF89009: ; PTHR13856:	NA
comp19874_c0_seq2.p1	Ec-21_004710.1	SH3 domain	GO:0005515	IPR001452: SH3 domain; SSF103657: ; IPR027267: Arfaptin homology (AH) domain/BAR domain; G3DSA:2.30.30.40: ; Coil:	NA
comp14393_c0_seq1.p1	Ec-21_004720.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp59515_c0_seq1.p1	Ec-21_004750.1	FAM227 Protein	n/a;n/a;n/a	IPR029417: FAM227 Protein	NA
comp28946_c0_seq1.p1	Ec-21_004770.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32158_c1_seq23.p1	Ec-21_004790.1	ammonium transporter	GO:0006810;GO:0008519;GO:0016020	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001905: Ammonium transporter; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11730:SF6: ; IPR018047: Ammonium transporter, conserved site; IPR024041: Ammonium transporter AmtB-like domain; IPR029020: Ammonium/urea transporter; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31867_c1_seq2.p1	Ec-21_004820.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31867_c1_seq5.p2	Ec-21_004840.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp47718_c0_seq1.p2	Ec-21_004850.1	Protein kinase-like domain	GO:0005524;GO:0006468;GO:0004672;GO:0016772	IPR017441: Protein kinase, ATP binding site; G3DSA:3.30.200.20: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; IPR000961: AGC-kinase, C-terminal; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR016137: RGS domain; IPR000719: Protein kinase domain; G3DSA:1.10.167.10: ; G3DSA:1.10.510.10: ; PTHR24351:	NA
comp33092_c0_seq18.p1	Ec-21_004870.1	Cyclic nucleotide-binding domain	n/a;n/a;n/a	IPR000595: Cyclic nucleotide-binding domain; PTHR10217: ; G3DSA:1.10.287.70: ; IPR003938: Potassium channel, voltage-dependent, EAG/ELK/ERG; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF81324: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018490: Cyclic nucleotide-binding-like; G3DSA:1.10.287.630: ; IPR013099: Two pore domain potassium channel domain; Coil: ; IPR014710: RmlC-like jelly roll fold; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34064_c0_seq1.p1	Ec-21_004880.1	NADH dehydrogenase (ubiquinone)	GO:0055114;GO:0016491	SIGNAL_PEPTIDE: Signal peptide region; PR00368: FAD-dependent pyridine nucleotide reductase signature; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PR00411: Pyridine nucleotide disulphide reductase class-I signature; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001327: Pyridine nucleotide-disulphide oxidoreductase, NAD-binding domain; SignalP-noTM: ; G3DSA:3.50.50.60: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR22915: ; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	KOG2495
comp12193_c0_seq1.p1	Ec-21_004890.1	Protein disulfide-isomerase fusion protein	GO:0045454	IPR005788: Disulphide isomerase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013766: Thioredoxin domain; IPR017937: Thioredoxin, conserved site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PR00421: Thioredoxin family signature; PTHR18929: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32513_c0_seq3.p1	Ec-21_004900.1	Galactose-binding domain-like	GO:0004867	IPR011050: Pectin lyase fold/virulence factor; IPR008979: Galactose-binding domain-like	NA
comp25469_c0_seq2.p1	Ec-21_004920.1	Peroxyredoxin	GO:0016491	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10430: ; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013740: Redoxin	NA
comp26423_c0_seq1.p1	Ec-21_004930.1	Carotenoid oxygenase	n/a;n/a;n/a	IPR004294: Carotenoid oxygenase	NA
comp27598_c0_seq1.p1	Ec-21_004940.1	Zinc finger, RING-type	GO:0005515;GO:0008270	IPR001841: Zinc finger, RING-type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR14155: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24741_c0_seq7.p2	Ec-21_004950.1	Organic solute transporter subunit alpha/Transmembrane protein 184	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005178: Organic solute transporter subunit alpha/Transmembrane protein 184; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24741_c0_seq2.p1	Ec-21_004960.1	Oxoglutarate/iron-dependent dioxygenase	GO:0055114;GO:0016706;GO:0016491	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005123: Oxoglutarate/iron-dependent dioxygenase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp24590_c1_seq1.p1	Ec-21_004980.1	CRAL-TRIO domain protein	GO:0031072	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011074: CRAL/TRIO, N-terminal domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001251: CRAL-TRIO lipid binding domain; IPR007905: Emopamil-binding protein; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR23324: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19438_c0_seq2.p1	Ec-21_004990.1	Vesicle transport protein, Got1/SFT2-like	GO:0006810;GO:0016192;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR007305: Vesicle transport protein, Got1/SFT2-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011691: Vesicle transport protein, SFT2-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24002_c0_seq5.p1	Ec-21_005000.1	Pleckstrin homology domain	n/a;n/a;n/a	IPR011993: PH domain-like; IPR001849: Pleckstrin homology domain	NA
comp21041_c0_seq1.p1	Ec-21_005010.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp19464_c0_seq1.p1	Ec-21_005020.1	cytochrome c oxidase subunit 6b	GO:0004129;GO:0006118;GO:0005739	IPR003213: Cytochrome c oxidase, subunit VIb; PTHR11387: ; PD015172: OXIDASE C CYTOCHROME SUBUNIT ISOFORM VIB OXIDOREDUCTASE MITOCHONDRION COX ACETYLATION	KOG3057
comp27841_c0_seq1.p1	Ec-21_005040.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp24584_c0_seq1.p1	Ec-21_005050.1	NAD(P)-binding domain	GO:0003824;GO:0005488;GO:0008152	SSF51735: ; IPR016040: NAD(P)-binding domain; PTHR12126: ; PF13460: NADH(P)-binding	NA
comp27154_c0_seq1.p1	Ec-21_005080.1	Glutaredoxin	GO:0009055;GO:0015035;GO:0045454	IPR002109: Glutaredoxin; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR004480: Monothiol glutaredoxin-related; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR012336: Thioredoxin-like fold	NA
comp26271_c0_seq1.p1	Ec-21_005090.1	Mediator complex, subunit Med10	GO:0016592;GO:0001104;GO:0006357	Coil: ; IPR019145: Mediator complex, subunit Med10	NA
comp32916_c0_seq10.p1	Ec-21_005100.1	manganese stabilising protein	GO:0009523;GO:0019898;GO:0009654;GO:0042549;GO:0005509;GO:0016021;GO:0015979	G3DSA:2.40.160.30: ; SIGNAL_PEPTIDE: Signal peptide region; IPR002628: Photosystem II PsbO, manganese-stabilising; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR011250: Outer membrane protein/outer membrane enzyme PagP, beta-barrel; G3DSA:3.30.2050.10:	NA
comp32374_c6_seq6.p1	Ec-21_005110.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PF06664: Wnt-binding factor required for Wnt secretion; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR31918: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19563_c0_seq1.p1	Ec-21_005180.1	Armadillo-type fold	GO:0000339;GO:0045292;GO:0005488;GO:0051028;GO:0005846	IPR015172: MIF4G-like, type 1; IPR016021: MIF4-like, type 1/2/3; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; IPR015174: MIF4G-like, type 2; IPR016024: Armadillo-type fold; IPR027159: Nuclear cap-binding protein subunit 1; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21563_c0_seq1.p1	Ec-21_005190.1	Mob1/phocein	GO:0005515	IPR005301: MOB kinase activator family	NA
comp30685_c0_seq1.p1	Ec-21_005200.1	K Homology domain, type 1	GO:0003723	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004087: K Homology domain; IPR004088: K Homology domain, type 1; PTHR10288: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24209_c0_seq1.p1	Ec-21_005210.1	Fatty acid elongase	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PS01188: ELO family signature.; IPR002076: ELO family; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3072
comp32840_c2_seq46.p1	Ec-21_005220.1	von Hippel-Lindau disease tumour suppressor, beta domain	GO:0005506;GO:0016705;GO:0016706;GO:0019538;GO:0031418;GO:0055114	IPR006620: Prolyl 4-hydroxylase, alpha subunit; IPR024053: von Hippel-Lindau disease tumour suppressor, beta domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR10869:	NA
comp12933_c0_seq1.p1	Ec-21_005230.1	Protein kinase domain containing protein	NA	G3DSA:3.30.1120.30: ; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; SSF82615: ; IPR000959: POLO box duplicated domain; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; PTHR24345:	NA
comp30568_c0_seq5.p1	Ec-21_005250.1	BEACH domain	n/a;n/a;n/a	PTHR13743: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000409: BEACH domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023362: PH-BEACH domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp125345_c0_seq1.p1	Ec-21_005310.1	von Hippel-Lindau disease tumour suppressor, beta/alpha domain	GO:0005515	IPR024053: von Hippel-Lindau disease tumour suppressor, beta domain; IPR001478: PDZ domain; Coil: ; IPR022772: von Hippel-Lindau disease tumour suppressor, beta/alpha domain	NA
comp24403_c0_seq1.p1	Ec-21_005320.1	Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain	GO:0045454;GO:0055114	IPR016156: FAD/NAD-linked reductase, dimerisation domain; PR00368: FAD-dependent pyridine nucleotide reductase signature; IPR004099: Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain; PTHR22912: ; PR00411: Pyridine nucleotide disulphide reductase class-I signature; IPR023753: FAD/NAD(P)-binding domain	NA
comp26620_c0_seq2.p1	Ec-21_005350.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp11706_c0_seq1.p1	Ec-21_005360.1	HAD-like domain	GO:0005524;GO:0006754;GO:0006810;GO:0015662;GO:0016020	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF12710: haloacid dehalogenase-like hydrolase; IPR008250: P-type ATPase, A domain; IPR023299: P-type ATPase, cytoplasmic domain N; PTHR24093: ; SSF81653: ; IPR023214: HAD-like domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006544: P-type ATPase, subfamily V; IPR001757: P-type ATPase; SSF81665: ; Coil: ; IPR018303: P-type ATPase, phosphorylation site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30779_c2_seq3.p1	Ec-21_005370.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR025313: Domain of unknown function DUF4217; IPR000629: ATP-dependent RNA helicase DEAD-box, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; PTHR24031:	KOG0348
comp24221_c0_seq1.p1	Ec-21_005380.1	TCP-1-like chaperonin intermediate domain	GO:0005524;GO:0006457;GO:0051082	IPR017998: Chaperone tailless complex polypeptide 1 (TCP-1); IPR027410: TCP-1-like chaperonin intermediate domain; IPR027409: GroEL-like apical domain; IPR002194: Chaperonin TCP-1, conserved site; IPR012721: T-complex protein 1, theta subunit; IPR002423: Chaperonin Cpn60/TCP-1 family; SSF54849: ; IPR027413: GroEL-like equatorial domain; SSF48592:	NA
comp11768_c0_seq1.p1	Ec-21_005390.1	WD40/YVTN repeat-like-containing domain	GO:0005515	NA	NA
comp30645_c0_seq2.p1	Ec-21_005410.1	Jumonji and zinc finger domain protein	GO:0003677;GO:0005515;GO:0005622	NA	NA
comp30514_c0_seq1.p2	Ec-21_005420.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp30514_c0_seq1.p1	Ec-21_005430.1	Sirtuin family, catalytic core small domain	GO:0003677;GO:0005677;GO:0006342;GO:0006355;GO:0006476;GO:0008270;GO:0016811;GO:0017136;GO:0045449;GO:0051287;GO:0070403	IPR003000: Sirtuin family; IPR029035: DHS-like NAD/FAD-binding domain; IPR026590: Sirtuin family, catalytic core domain; IPR026591: Sirtuin family, catalytic core small domain	NA
comp32070_c1_seq1.p1	Ec-21_005440.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31728_c0_seq3.p1	Ec-21_005510.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12309_c0_seq1.p1	Ec-21_005540.1	Peptidyl-prolyl cis-trans isomerase	GO:0003755;GO:0006457	SIGNAL_PEPTIDE: Signal peptide region; IPR029000: Cyclophilin-like domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR024936: Cyclophilin-type peptidyl-prolyl cis-trans isomerase; IPR002130: Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30884_c0_seq9.p1	Ec-21_005550.1	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	GO:0003755;GO:0006457	IPR024936: Cyclophilin-type peptidyl-prolyl cis-trans isomerase; IPR002130: Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain; IPR029000: Cyclophilin-like domain; IPR020892: Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site	NA
comp31584_c0_seq5.p2	Ec-21_005560.1	EGF-like domain, extracellular	n/a;n/a;n/a	G3DSA:2.10.25.10: ; PTHR24035: ; SIGNAL_PEPTIDE: Signal peptide region; IPR000742: Epidermal growth factor-like domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013032: EGF-like, conserved site; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PR00011: Type III EGF-like signature; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013111: EGF-like domain, extracellular; SignalP-noTM: ; G3DSA:2.170.300.10: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31592_c3_seq1.p1	Ec-21_005570.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp33907_c0_seq1.p1	Ec-21_005600.1	Sedlin	GO:0006810;GO:0005622;GO:0006888	IPR006722: Trafficking protein particle complex subunit 2; IPR011012: Longin-like domain; G3DSA:3.30.450.70:	NA
comp31584_c0_seq5.p1	Ec-21_005610.1	similar to Structural maintenance of chromosome 3	GO:0005515;GO:0005524;GO:0005694;GO:0051276	IPR029685: Structural maintenance of chromosomes protein 3; IPR010935: SMCs flexible hinge; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR003395: RecF/RecN/SMC, N-terminal; PTHR18937:	NA
comp12327_c0_seq1.p1	Ec-21_005640.1	cysteine desulfurase	GO:0008152;GO:0003824	PTHR11601: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR015424: Pyridoxal phosphate-dependent transferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000192: Aminotransferase class V domain; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG1549
comp32370_c0_seq7.p1	Ec-21_005670.1	Peptidyl-prolyl cis-trans isomerase, PpiC-type	GO:0016853	PTHR10657: ; SSF54534: ; G3DSA:3.10.50.40: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR000297: Peptidyl-prolyl cis-trans isomerase, PpiC-type; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25518_c0_seq3.p1	Ec-21_005690.2	transcription factor E2F	n/a;n/a;n/a	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR003316: E2F/DP family, winged-helix DNA-binding domain; SSF144074: ; IPR032198: E2F transcription factor, CC-MB domain; Coil: ; PTHR12081:SF18: ; IPR015633: E2F Family	KOG2578
comp26327_c0_seq2.p1	Ec-21_005700.1	C2 domain	GO:0005515	PTHR10774: ; Coil: ; IPR000008: C2 domain; IPR000048: IQ motif, EF-hand binding site	NA
comp14379_c0_seq2.p1	Ec-21_005710.1	Phosphoglycerate kinase	GO:0006096;GO:0004618	IPR001576: Phosphoglycerate kinase; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR015824: Phosphoglycerate kinase, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR015901: Phosphoglycerate kinase, C-terminal; IPR015911: Phosphoglycerate kinase, conserved site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1367
comp27901_c0_seq4.p2	Ec-21_005720.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp31181_c0_seq2.p1	Ec-21_005730.2	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp14379_c0_seq2.p2	Ec-21_005760.1	20S proteasome subunit	GO:0051603;GO:0004298;GO:0005839;GO:0006511	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001353: Proteasome, subunit alpha/beta; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029055: Nucleophile aminohydrolases, N-terminal; IPR000426: Proteasome alpha-subunit, N-terminal domain; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11599:	NA
comp20850_c0_seq2.p1	Ec-21_005770.1	Domain of unknown function DUF4033	n/a;n/a;n/a	IPR025114: Domain of unknown function DUF4033; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp19600_c0_seq1.p1	Ec-21_005790.1	serine/threonine-protein kinase 38 (ndr2 protein kinase)	GO:0004672;GO:0005524;GO:0006468	PTHR24356: ; IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR017892: Protein kinase, C-terminal; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000961: AGC-kinase, C-terminal; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	NA
comp29810_c0_seq1.p1	Ec-21_005800.2	Protein phosphatase 2C (PP2C)-like domain	GO:0003824	IPR000222: PPM-type phosphatase, divalent cation binding; IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C family; Coil:	KOG0698
comp24589_c0_seq1.p1	Ec-21_005810.1	SPRY domain	GO:0005515	PF13297: Telomere stability C-terminal; IPR000571: Zinc finger, CCCH-type; IPR001870: B30.2/SPRY domain; IPR024974: Sde2 N-terminal domain; IPR013320: Concanavalin A-like lectin/glucanase domain; IPR003877: SPRY domain; PTHR13363:	NA
comp33179_c0_seq2.p2	Ec-21_005820.1	Rab22, RAB family GTPase	GO:0016020;GO:0007165;GO:0007264;GO:0005525;GO:0015031	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR025662: Sigma-54 interaction domain, ATP-binding site 1; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; IPR020849: Small GTPase superfamily, Ras type; PS51419: small GTPase Rab1 family profile.; IPR003579: Small GTPase superfamily, Rab type; PTHR24073:	NA
comp33179_c0_seq12.p1	Ec-21_005830.1	CDT1 Geminin-binding domain-like	n/a;n/a;n/a	SSF46785: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; IPR014939: CDT1 Geminin-binding domain-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33246_c0_seq8.p1	Ec-21_005840.2	conserved unknown protein	GO:0004221;GO:0006511;n/a	SignalP-TM:	NA
comp21078_c0_seq1.p3	Ec-21_005870.1	WASH complex, subunit CCDC53	GO:0071203	IPR019309: WASH complex, subunit CCDC53	NA
comp31161_c5_seq3.p4	Ec-21_005880.2	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp30640_c1_seq1.p1	Ec-21_005890.1	ARID DNA-binding domain	GO:0003677	Coil: ; SM01014: ARID/BRIGHT DNA binding domain; IPR001606: ARID DNA-binding domain	NA
comp21235_c0_seq2.p2	Ec-21_005900.1	Prenylated rab acceptor PRA1	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR19317: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004895: Prenylated rab acceptor PRA1; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27729_c0_seq1.p1	Ec-21_005910.1	Dyskerin pseudouridine synthase	GO:0006396;GO:0003723;GO:0009451;GO:0001522;GO:0009982	NA	NA
comp31425_c0_seq3.p1	Ec-21_005940.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	IPR001841: Zinc finger, RING-type; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14155: ; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp14912_c0_seq1.p1	Ec-21_005970.1	Nonaspanin (TM9SF)	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004240: Nonaspanin (TM9SF); TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-TM:	NA
comp11814_c0_seq1.p1	Ec-21_005990.1	Histidine phosphatase superfamily	GO:0003993	IPR029033: Histidine phosphatase superfamily; IPR000560: Histidine phosphatase superfamily, clade-2; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11567:SF110: ; SignalP-noTM: ; PTHR11567: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp34516_c0_seq1.p2	Ec-21_006010.1	SIT4 phosphatase-associated protein family	GO:0005525;GO:0005874;GO:0007017	IPR007587: SIT4 phosphatase-associated protein family; Coil:	NA
comp12730_c0_seq1.p1	Ec-21_006020.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp25197_c0_seq1.p1	Ec-21_006030.1	C2H2 zinc finger protein	GO:0005622;GO:0003676;GO:0046872;GO:0008270	IPR007087: Zinc finger, C2H2; Coil:	KOG1721
comp32696_c4_seq1.p1	Ec-21_006040.1	DnaJ domain	GO:0031072	IPR001623: DnaJ domain	NA
comp29773_c0_seq3.p1	Ec-21_006060.1	Mini-chromosome maintenance complex-binding protein	NA	IPR019140: Mini-chromosome maintenance complex-binding protein; PF13615: Putative alanine racemase	NA
comp29208_c0_seq1.p2	Ec-21_006070.1	SGNH hydrolase-type esterase domain	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PF13472: GDSL-like Lipase/Acylhydrolase family; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013830: SGNH hydrolase-type esterase domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp29141_c1_seq2.p2	Ec-21_006080.1	Aspartyl/glutamyl-tRNA amidotransferase subunit B-related	GO:0016874;GO:0016884	IPR004413: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, B subunit; IPR003789: Aspartyl/glutamyl-tRNA amidotransferase subunit B-related; IPR017959: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, subunit B /E; SSF55931: ; IPR018027: Asn/Gln amidotransferase; IPR006075: Aspartyl/Glutamyl-tRNA(Gln) amidotransferase, subunit B/E, catalytic	NA
comp29141_c1_seq4.p1	Ec-21_006100.1	SH2 domain containing protein	GO:0003700;GO:0004871;GO:0005634;GO:0006355;GO:0007165	IPR024983: CHAT domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase	KOG3667
comp24724_c0_seq1.p1	Ec-21_006110.1	Vacuole morphology and inheritance protein 14	GO:0005488;GO:0070772;GO:0043550	IPR026825: Vacuole morphology and inheritance protein 14; IPR011989: Armadillo-like helical; IPR021841: Vacuolar protein 14 C-terminal Fig4-binding domain; IPR021133: HEAT, type 2; PF12755: Vacuolar 14 Fab1-binding region; IPR016024: Armadillo-type fold	NA
comp29208_c0_seq1.p1	Ec-21_006120.1	Helicase, C-terminal	n/a;n/a;n/a	IPR007502: Helicase-associated domain; IPR011545: DEAD/DEAH box helicase domain; IPR011709: Domain of unknown function DUF1605; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR18934: ; IPR002464: DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal	NA
comp12874_c0_seq1.p1	Ec-21_006130.2	conserved unknown protein	n/a;n/a;n/a	PTHR24089:SF234: ; PTHR24089: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24481_c0_seq4.p1	Ec-21_006150.1	Carnitine/choline O-acyltransferase	GO:0016746	IPR000542: Acyltransferase ChoActase/COT/CPT; SSF52777:	KOG3717
comp24358_c0_seq2.p1	Ec-21_006160.1	Histone H2A variant	GO:0003677	NA	NA
comp12900_c0_seq1.p1	Ec-21_006170.1	Nucleotide-binding alpha-beta plait domain	GO:0006397;GO:0005634;GO:0003723;GO:0000166	PF13893: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain); SSF54928: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; PTHR23139: ; IPR006529: U2 snRNP auxiliary factor, large subunit, splicing factor	NA
comp33876_c0_seq1.p1	Ec-21_006180.1	Isochorismatase-like	GO:0008152;GO:0003824	PTHR22937: ; IPR000868: Isochorismatase-like	NA
comp106201_c0_seq1.p1	Ec-21_006190.1	Armadillo-like helical	n/a;GO:0005488	IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold	NA
comp27907_c0_seq2.p1	Ec-21_006210.1	Acetyl-coenzyme A synthetase	GO:0019427;GO:0003987;GO:0008152;GO:0016208;GO:0003824	G3DSA:3.40.50.980: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR025110: AMP-binding enzyme C-terminal domain; IPR020845: AMP-binding, conserved site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF56801: ; PTHR24095: ; SIGNAL_PEPTIDE: Signal peptide region; IPR011904: Acetate-CoA ligase; G3DSA:2.30.38.10: ; IPR000873: AMP-dependent synthetase/ligase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-noTM: ; G3DSA:3.30.300.30:	KOG1175
comp27478_c0_seq6.p1	Ec-21_006220.1	gamma-glutamyl transpeptidase	GO:0006749;GO:0003840	IPR029055: Nucleophile aminohydrolases, N-terminal; IPR000101: Gamma-glutamyltranspeptidase	KOG2410
comp26559_c0_seq1.p2	Ec-21_006230.1	Nucleophile aminohydrolases, N-terminal	GO:0051603;GO:0004298;GO:0005839;GO:0006511	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001353: Proteasome, subunit alpha/beta; IPR023333: Proteasome B-type subunit; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016050: Proteasome beta-type subunit, conserved site; IPR029055: Nucleophile aminohydrolases, N-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11599:	NA
comp26559_c0_seq1.p1	Ec-21_006250.1	SGT1 homologue	n/a;GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; IPR007699: SGS; IPR008978: HSP20-like chaperone; IPR007052: CS domain; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; Coil: ; IPR019734: Tetratricopeptide repeat; PTHR22904:	KOG1309
comp29567_c0_seq3.p1	Ec-21_006260.1	Diphthine synthase, putative	GO:0008152;GO:0008168	IPR004551: Diphthine synthase; PTHR10882: ; IPR000878: Tetrapyrrole methylase; IPR014777: Tetrapyrrole methylase, subdomain 1; IPR014776: Tetrapyrrole methylase, subdomain 2	NA
comp29567_c0_seq7.p1	Ec-21_006270.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp25250_c0_seq2.p1	Ec-21_006280.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp25250_c0_seq2.p2	Ec-21_006290.1	Domain of unknown function DUF1279	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR009688: Domain of unknown function DUF1279; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30022_c0_seq3.p2	Ec-21_006300.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30022_c0_seq3.p1	Ec-21_006310.1	TB2/DP1/HVA22-related protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004345: TB2/DP1/HVA22-related protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12157_c0_seq1.p1	Ec-21_006320.1	Putative: flagellar basal body protein [Chlamydomonas reinhardtii].	n/a;n/a;n/a	IPR021298: Protein of unknown function DUF2870; PTHR13238: ; Coil:	NA
comp32228_c0_seq1.p1	Ec-21_006350.1	PDZ domain	GO:0005515	IPR001478: PDZ domain; Coil:	NA
comp32228_c0_seq2.p2	Ec-21_006370.1	WD40-repeat-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp33767_c0_seq1.p1	Ec-21_006380.1	THO complex, subunit 5	n/a;n/a;n/a	IPR019163: THO complex, subunit 5; PTHR13375:	NA
comp30798_c0_seq2.p1	Ec-21_006390.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR014014: RNA helicase, DEAD-box type, Q motif; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001650: Helicase, C-terminal; Coil: ; PTHR24031:	KOG0331
comp30798_c0_seq2.p2	Ec-21_006400.1	Serine/threonine protein kinase	GO:0004674	IPR010440: Lipopolysaccharide kinase; IPR000719: Protein kinase domain; IPR008266: Tyrosine-protein kinase, active site; G3DSA:1.10.510.10: ; IPR022495: Serine/threonine-protein kinase Bud32; IPR011009: Protein kinase-like domain	KOG3087
comp32115_c0_seq2.p2	Ec-21_006420.1	Glycosyltransferase family 18	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR026116: Glycosyltransferase family 18; PTHR15075:SF2: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF15024: Glycosyltransferase family 18; G3DSA:3.40.50.2300: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32115_c0_seq2.p1	Ec-21_006430.1	Amine oxidase domain protein	GO:0055114;GO:0016491	NA	KOG0029
comp77059_c0_seq1.p1	Ec-21_006440.1	Flagellar WD repeat-containing protein Pf 20	n/a;n/a;n/a	PTHR14604: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; Coil: ; IPR020472: G-protein beta WD-40 repeat	NA
comp29163_c0_seq5.p1	Ec-21_006450.2	dynein heavy chain	GO:0003341;GO:0003777;GO:0005858;GO:0016887	IPR004273: Dynein heavy chain domain; PF12774: Hydrolytic ATP binding site of dynein motor region D1; PF12781: ATP-binding dynein motor region D5; IPR013602: Dynein heavy chain, domain-2; PF12775: P-loop containing dynein motor region D3; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR024317: Dynein heavy chain, P-loop containing D4 domain; IPR003593: AAA+ ATPase domain; IPR026975: Dynein heavy chain 1, axonemal; IPR024743: Dynein heavy chain, coiled coil stalk; Coil: ; IPR026983: Dynein heavy chain	NA
comp9524_c0_seq1.p1	Ec-21_006460.1	hypothetical protein	n/a;n/a;n/a	IPR011992: EF-hand domain pair; Coil: ; SSF47473:	NA
comp12962_c0_seq1.p1	Ec-21_006470.1	conserved unknown protein	n/a;n/a;n/a	Coil: ; IPR013885: Protein of unknown function DUF1764, eukaryotic	NA
comp28402_c0_seq2.p1	Ec-21_006480.1	flagellar associated protein	GO:0016787	IPR029067: CDC48 domain 2-like; IPR003959: ATPase, AAA-type, core; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003338: CDC48, N-terminal subdomain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR003960: ATPase, AAA-type, conserved site; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR23077: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003593: AAA+ ATPase domain; IPR009010: Aspartate decarboxylase-like domain; G3DSA:1.10.8.60: ; G3DSA:2.40.40.20: ; Coil: ; IPR005938: AAA ATPase, CDC48 family	KOG0730
comp28402_c2_seq2.p1	Ec-21_006490.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp33736_c0_seq1.p2	Ec-21_006500.1	tRNA-splicing endonuclease subunit Sen15	n/a;n/a;n/a	IPR018593: tRNA-splicing endonuclease subunit Sen15	NA
comp30040_c0_seq2.p1	Ec-21_006510.1	Baculoviral inhibition of apoptosis protein repeat	GO:0005634;GO:0008270	SSF57924: ; PTHR15835: ; IPR001370: Baculoviral inhibition of apoptosis protein repeat; IPR012935: Zinc finger, C3HC-like	NA
comp30040_c0_seq2.p2	Ec-21_006520.1	Amidohydrolase 1	GO:0016787;GO:0016810	IPR014311: Guanine deaminase; IPR006680: Amidohydrolase 1; SSF51556: ; PTHR11271: ; G3DSA:3.20.20.140: ; IPR011059: Metal-dependent hydrolase, composite domain	NA
comp29525_c0_seq4.p1	Ec-22_000020.1	Nucleotidyl transferase domain	GO:0016779	SSF81631: ; IPR002934: Polymerase, nucleotidyl transferase domain; PTHR12271:SF58: ; PTHR12271: ; Coil: ; G3DSA:3.30.460.10: ; SSF81301:	NA
comp29525_c0_seq8.p2	Ec-22_000030.1	Dolichyl-P-Glc:Glc1Man9GlcNAc2-PP-dolichyl glucosyltransferase ALG8, family GT57	GO:0016758;GO:0005789	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SignalP-noTM: ; IPR004856: Glycosyl transferase, ALG6/ALG8; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2576
comp27398_c0_seq2.p1	Ec-22_000060.1	phycoerythrobilin:ferredoxin oxidoreductase	GO:0010024;GO:0055114;GO:0050897;GO:0016636	SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; IPR009249: Ferredoxin-dependent bilin reductase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF101447: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp11834_c0_seq1.p1	Ec-22_000070.1	6-phosphofructokinase	GO:0003872;GO:0006096;GO:0006002	SIGNAL_PEPTIDE: Signal peptide region; PTHR13697: ; IPR022953: ATP-dependent 6-phosphofructokinase; G3DSA:3.40.50.450: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000023: Phosphofructokinase domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31752_c1_seq9.p1	Ec-22_000080.1	Trehalase N-terminal fragment, family GH37	GO:0000049	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR001661: Glycoside hydrolase, family 37; IPR008928: Six-hairpin glycosidase-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR23403:SF1:	KOG0602
comp12099_c0_seq1.p1	Ec-22_000090.1	aspartyl protease	GO:0004190;GO:0006508	IPR021109: Aspartic peptidase domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001461: Aspartic peptidase; IPR001969: Aspartic peptidase, active site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1339
comp30695_c1_seq3.p1	Ec-22_000110.3	Xaa-Pro dipeptidyl-peptidase-like domain	GO:0016787	PTHR11731: ; IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11731:SF152: ; IPR000383: Xaa-Pro dipeptidyl-peptidase-like domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR013736: Xaa-Pro dipeptidyl-peptidase, C-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005674: CocE/Serine esterase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR008979: Galactose-binding domain-like	NA
comp26754_c1_seq1.p1	Ec-22_000120.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR014014: RNA helicase, DEAD-box type, Q motif; IPR000629: ATP-dependent RNA helicase DEAD-box, conserved site; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001650: Helicase, C-terminal; PTHR24031:	NA
comp27278_c0_seq1.p1	Ec-22_000150.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp28525_c0_seq2.p1	Ec-22_000160.1	Protein of unknown function DUF2373	n/a;n/a;n/a	PTHR22306: ; IPR019327: Protein of unknown function DUF2373	NA
comp25825_c0_seq2.p1	Ec-22_000180.1	Beta-lactamase-like	GO:0006520	G3DSA:3.30.70.20: ; SIGNAL_PEPTIDE: Signal peptide region; IPR001279: Beta-lactamase-like; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PF13370: 4Fe-4S single cluster domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR11935: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21576_c0_seq1.p1	Ec-22_000190.2	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20915_c0_seq1.p1	Ec-22_000250.1	ATP-NAD kinase, PpnK-type, all-beta	GO:0003951;GO:0008152;GO:0019674	IPR018247: EF-Hand 1, calcium-binding site; IPR002504: NAD kinase; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR017437: ATP-NAD kinase, PpnK-type, all-beta; SSF47473: ; IPR017438: Inorganic polyphosphate/ATP-NAD kinase, domain 1; IPR016064: NAD kinase/diacylglycerol kinase-like domain	NA
comp21466_c0_seq1.p1	Ec-22_000260.1	Autophagy-related protein3	NA	PTHR12866: ; IPR007135: Autophagy-related protein 3; IPR019461: Autophagy-related protein 3, C-terminal; IPR007134: Autophagy-related protein 3, N-terminal	NA
comp32160_c0_seq18.p1	Ec-22_000270.1	GTP cyclohydrolase N-terminal	n/a;n/a;n/a	IPR022163: GTP cyclohydrolase N-terminal; SSF142695: ; PTHR21327:	NA
comp26993_c0_seq1.p1	Ec-22_000280.1	Thioredoxin-like fold	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; IPR012336: Thioredoxin-like fold; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32785_c1_seq2.p1	Ec-22_000290.1	40S ribosomal protein S4	GO:0005840;n/a;GO:0005622;GO:0006412;GO:0003735	IPR013845: Ribosomal protein S4e, central region; IPR018199: Ribosomal protein S4e, N-terminal, conserved site; IPR005824: KOW; IPR002942: RNA-binding S4 domain; IPR013843: Ribosomal protein S4e, N-terminal; IPR000876: Ribosomal protein S4e	KOG0378
comp12107_c0_seq1.p2	Ec-22_000310.1	Eukaryotic initiation factor 1	GO:0006413;GO:0003743	IPR012340: Nucleic acid-binding, OB-fold; IPR006196: RNA-binding domain, S1, IF1 type; IPR018104: Translation initiation factor 1A (eIF-1A), conserved site; IPR001253: Translation initiation factor 1A (eIF-1A)	KOG3403
comp10840_c0_seq1.p1	Ec-22_000320.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13414: TPR repeat; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; Coil: ; IPR019734: Tetratricopeptide repeat; PTHR23083:	NA
comp12496_c0_seq1.p1	Ec-22_000330.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp33358_c0_seq1.p1	Ec-22_000360.1	Sedoheptulose-bisphosphatase	GO:0042578;GO:0005975;GO:0042132	G3DSA:3.30.540.10: ; IPR023079: Sedoheptulose-1,7-bisphosphatase; SSF56655: ; IPR020548: Fructose-1,6-bisphosphatase, active site; IPR000146: Fructose-1,6-bisphosphatase class 1/Sedoheputulose-1,7-bisphosphatase; G3DSA:3.40.190.80:	NA
comp12294_c0_seq1.p1	Ec-22_000370.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp30987_c0_seq2.p1	Ec-22_000380.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp20000_c0_seq1.p3	Ec-22_000410.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:1.20.5.110: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF58038: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28809_c0_seq1.p1	Ec-22_000420.1	SET and ADD zinc finger domain protein	GO:0005634;GO:0005515;GO:0008270;GO:0034968;GO:0018024	NA	NA
comp29487_c0_seq1.p1	Ec-22_000440.1	carnitine/acylcarnitine carrier protein	GO:0005488;GO:0006810;GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR24089: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0758
comp33084_c0_seq13.p1	Ec-22_000460.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	PTHR23257: ; IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR011009: Protein kinase-like domain	NA
comp30640_c1_seq1.p2	Ec-22_000470.1	expressed unknown protein	n/a;n/a;n/a	IPR001138: Zn(2)-C6 fungal-type DNA-binding domain; Coil:	NA
comp19377_c0_seq2.p1	Ec-22_000510.1	B-domain containing protein Kua	GO:0019787;GO:0043687;GO:0051246	IPR019547: B domain of TMEM189, localisation domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR24067: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR24067:SF41:	NA
comp29505_c0_seq5.p1	Ec-22_000540.1	conserved unknown protein	n/a;n/a;n/a	Coil: ; PTHR15107:	NA
comp19365_c0_seq1.p1	Ec-22_000550.1	SPG1, Ras superfamily GTPase	GO:0016020;GO:0007165;GO:0007264;GO:0005525	IPR002041: Ran GTPase; PIRSF037527: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; IPR020849: Small GTPase superfamily, Ras type; IPR003579: Small GTPase superfamily, Rab type; PS51419: small GTPase Rab1 family profile.; PTHR24073:	NA
comp32091_c0_seq10.p1	Ec-22_000560.1	CLU domain	n/a;n/a;n/a	PTHR12601: ; IPR025697: CLU domain	NA
comp30817_c0_seq2.p1	Ec-22_000690.2	SAP domain	GO:0003676	IPR003034: SAP domain	NA
comp20270_c0_seq1.p1	Ec-22_000720.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30370_c0_seq4.p1	Ec-22_000740.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR025313: Domain of unknown function DUF4217; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001650: Helicase, C-terminal; Coil: ; PTHR24031:	KOG0345
comp24712_c0_seq2.p1	Ec-22_000760.1	RGS domain	GO:0038032	IPR016137: RGS domain	NA
comp12396_c0_seq1.p1	Ec-22_000790.1	Ribosomal RNA-processing protein 7	n/a;n/a;n/a	IPR024326: Ribosomal RNA-processing protein 7; IPR012677: Nucleotide-binding alpha-beta plait domain; Coil:	NA
comp21313_c0_seq1.p2	Ec-22_000800.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	IPR000571: Zinc finger, CCCH-type; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; IPR003954: RNA recognition motif domain, eukaryote; Coil: ; IPR009145: U2 auxiliary factor small subunit	NA
comp12040_c0_seq1.p1	Ec-22_000820.1	zeaxanthin epoxidase, chloroplast precursor	GO:0008152;GO:0016740	IPR002938: Monooxygenase, FAD-binding; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; G3DSA:3.50.50.60: ; PTHR13789: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF51905: ; PR00420: Aromatic-ring hydroxylase (flavoprotein monooxygenase) signature	NA
comp19912_c0_seq1.p1	Ec-22_000830.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31628_c0_seq6.p2	Ec-22_000840.1	Protein of unknown function DUF778	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR008496: Protein of unknown function DUF778; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31628_c0_seq6.p1	Ec-22_000850.1	Basic-leucine zipper domain	GO:0006355;GO:0043565;GO:0003700	IPR004827: Basic-leucine zipper domain; SSF57959: ; G3DSA:1.20.5.170: ; Coil:	NA
comp29241_c0_seq2.p1	Ec-22_000860.1	Cyclophilin-like domain	GO:0003755;GO:0006457	IPR024936: Cyclophilin-type peptidyl-prolyl cis-trans isomerase; IPR002130: Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain; IPR029000: Cyclophilin-like domain; SignalP-TM:	NA
comp31796_c0_seq1.p1	Ec-22_000880.2	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30727_c0_seq3.p1	Ec-22_000900.1	F-box domain	GO:0005515	IPR001810: F-box domain; G3DSA:1.20.1280.50: ; SSF50993: ; IPR017986: WD40-repeat-containing domain; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; PTHR22838:	NA
comp31346_c0_seq7.p1	Ec-22_000910.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp92133_c0_seq1.p1	Ec-22_000940.1	Hypothetical leucine rich repeat calcium binding protein	NA	PTHR24114:SF2: ; PTHR24114: ; IPR018247: EF-Hand 1, calcium-binding site; SSF52047: ; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR032675: Leucine-rich repeat domain, L domain-like; IPR003590: Leucine-rich repeat, ribonuclease inhibitor subtype; Coil:	NA
comp30636_c0_seq5.p1	Ec-22_000950.1	Cysteine desulfurase	GO:0003824;GO:0031071;GO:0019448;GO:0030170	PTHR11601: ; IPR010970: Cysteine desulfurase, SufS; SignalP-TM: ; IPR015424: Pyridoxal phosphate-dependent transferase; IPR000192: Aminotransferase class V domain; SignalP-noTM: ; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1; IPR015422: Pyridoxal phosphate-dependent transferase, major region, subdomain 2	KOG1549
comp30004_c0_seq3.p1	Ec-22_000960.1	Uncharacterised protein family UPF0434/Trm112	n/a;n/a;n/a	IPR005651: Uncharacterised protein family UPF0434/Trm112; SSF158997: ; PTHR12773: ; G3DSA:2.20.25.10:	NA
comp32529_c0_seq10.p1	Ec-22_000980.1	Bromodomain	GO:0005515	IPR001965: Zinc finger, PHD-type; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001487: Bromodomain; IPR006311: Twin-arginine translocation pathway, signal sequence; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR22880: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR019787: Zinc finger, PHD-finger	NA
comp29030_c0_seq2.p1	Ec-22_000990.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp30004_c0_seq1.p1	Ec-22_001020.1	RME1L2, RME1-like GTPase/ATPase without a C-terminal EH domain	GO:0003924;GO:0005506;GO:0005525;GO:0006118;GO:0008901;GO:0009055;GO:0042597;GO:0051536	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR030381: Dynamin-type guanine nucleotide-binding (G) domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR11216: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF00350: Dynamin family	NA
comp30216_c0_seq1.p1	Ec-22_001040.1	Scaper protein	GO:0004197;GO:0006508;n/a	Coil: ; PTHR31434:	NA
comp26635_c0_seq3.p1	Ec-22_001050.1	Helicase-associated	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR37066: ; SignalP-noTM: ; PTHR37066:SF1: ; IPR005114: Helicase-associated; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12172_c0_seq1.p1	Ec-22_001060.1	Mog1/PsbP, alpha/beta/alpha sandwich	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR016123: Mog1/PsbP, alpha/beta/alpha sandwich; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp48444_c0_seq1.p1	Ec-22_001070.1	conserved unknown protein	GO:0005509	IPR018247: EF-Hand 1, calcium-binding site; PTHR10891: ; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; SSF47473: ; Coil:	NA
comp31108_c0_seq1.p1	Ec-22_001080.1	Presumed helicase required for RNA polymerase II transcription termination and processing of RNAs	n/a;n/a;n/a	PTHR10887: ; PF13086: AAA domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR026852: Helicase Sen1-like; IPR024481: Helicase Sen1, N-terminal; Coil: ; PF13087: AAA domain	NA
comp21185_c0_seq1.p1	Ec-22_001090.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30642_c0_seq4.p1	Ec-22_001130.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp11674_c0_seq1.p1	Ec-22_001140.1	START domain	GO:0008289	PTHR12136: ; SSF55961: ; IPR002913: START domain; IPR023393: START-like domain; Coil:	NA
comp26041_c0_seq1.p1	Ec-22_001150.1	carbonic anhydrase	GO:0008270;GO:0004089	IPR001765: Carbonic anhydrase	KOG1578
comp30124_c0_seq2.p1	Ec-22_001160.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR023270: tRNA (C5-cytosine) methyltransferase, NCL1; SIGNAL_PEPTIDE: Signal peptide region; IPR023267: RNA (C5-cytosine) methyltransferase; PTHR22808: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001678: SAM-dependent methyltransferase RsmB/NOP2-type; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR018314: Bacterial Fmu (Sun)/eukaryotic nucleolar NOL1/Nop2p, conserved site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26337_c0_seq1.p1	Ec-22_001230.1	enoyl-ACP reductase enoyl-ACP reductase	GO:0008152;GO:0016491	PTHR24322: ; SSF51735: ; PF13561: Enoyl-(Acyl carrier protein) reductase; IPR016040: NAD(P)-binding domain	KOG0725
comp55175_c0_seq1.p1	Ec-22_001260.1	hypothetical protein	NA	IPR027912: Protein of unknown function DUF4486; Coil:	NA
comp31422_c0_seq3.p1	Ec-22_001270.1	Armadillo-type fold	GO:0005488	PTHR18460: ; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold; Coil:	NA
comp30535_c0_seq4.p1	Ec-22_001320.1	EamA domain	GO:0016020;GO:0016021	SSF103481: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000620: EamA domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR029044: Nucleotide-diphospho-sugar transferases; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29831_c0_seq1.p1	Ec-22_001370.1	Ribonuclease P/MRP, subunit POP1	GO:0004526;GO:0001682	PTHR22731: ; IPR012590: POPLD; IPR009723: Ribonuclease P/MRP, subunit POP1	NA
comp34057_c0_seq1.p1	Ec-22_001380.1	molybdopterin-synthase adenylyltransferase / sulfurtransferase	NA	IPR001763: Rhodanese-like domain; PTHR10953: ; IPR000594: THIF-type NAD/FAD binding fold; IPR016040: NAD(P)-binding domain; Coil:	NA
comp32528_c0_seq4.p1	Ec-22_001400.1	Ribonuclease domain protein	GO:0005488	IPR021869: Ribonuclease Zc3h12a-like; PTHR12876: ; Coil: ; PF01217: Proline rich extensin signature	NA
comp32710_c0_seq23.p1	Ec-22_001440.1	Riboflavin synthase-like beta-barrel	GO:0055114;GO:0016491	IPR017927: Ferredoxin reductase-type FAD-binding domain; PTHR19370: ; IPR008333: Oxidoreductase, FAD-binding domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:2.40.30.10: ; IPR001834: NADH:cytochrome b5 reductase (CBR); SSF52343: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001433: Oxidoreductase FAD/NAD(P)-binding; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.40.50.80: ; IPR017938: Riboflavin synthase-like beta-barrel; IPR001709: Flavoprotein pyridine nucleotide cytochrome reductase; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28681_c0_seq3.p1	Ec-22_001460.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; G3DSA:1.10.601.10: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR24031: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR014014: RNA helicase, DEAD-box type, Q motif; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG0346
comp30050_c0_seq4.p1	Ec-22_001510.1	alpha-1,2-fucosyltransferase, putative	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA

comp31610_c0_seq5.p1	Ec-22_001530.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp30784_c0_seq4.p1	Ec-22_001570.1	Bicarbonate transporter, eukaryotic	GO:0016020;GO:0006820;GO:0005452;GO:0016021	[illegible]	NA
comp29064_c0_seq2.p1	Ec-22_001580.1	glycine/D-amino acid oxidase-like protein	n/a;n/a;n/a	[illegible]	NA
comp29178_c0_seq1.p1	Ec-22_001610.1	Rhodanese-like domain	GO:0008272;GO:0004792	IPR001763: Rhodanese-like domain; IPR010916: TonB box, conserved site; IPR001307: Thiosulphate sulfurtransferase, conserved site; PTHR11364:	NA
comp56440_c0_seq1.p1	Ec-22_001630.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp30995_c0_seq2.p1	Ec-22_001640.1	Protein of unknown function DUF1415	n/a;n/a;n/a	IPR009858: Protein of unknown function DUF1415	NA
comp37231_c0_seq1.p2	Ec-22_001650.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp12439_c0_seq1.p1	Ec-22_001710.1	hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp32297_c0_seq9.p1	Ec-22_001730.1	Tetratricopeptide-like helical domain	GO:0005506;GO:0005515;GO:0016491;GO:0016705;GO:0031418;GO:0055114	[illegible]	NA
comp31150_c0_seq1.p1	Ec-22_001750.1	Jumonji domain protein	n/a;n/a;n/a	NA	NA
comp19625_c0_seq1.p1	Ec-22_001770.1	Two pore domain potassium channel domain	n/a;n/a;n/a	[illegible]	NA
comp31266_c0_seq9.p1	Ec-22_001780.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30812_c1_seq1.p2	Ec-22_001810.1	Tetratricopeptide-like helical domain	GO:0005515	PTHR26312: ; SSF48452: ; PF13414: TPR repeat; IPR011990: Tetratricopeptide-like helical domain; IPR019734: Tetratricopeptide repeat	NA
comp32745_c0_seq2.p1	Ec-22_001840.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	PF13637: Ankyrin repeats (many copies); IPR020683: Ankyrin repeat-containing domain; PF13857: Ankyrin repeats (many copies); PTHR24123: ; IPR002110: Ankyrin repeat	NA
comp34390_c0_seq1.p1	Ec-22_001850.1	Armadillo-like helical	n/a;GO:0005524;GO:0016887	[illegible]	NA
comp28344_c1_seq3.p1	Ec-22_001880.1	Hook-related protein family	GO:0000226;GO:0005737;GO:0008017	SSF116907: ; IPR008636: Hook-related protein family; Coil:	NA
comp32777_c2_seq14.p2	Ec-22_001910.1	SH3-like domain, bacterial-type	GO:0000772;GO:0016020	IPR003646: SH3-like domain, bacterial-type; IPR013761: Sterile alpha motif/pointed domain; IPR021129: Sterile alpha motif, type 1	NA
comp28345_c0_seq2.p1	Ec-22_001920.2	RanBP, RRM1, C2H2 zinc finger protein	GO:0008270	IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; IPR007087: Zinc finger, C2H2; PTHR13948: ; IPR001876: Zinc finger, RanBP2-type	KOG0154/
comp30565_c0_seq8.p2	Ec-22_001940.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp30565_c0_seq9.p1	Ec-22_001960.1	Homologue of Arabidopsis MOS2 (MODIFIER OF SNC1, 2)	GO:0005622;GO:0003676	[illegible]	NA
comp29542_c0_seq4.p1	Ec-22_001970.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp34763_c0_seq1.p1	Ec-22_002050.1	Tetratricopeptide-like helical domain	GO:0005515	NA	NA
comp20926_c0_seq2.p1	Ec-22_002060.1	Ribosomal protein L13e	GO:0005840;GO:0005622;GO:0006412;GO:0003735	[illegible]	NA
comp28167_c0_seq1.p1	Ec-22_002070.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30142_c0_seq5.p1	Ec-22_002080.1	MYST-type histone acetyltransferase and chromo domain protein	GO:0006333;GO:0005634;GO:0003682;GO:0000785	NA	NA
comp30236_c0_seq5.p1	Ec-22_002100.1	Initiator tRNA phosphoribosyl transferase	GO:0016763;GO:0043399;GO:0019988	[illegible]	NA
comp30236_c0_seq8.p1	Ec-22_002100.2	Initiator tRNA phosphoribosyl transferase	GO:0016763	[illegible]	NA
comp32602_c1_seq3.p1	Ec-22_002110.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp32602_c1_seq4.p1	Ec-22_002130.1	FMP27, C-terminal	n/a;n/a;n/a	[illegible]	NA
comp28302_c0_seq1.p1	Ec-22_002140.1	Protein of unknown function DUF2358	n/a;n/a;n/a	[illegible]	NA
comp30501_c0_seq1.p1	Ec-22_002150.1	nucleolar complex associated 2 homolog	NA	[illegible]	NA
comp33225_c0_seq1.p1	Ec-22_002160.2	Hypothetical leucine rich repeat protein	GO:0005515	[illegible]	NA
comp33266_c0_seq6.p1	Ec-22_002160.4	Hypothetical leucine rich repeat protein	GO:0005515	[illegible]	NA
comp26254_c0_seq1.p1	Ec-22_002190.1	C2 domain	GO:0005515	[illegible]	NA
comp32164_c0_seq2.p1	Ec-22_002250.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp28686_c0_seq1.p1	Ec-22_002280.1	BTB/POZ fold	GO:0005515	[illegible]	NA
comp26367_c0_seq1.p1	Ec-22_002310.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp33461_c0_seq1.p1	Ec-22_002330.1	60S ribosomal protein L26	GO:0005840;GO:0006412;GO:0005622;GO:0003735	[illegible]	NA
comp33817_c0_seq1.p1	Ec-22_002360.1	eukaryotic translation initiation factor eIF3 e subunit	GO:0005515	[illegible]	NA
comp32550_c0_seq12.p1	Ec-22_002370.1	Protein of unknown function DUF1997	n/a;n/a;n/a	[illegible]	NA
comp30335_c0_seq2.p1	Ec-22_002380.1	calcium/ calmodulin-dependent protein kinase 1	n/a;GO:0006468;GO:0004672	[illegible]	NA
comp25787_c1_seq2.p1	Ec-22_002400.1	Methylcrotonoyl-CoA carboxylase beta chain	GO:0016874;GO:0005739	[illegible]	KOG0540
comp24230_c0_seq1.p1	Ec-22_002410.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp12000_c0_seq1.p1	Ec-22_002440.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp30545_c4_seq3.p1	Ec-22_002450.1	manganese superoxide dismutase	GO:0006801;GO:0004784;GO:0055114;GO:0046872	[illegible]	KOG0876
comp25082_c0_seq2.p1	Ec-22_002490.1	Oligosaccharyltransferase, OST48 subunit (or beta subunit)	GO:0018279;GO:0004579;GO:0005789	[illegible]	KOG2754
comp32203_c1_seq2.p1	Ec-22_002500.2	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp28775_c0_seq1.p1	Ec-22_002520.1	S-Adenosylmethionine decarboxylase	GO:0004014;GO:0006597;GO:0008295	[illegible]	KOG0788
comp27804_c0_seq1.p1	Ec-22_002530.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp27804_c0_seq1.p2	Ec-22_002540.1	UBA-like	GO:0005515	[illegible]	NA
comp28328_c0_seq1.p1	Ec-22_002550.1	WW domain	GO:0005515	[illegible]	NA
comp21011_c0_seq1.p1	Ec-22_002580.1	Cyclin-like	n/a;n/a;n/a	[illegible]	NA
comp33963_c0_seq1.p1	Ec-22_002600.1	39S ribosomal protein L46, mitochondrial	GO:0016787	[illegible]	NA
comp20319_c0_seq1.p1	Ec-22_002610.1	S-Adenosyl homocysteine hydrolase	n/a;n/a;n/a	[illegible]	KOG1370
comp32424_c0_seq5.p1	Ec-22_002630.1	Mediator complex, subunit Med20	GO:0001104;GO:0006357;GO:0016592	[illegible]	NA
comp30060_c0_seq5.p2	Ec-22_002640.1	FKBP-type peptidyl-prolyl cis-trans isomerase	GO:0006457	[illegible]	KOG0549
comp30060_c0_seq5.p1	Ec-22_002650.2	SGT1	n/a;n/a;n/a	[illegible]	NA
comp32360_c0_seq9.p1	Ec-22_002660.1	Ankyrin repeat	GO:0005515	[illegible]	NA
comp28636_c0_seq8.p1	Ec-22_002670.1	Small Conductance Mechanosensitive Ion channel	GO:0016020;GO:0055085	[illegible]	NA
comp28636_c0_seq8.p2	Ec-22_002680.1	Macro domain	n/a;n/a;n/a	[illegible]	NA
comp32062_c0_seq29.p1	Ec-22_002690.1	FMN-binding split barrel	GO:0055114;GO:0010181;GO:0016491	[illegible]	NA
comp29874_c0_seq1.p1	Ec-22_002730.1	Coatomer, gamma subunit, appendage, Ig-like subdomain	GO:0005198;GO:0006886;GO:0016192;GO:0030126	[illegible]	KOG2063
comp24969_c0_seq1.p1	Ec-22_002740.1	Acetyltransferase (GNAT) domain protein	n/a;n/a;n/a	NA	NA
comp30607_c0_seq1.p2	Ec-22_002780.1	Heat shock protein DnaJ, cysteine-rich domain	GO:0031072;GO:0051082	[illegible]	NA
comp30607_c0_seq1.p1	Ec-22_002800.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	[illegible]	NA
comp26361_c1_seq3.p3	Ec-22_002820.1	V-ATPase proteolipid subunit C-like domain	GO:0033179;GO:0015991;GO:0033177;GO:0015078	[illegible]	NA
comp26361_c1_seq1.p1	Ec-22_002830.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0006139;GO:0019205;GO:0019201	[illegible]	NA
comp26917_c0_seq3.p1	Ec-22_002840.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp30788_c0_seq2.p1	Ec-22_002850.1	Acetyl-CoA acetyltransferase	GO:0008152;GO:0003824;GO:0016747	[illegible]	NA
comp32794_c0_seq1.p1	Ec-22_002860.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp29632_c0_seq7.p1	Ec-22_002870.1	Coagulation factor 5/8 C-terminal type domain	n/a;n/a;n/a	[illegible]	NA
comp31397_c0_seq3.p1	Ec-22_002910.3	BTB/POZ fold	GO:0005515	[illegible]	NA
comp25153_c0_seq1.p1	Ec-22_002920.1	acyl-CoA oxidase	GO:0016627;GO:0006118;GO:0055114	[illegible]	KOG0136
comp28406_c0_seq2.p1	Ec-22_002940.1	AP2/ERF domain	GO:0003700;GO:0006355	[illegible]	NA
comp25000_c0_seq1.p1	Ec-22_002960.1	Homeodomain-like	GO:0003677	[illegible]	NA
comp24933_c0_seq2.p1	Ec-22_002980.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30566_c0_seq1.p1	Ec-22_003010.1	Hypothetical leucine rich repeat protein	NA	[illegible]	NA
comp20681_c0_seq1.p1	Ec-22_003050.1	Ribosomal protein L36e	GO:0005840;GO:0005622;GO:0006412;GO:0003735	[illegible]	NA
comp12415_c0_seq1.p1	Ec-22_003080.1	Cwf19-like protein, C-terminal domain-2	n/a;n/a;n/a	[illegible]	NA
comp28993_c0_seq1.p1	Ec-22_003090.1	Cation efflux protein	GO:0055085;GO:0006812;GO:0016021;GO:0008324	[illegible]	NA
comp32109_c0_seq10.p1	Ec-22_003140.3	von Willebrand factor, type A	n/a;n/a;n/a	[illegible]	NA
comp17598_c0_seq2.p1	Ec-22_003250.1	similar to importin 11	GO:0005488	[illegible]	NA
comp28718_c0_seq1.p1	Ec-22_003260.1	RNA recognition motif domain	GO:0003676;GO:0000166	[illegible]	NA
comp28718_c0_seq1.p2	Ec-22_003270.1	Tubby, C-terminal	n/a;n/a;n/a	[illegible]	NA
comp20791_c0_seq1.p3	Ec-22_003280.1	Nucleoside diphosphate kinase	GO:0005524;GO:0006241;GO:0006165;GO:0004550;GO:0006228;GO:0006183	[illegible]	NA
comp29746_c0_seq4.p1	Ec-22_003290.1	Rhodanese-like domain	n/a;n/a;n/a	[illegible]	NA
comp26765_c0_seq1.p1	Ec-22_003300.1	Ankyrin repeat-containing domain	n/a;GO:0005515	[illegible]	NA
comp30818_c0_seq5.p1	Ec-22_003320.1	Trehalose 6-phosphate synthase, family GT20 / Trehalose 6-phosphate phosphatase	GO:0003824;GO:0005992	[illegible]	KOG1050
comp23689_c0_seq1.p1	Ec-22_003360.1	ExV-1-7 domain protein	NA	NA	NA
comp30619_c1_seq5.p1	Ec-22_003380.1	Sup35, eukaryotic translation termination factor eRF3	n/a;n/a;n/a	[illegible]	NA
comp20885_c0_seq1.p1	Ec-22_003400.1	Basic-leucine zipper domain	GO:0005634;GO:0006355;GO:0043565;GO:0003700;GO:0046983	NA	NA
comp34444_c0_seq1.p1	Ec-22_003405.1	hypothetical protein	NA	Coil:	NA
comp30215_c0_seq1.p2	Ec-22_003450.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp10905_c0_seq1.p1	Ec-22_003470.1	coiled-coil flagellar protein, move backward only 2	n/a;n/a;n/a	[illegible]	NA
comp19567_c0_seq1.p1	Ec-22_003530.1	pepsinogen	GO:0004190;GO:0006508	[illegible]	KOG1339
comp30742_c1_seq2.p1	Ec-22_003540.1	DENN domain	n/a;n/a;n/a	[illegible]	NA
comp31870_c0_seq1.p1	Ec-22_003570.1	Ribonuclease H1, N-terminal	GO:0003676;GO:0004523	[illegible]	NA
comp26342_c0_seq1.p1	Ec-22_003610.1	RmlC-like cupin domain	GO:0006355	[illegible]	NA
comp32203_c1_seq8.p1	Ec-22_003620.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp30612_c0_seq2.p1	Ec-22_003630.1	XPG-I domain	GO:0003677;GO:0003824;GO:0004518	[illegible]	NA
comp32865_c0_seq12.p1	Ec-22_003640.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp31729_c1_seq5.p1	Ec-22_003650.2	hypothetical protein	n/a;n/a;n/a	NA	NA
comp12498_c0_seq1.p1	Ec-22_003660.1	Phytanoyl-CoA dioxygenase	n/a;n/a;n/a	[illegible]	NA
comp32165_c1_seq1.p1	Ec-22_003680.1	Helicase, C-terminal	n/a;n/a;n/a	[illegible]	NA
comp34050_c0_seq1.p1	Ec-22_003710.1	hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp26574_c0_seq1.p1	Ec-22_003740.1	Tyrosine kinase, EPH (ephrin) receptor family	NA	[illegible]	KOG0196
comp19978_c0_seq2.p1	Ec-22_003750.1	NB-ARC and TPR repeat-containing protein	GO:0051539	[illegible]	NA
comp11871_c0_seq2.p1	Ec-22_003780.2	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp11871_c0_seq2.p2	Ec-22_003790.1	similar to Vacuolar protein sorting 29 (Vesicle protein sorting 29)	n/a;n/a;n/a	[illegible]	NA
comp18504_c0_seq1.p1	Ec-22_003810.1	FMN-binding split barrel	GO:0010181;GO:0016491;GO:0055114	[illegible]	NA
comp28099_c0_seq1.p1	Ec-22_003820.1	Complex I intermediate-associated protein 30, mitochondrial precursor (NADH dehydrogenase [ubiquinon])	n/a;n/a;n/a	[illegible]	KOG2435
comp32018_c0_seq7.p1	Ec-22_003830.1	Nucleic acid-binding, OB-fold	GO:0003677;GO:0005524;GO:0006260;n/a	[illegible]	NA
comp32764_c5_seq2.p1	Ec-22_003850.1	Monodehydroascorbate reductase-like	GO:0050660;GO:0016656;GO:0055114;GO:0016491	[illegible]	NA
comp32018_c0_seq7.p4	Ec-22_003860.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp32743_c0_seq5.p1	Ec-22_003870.2	dicer-like 3	GO:0003723;GO:0004525;GO:0006396	[illegible]	NA
comp32710_c0_seq47.p1	Ec-22_003880.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp13110_c0_seq1.p1	Ec-22_003890.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp25669_c0_seq1.p1	Ec-22_003910.3	FNIP	n/a;n/a;n/a	[illegible]	NA
comp32140_c0_seq5.p1	Ec-22_003930.1	Carbohydrate-binding WSC	n/a;n/a;n/a	[illegible]	NA
comp126944_c0_seq1.p1	Ec-23_000040.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp31258_c0_seq10.p1	Ec-23_000050.1	expressed unknown protein	GO:0005634;GO:0003677;GO:0006355;GO:0003682	[illegible]	NA
comp20360_c0_seq2.p1	Ec-23_000060.2	RNA recognition motif domain	GO:0003676	[illegible]	NA
comp26661_c1_seq1.p1	Ec-23_000070.1	Putative NIN-like transcription factor	n/a;n/a;n/a	[illegible]	NA
comp24732_c0_seq1.p1	Ec-23_000110.1	orotidine-5'-phosphate decarboxylase	GO:0004590;GO:0003824;GO:0006207	[illegible]	KOG1377
comp30899_c0_seq1.p1	Ec-23_000130.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp20573_c0_seq1.p1	Ec-23_000150.1	NAD(P)-binding domain	GO:0003824;GO:0005488;GO:0008152	[illegible]	KOG4288
comp30113_c0_seq1.p1	Ec-23_000170.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp29838_c1_seq2.p1	Ec-23_000180.1	General substrate transporter	GO:0016020;GO:0055085;GO:0016021;GO:0022857;GO:0022891	[illegible]	NA
comp32731_c0_seq1.p1	Ec-23_000190.1	Similar to calmodulin	GO:0005509	[illegible]	NA
comp31310_c0_seq1.p1	Ec-23_000200.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp29630_c0_seq4.p1	Ec-23_000210.1	SAP domain	GO:0003676	[illegible]	NA
comp31097_c0_seq1.p1	Ec-23_000220.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp35357_c0_seq1.p1	Ec-23_000250.1	hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp30416_c0_seq2.p1	Ec-23_000260.1	conserved unknown protein	GO:0005515	[illegible]	NA
comp32083_c0_seq4.p1	Ec-23_000290.1	Bacterial bifunctional deaminase-reductase, C-terminal	GO:0009231;GO:0008703;GO:0055114	[illegible]	NA
comp12548_c0_seq1.p1	Ec-23_000300.2	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp23934_c0_seq1.p1	Ec-23_000310.1	ALIX V-shaped and BRO1-like domain protein	n/a;n/a;n/a	[illegible]	NA
comp32083_c0_seq6.p1	Ec-23_000320.1	ALIX V-shaped and BRO1-like domain protein	n/a;n/a;n/a	[illegible]	NA
comp32157_c0_seq5.p1	Ec-23_000340.1	dDENN domain	n/a;n/a;n/a	[illegible]	NA
comp27749_c0_seq2.p1	Ec-23_000360.1	aureochrome 1	GO:0004871;GO:0007165	[illegible]	NA
comp31054_c0_seq6.p3	Ec-23_000370.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp24160_c0_seq1.p1	Ec-23_000380.1	Cupin-like domain protein	n/a;n/a;n/a	NA	NA
comp32579_c0_seq35.p1	Ec-23_000390.1	Xylosyltransferase, family GT14	GO:0016020;GO:0008375	[illegible]	NA
comp32579_c0_seq32.p2	Ec-23_000410.1	HAD-superfamily hydrolase, subfamily IIA	n/a;n/a;n/a	[illegible]	NA
comp11933_c0_seq1.p1	Ec-23_000420.1	FUN14	GO:0005509	[illegible]	NA
comp26787_c0_seq4.p2	Ec-23_000440.1	Golgi apparatus membrane protein TVP15	GO:0004553;GO:0005975	[illegible]	NA
comp26787_c0_seq4.p1	Ec-23_000460.1	Glycolate Oxidase	GO:0003973;GO:0005777;GO:0055114;GO:0010181;GO:0009853;GO:0016491	[illegible]	KOG0538
comp31607_c0_seq2.p1	Ec-23_000470.2	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp31258_c0_seq4.p1	Ec-23_000480.1	Endonuclease/exonuclease/phosphatase domain protein	n/a;n/a;n/a	[illegible]	NA
comp26299_c0_seq3.p1	Ec-11_005180.5	Mannuronan C-5-epimerase internal fragment	NA	[illegible]	NA
comp31204_c0_seq4.p1	Ec-23_000500.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp25175_c0_seq3.p1	Ec-23_000520.1	Major facilitator superfamily domain	n/a;n/a;n/a	[illegible]	NA
comp32133_c2_seq7.p1	Ec-23_000540.1	Conserved hypothetical protein CHP02464	n/a;n/a;n/a	[illegible]	NA
comp21302_c0_seq2.p1	Ec-23_000570.1	mannitol 1-phosphate dehydrogenase	n/a;n/a;n/a	NA	NA
comp55946_c0_seq1.p1	Ec-23_000610.1	cAMP-dependent protein kinase catalytic subunit (PKA)	GO:0004672;GO:0005524;GO:0006468	[illegible]	KOG0616
comp30063_c0_seq1.p1	Ec-23_000620.1	Possible CBL-interacting-like PK	GO:0006468;GO:0004674;GO:0004672	[illegible]	KOG0583
comp31623_c0_seq1.p1	Ec-23_000630.1	Probable 16S rRNA-processing protein rimM	GO:0005840;GO:0006364;GO:0043022	[illegible]	NA
comp30722_c0_seq5.p1	Ec-23_000640.1	Mediator complex, subunit Med14	GO:0001104;GO:0006357;GO:0016592	[illegible]	NA
comp32370_c0_seq35.p1	Ec-23_000660.1	ATPase, AAA-type, core	GO:0005524;GO:0019538	[illegible]	NA
comp24880_c0_seq1.p1	Ec-23_000670.1	ABC transporter	GO:0005524;GO:0016887	[illegible]	NA
comp24880_c0_seq1.p2	Ec-23_000680.1	HCF101 (HIGH-CHLOROPHYLL-FLUORESCENCE 101); ATP binding	NA	[illegible]	NA
comp25142_c0_seq2.p1	Ec-23_000690.1	UV excision repair protein RAD23B homolog	GO:0005515	[illegible]	NA
comp25142_c0_seq4.p1	Ec-23_000700.1	putative Glutathione S-transferase	GO:0005515	[illegible]	KOG0406
comp11711_c0_seq1.p1	Ec-23_000710.1	photosystem II stability/assembly factor HCF136	n/a;n/a;n/a	[illegible]	NA
comp35022_c0_seq1.p1	Ec-23_000720.1	cytoplasmic ribosomal protein L18	GO:0005840;GO:0005622;GO:0006412;GO:0003735	[illegible]	NA
comp24784_c0_seq2.p1	Ec-23_000740.1	Serine/threonine-protein phosphatase PP2A catalytic subunit	GO:0016787	[illegible]	KOG0376
comp19901_c0_seq2.p1	Ec-23_000750.1	putative: similar to cytoplasmic dynein intermediate chain	GO:0005515	[illegible]	KOG1587
comp25047_c0_seq1.p1	Ec-23_000760.1	eukaryotic initiation factor 4B	GO:0000166	[illegible]	NA
comp16251_c0_seq1.p1	Ec-23_000810.1	Ankyrin repeat-containing domain	n/a;GO:0005515	[illegible]	NA
comp32353_c2_seq3.p1	Ec-23_000820.1	Monooxygenase	GO:0008152;GO:0016491	[illegible]	KOG3855
comp24352_c0_seq1.p1	Ec-23_000830.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp26653_c0_seq1.p1	Ec-23_000840.1	AAA+ ATPase domain	GO:0003684;GO:0004176;GO:0004252;GO:0005524;GO:0006281;GO:0006508	[illegible]	NA
comp29340_c0_seq10.p1	Ec-23_000850.1	Histidine kinase-like ATPase, C-terminal domain	GO:0005524	[illegible]	NA
comp24892_c0_seq3.p2	Ec-23_000860.1	Protein of unknown function DUF1295	n/a;n/a;n/a	[illegible]	NA
comp31291_c0_seq13.p1	Ec-23_000870.1	Ankyrin repeat-containing domain	n/a;GO:0005515	[illegible]	NA
comp20692_c0_seq2.p1	Ec-23_000910.1	COQ9	n/a;GO:0006744	[illegible]	NA
comp31169_c0_seq16.p1	Ec-23_000920.1	Multi antimicrobial extrusion protein	GO:0016020;GO:0055085;GO:0015238;GO:0015297;GO:0006855	[illegible]	NA
comp31136_c0_seq1.p1	Ec-23_000930.1	similar to ATP synthase mitochondrial F1 complex assembly factor 2	GO:0005515;GO:0043461	[illegible]	NA
comp28627_c0_seq1.p1	Ec-23_000950.1	Casein kinase (serine/threonine/tyrosine protein kinase)	GO:0005524;GO:0006468;GO:0004672	[illegible]	KOG1164
comp32294_c1_seq13.p1	Ec-23_000970.1	Ribosome biogenesis regulatory protein homolog	GO:0005634;GO:0042254	[illegible]	NA
comp27827_c0_seq1.p1	Ec-23_001000.1	AhpD-like	n/a;n/a;n/a	[illegible]	NA
comp24223_c0_seq1.p1	Ec-23_001010.2	Ubiquitin-conjugating enzyme/RWD-like	GO:0019787;GO:0043687;GO:0051246;n/a	[illegible]	NA
comp24993_c0_seq1.p1	Ec-23_001020.1	Gem-associated protein 2	GO:0000398;GO:0005681;GO:0000387	[illegible]	NA
comp19379_c0_seq1.p1	Ec-23_001040.1	Homeodomain-like	GO:0003677	[illegible]	NA
comp30180_c0_seq2.p1	Ec-23_001060.1	Cysteamine dioxygenase	GO:0016702;GO:0055114;GO:0047800	[illegible]	NA
comp20109_c0_seq1.p1	Ec-23_001080.1	ER membrane protein complex subunit 6	GO:0005783;GO:0016021;GO:0072546	[illegible]	NA
comp25191_c0_seq1.p1	Ec-23_001100.1	Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote	n/a;GO:0005515	[illegible]	NA
comp28420_c0_seq2.p1	Ec-23_001120.1	ExV-1-7 domain protein	NA	NA	NA
comp30993_c1_seq3.p2	Ec-23_001170.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp13139_c0_seq1.p1	Ec-23_001190.1	Rab6, RAB family GTPase	GO:0005622;GO:0007264;GO:0005525;GO:0015031	[illegible]	NA
comp34458_c0_seq1.p1	Ec-23_001220.1	Dihydroflavonol-4-reductase	GO:0003824;GO:0005488;GO:0008152	[illegible]	KOG1502
comp32447_c1_seq6.p1	Ec-23_001230.1	CDP-diacylglycerol-inositol 3-phosphatidyltransferase	GO:0016020;GO:0008654;GO:0016780	[illegible]	KOG3240
comp31223_c0_seq1.p1	Ec-23_001240.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	[illegible]	NA
comp31076_c3_seq1.p1	Ec-23_001250.1	Aquarius intron-binding protein similar to aquarius	GO:0003677;GO:0005524;GO:0016787	[illegible]	KOG1806
comp12884_c0_seq1.p1	Ec-23_001260.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31442_c1_seq2.p1	Ec-23_001270.1	PDZ domain	GO:0005515	[illegible]	NA
comp32821_c2_seq19.p1	Ec-23_001310.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp31880_c0_seq7.p1	Ec-23_001350.1	PAS domain	GO:0004871;GO:0007165	[illegible]	NA
comp27499_c0_seq3.p1	Ec-23_001360.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp24519_c0_seq1.p1	Ec-23_001400.1	Glyoxalase/bleomycin resistance protein/dioxygenase	n/a;n/a;n/a	[illegible]	KOG3105
comp30669_c0_seq1.p1	Ec-23_001420.1	WD40-repeat-containing domain	GO:0005515	NA	NA
comp30669_c0_seq1.p2	Ec-23_001430.1	Protein of unknown function DUF4336	n/a;n/a;n/a	[illegible]	NA
comp24625_c0_seq1.p1	Ec-23_001460.1	NOP58 subunit of the C/D ribonucleoprotein complex	n/a;n/a;n/a	NA	NA
comp24994_c0_seq2.p1	Ec-23_001480.1	HSP40/DnaJ peptide-binding	GO:0006457;GO:0051082	[illegible]	NA
comp19612_c0_seq1.p1	Ec-23_001490.1	Hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp32898_c0_seq9.p1	Ec-23_001500.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp26743_c0_seq6.p2	Ec-23_001580.1	Protein of unknown function DUF1118	n/a;n/a;n/a	[illegible]	NA
comp26743_c0_seq6.p1	Ec-23_001600.1	WD40/YVTN repeat-like-containing domain	GO:0005515	[illegible]	NA
comp31772_c0_seq9.p1	Ec-23_001670.1	Helicase, C-terminal	GO:0003677;GO:0005524	[illegible]	NA
comp29914_c0_seq3.p1	Ec-23_001700.1	Protein of unknown function UPF0301	n/a;n/a;n/a	[illegible]	NA
comp28364_c0_seq1.p1	Ec-23_001710.1	Chromo domain-like	GO:0004221;GO:0006511	[illegible]	NA
comp32878_c0_seq13.p1	Ec-23_001730.1	EF-hand domain pair	GO:0005509	[illegible]	NA
comp28102_c0_seq2.p1	Ec-23_001820.1	DNA topoisomerase II	GO:0003677;GO:0005524;GO:0003918;GO:0006265	[illegible]	NA
comp30207_c0_seq5.p1	Ec-23_001830.1	Cyclophilin-like domain	GO:0003755;GO:0006457	[illegible]	NA
comp22880_c0_seq1.p1	Ec-23_001840.1	putative oxidoreductase	GO:0016491	[illegible]	NA
comp25067_c0_seq1.p2	Ec-23_001850.2	Prohibitin complex subunit 2	NA	[illegible]	NA
comp25067_c0_seq1.p1	Ec-23_001860.1	alpha-Glucosidase II, beta subunit	GO:0006491	[illegible]	KOG2397
comp86158_c0_seq1.p1	Ec-23_001870.2	WD40 repeat	GO:0005515	[illegible]	NA
comp32246_c4_seq15.p1	Ec-23_001880.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp31941_c0_seq2.p1	Ec-23_001890.4	Major facilitator superfamily domain	n/a;n/a;n/a	[illegible]	NA
comp27232_c0_seq2.p1	Ec-23_001940.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524;GO:0016887	[illegible]	NA
comp32935_c4_seq11.p1	Ec-23_001950.1	NUDIX hydrolase domain	GO:0016787	[illegible]	NA
comp32296_c0_seq19.p1	Ec-23_001960.1	EF-hand domain pair	GO:0005509;n/a	[illegible]	NA
comp25614_c0_seq1.p1	Ec-23_001970.1	Paired amphipathic helix	GO:0005634;GO:0006355	[illegible]	NA
comp12607_c0_seq1.p1	Ec-23_001970.2	Paired amphipathic helix	GO:0005634;GO:0006355	[illegible]	NA
comp34638_c0_seq1.p1	Ec-23_002000.1	Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain	GO:0000413;GO:0003755;GO:0006457	[illegible]	NA
comp46133_c0_seq1.p1	Ec-23_002020.1	Bulb-type lectin domain	n/a;n/a;n/a	[illegible]	NA
comp29410_c1_seq4.p1	Ec-23_002030.1	Putative lysophospholipase, monoglyceride lipase	GO:0005622;GO:0008152;GO:0016301;GO:0016310;GO:0016774	[illegible]	KOG1455
comp12417_c0_seq1.p1	Ec-23_002040.1	RNA recognition motif domain	GO:0003676;GO:0000166	[illegible]	NA
comp32296_c0_seq3.p1	Ec-23_002050.1	AAA+ ATPase domain protein	GO:0005524;GO:0006810;GO:0016021;GO:0016887;GO:0042626;GO:0055085	[illegible]	NA
comp32998_c0_seq8.p3	Ec-23_002100.1	High mobility group and SAP domain protein	GO:0003677;GO:0005634;GO:0005515;GO:0006355	[illegible]	NA
comp32998_c0_seq8.p1	Ec-23_002110.1	Electron transfer flavoprotein-ubiquinone oxidoreductase	GO:0004174;GO:0055114	[illegible]	KOG2415
comp20986_c1_seq3.p2	Ec-23_002130.1	Alkyl hydroperoxide reductase subunit C/ Thiol specific antioxidant	GO:0016209;GO:0016491;GO:0055114	[illegible]	NA
comp22268_c0_seq1.p1	Ec-23_002160.3	hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp23401_c0_seq2.p1	Ec-23_002170.1	CLASP N-terminal domain	GO:0005488	[illegible]	NA
comp20986_c1_seq2.p1	Ec-23_002180.1	Protein with LSm motif. Putative LSm11	NA	[illegible]	NA
comp31347_c0_seq5.p1	Ec-23_002190.1	NUDIX hydrolase domain-like	GO:0016787	[illegible]	NA
comp29134_c0_seq1.p1	Ec-23_002200.1	TATA-box binding protein	GO:0003677;GO:0006352	[illegible]	NA
comp32080_c0_seq3.p2	Ec-23_002250.1	Peptidase C19, ubiquitin-specific peptidase, DUSP domain	GO:0004843	[illegible]	NA
comp32974_c0_seq10.p2	Ec-23_002260.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32080_c0_seq3.p1	Ec-23_002270.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp30714_c0_seq3.p1	Ec-23_002340.1	Alpha/Beta hydrolase fold	GO:0003824;GO:0004806;GO:0006629	[illegible]	NA
comp12787_c0_seq1.p1	Ec-23_002380.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp12787_c1_seq1.p1	Ec-23_002380.2	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp20967_c0_seq1.p1	Ec-23_002410.1	glcerophosphoryl diester phosphodiesterase	GO:0008889;GO:0006071;GO:0008081;GO:0006629	[illegible]	KOG2258
comp31828_c0_seq1.p1	Ec-23_002450.1	Armadillo-type fold	GO:0005488	[illegible]	NA
comp26368_c0_seq1.p1	Ec-23_002470.1	ADF-H/Gelsolin-like domain	GO:0003779;GO:0005622;n/a	[illegible]	NA
comp25226_c0_seq2.p1	Ec-23_002490.1	Acyl transferase/acyl hydrolase/lysophospholipase	GO:0008152;GO:0006629	[illegible]	NA
comp55309_c0_seq1.p1	Ec-23_002510.1	hypothetical protein	GO:0005515;GO:0008270	[illegible]	NA
comp28961_c0_seq3.p1	Ec-23_002520.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	NA
comp25110_c0_seq1.p1	Ec-23_002530.1	Autophagy-related protein 11	n/a;n/a;n/a	[illegible]	NA
comp32015_c2_seq1.p1	Ec-23_002540.1	Forkhead domain protein	NA	[illegible]	NA
comp31966_c2_seq9.p2	Ec-23_002570.1	Nucleotide-diphospho-sugar transferases	GO:0008152;GO:0016779	[illegible]	NA
comp29852_c0_seq1.p1	Ec-23_002650.1	BTB/POZ fold	GO:0005515	[illegible]	NA
comp24251_c0_seq1.p1	Ec-23_002670.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020	[illegible]	NA
comp29100_c0_seq1.p1	Ec-23_002690.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp29100_c0_seq1.p2	Ec-23_002700.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0006457;GO:0051082;GO:0031072	[illegible]	NA
comp33724_c0_seq1.p1	Ec-23_002710.1	pyruvate dehydrogenase	GO:0003824;GO:0008152	[illegible]	KOG0524
comp47927_c0_seq1.p1	Ec-23_002720.1	glycerophosphoryl diester phosphodiesterase	GO:0008889;GO:0006071;GO:0008081;GO:0006629	[illegible]	NA
comp32391_c1_seq16.p1	Ec-23_002740.2	Phox homologous domain	GO:0035091	[illegible]	NA
comp21172_c0_seq1.p1	Ec-23_002750.1	Ribosomal protein L18e/L15P	GO:0003735;GO:0005622;GO:0005840;GO:0006412;GO:0015934	[illegible]	NA
comp26030_c0_seq1.p1	Ec-23_002780.1	Ubiquitin-related domain	n/a;n/a;n/a	[illegible]	NA
comp19387_c0_seq1.p1	Ec-23_002810.1	hypothetical protein	n/a;n/a;n/a	[illegible]	NA
comp31472_c1_seq1.p1	Ec-23_002820.4	Zinc finger, FYVE/PHD-type	n/a;n/a;n/a	[illegible]	NA
comp27183_c0_seq2.p1	Ec-23_002850.1	Mpv17/PMP22	GO:0016021	[illegible]	KOG1944
comp27183_c0_seq2.p2	Ec-23_002860.1	Exon junction complex, Pym	GO:0005515	[illegible]	NA
comp33024_c2_seq1.p1	Ec-23_002870.1	Tic22-like	n/a;n/a;n/a	[illegible]	NA
comp32117_c0_seq5.p1	Ec-23_002910.1	Alpha-(1,6)-fucosyltransferase, family GT23	NA	[illegible]	NA
comp63396_c0_seq1.p1	Ec-23_002920.1	Ammonium transporter	GO:0006810;GO:0008519;GO:0016020;GO:0055085	[illegible]	NA
comp22712_c0_seq1.p1	Ec-23_002950.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp28161_c0_seq1.p1	Ec-23_002960.2	Target of rapamycin 2	GO:0016773	[illegible]	KOG0891
comp28820_c0_seq1.p1	Ec-23_002970.1	Protein of unknown function DUF583	n/a;n/a;n/a	[illegible]	NA
comp33911_c0_seq1.p2	Ec-23_002980.1	Prefoldin beta-like	GO:0006457;GO:0016272;GO:0051082	[illegible]	NA
comp20957_c0_seq1.p2	Ec-23_003010.1	Ubiquitin-conjugating enzyme/RWD-like	GO:0019787;GO:0043687;GO:0051246	[illegible]	NA
comp31202_c1_seq5.p1	Ec-23_003030.2	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp34383_c0_seq1.p1	Ec-23_003040.1	Phytanoyl-CoA dioxygenase	n/a;n/a;n/a	[illegible]	NA
comp34653_c0_seq1.p1	Ec-23_003050.1	F-actin-capping protein subunit beta	GO:0051016;GO:0008290	[illegible]	NA
comp32696_c2_seq1.p1	Ec-23_003060.1	F-actin-capping protein subunit alpha	GO:0051016;GO:0008290	[illegible]	NA
comp35520_c0_seq1.p1	Ec-23_003070.1	Double-stranded RNA-binding domain	GO:0003723;GO:0003735;GO:0005622;GO:0005840;GO:0006412	[illegible]	NA
comp34597_c0_seq1.p1	Ec-23_003080.1	Cdc37, N-terminal domain	GO:0019901	[illegible]	NA
comp27272_c1_seq2.p1	Ec-23_003140.2	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28163_c0_seq1.p1	Ec-23_003160.1	Metallo-dependent phosphatase-like	GO:0016787	[illegible]	NA
comp113458_c0_seq1.p1	Ec-23_003180.1	Adenylyl cyclase class-3/4/guanylyl cyclase	GO:0009190;GO:0016849;GO:0035556	[illegible]	NA
comp23156_c0_seq1.p1	Ec-23_003190.1	Reduced growth phenotype protein 1	n/a;n/a;n/a	[illegible]	NA
comp32206_c0_seq7.p1	Ec-23_003200.1	Mrp/NBP35 ATP-binding protein	GO:0005524	[illegible]	NA

comp25026_c0_seq2.p1	Ec-23_003210.1	Hypothetical leucine rich repeat calcium binding protein	GO:0005509
comp29798_c0_seq1.p3	Ec-23_003230.1	Xylosyltransferase, family GT14	GO:0008375;GO:0016020
comp29798_c0_seq1.p1	Ec-23_003240.1	von Willebrand factor, type A	n/a;n/a;n/a
comp24704_c1_seq2.p1	Ec-23_003270.2	Chloride channel, core	GO:0005216;GO:0055085
comp20907_c0_seq3.p2	Ec-23_003280.1	Probable Spc2 homolog, Subunit of Signal Peptidase Complex	GO:0005792;GO:0008233;GO:0006465;GO:0005787;GO:0009003;GO:0016021
comp27050_c0_seq1.p1	Ec-23_003320.1	P-loop containing nucleoside triphosphate hydrolase	GO:0007018;GO:0005524;GO:0008017;GO:0005875;GO:0003777
comp10038_c0_seq1.p1	Ec-23_003330.1	Machado-Joseph disease protein MJD	GO:0008242
comp29434_c1_seq1.p1	Ec-23_003340.1	protein involved in intra-Golgi vesicle-mediated transport	GO:0006891;GO:0030173
comp26943_c0_seq3.p1	Ec-23_003360.1	conserved unknown protein	n/a;n/a;n/a
comp33138_c0_seq13.p1	Ec-23_003420.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777
comp20168_c0_seq1.p1	Ec-23_003430.1	Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase	GO:0016787
comp20986_c1_seq3.p1	Ec-23_003460.1	Fumarate hydratase (Fumarase)	n/a;GO:0003824;GO:0006099;GO:0016829
comp29469_c0_seq3.p1	Ec-23_003470.1	Exocyst complex protein Exo70	GO:0000145;GO:0006887
comp20635_c0_seq1.p1	Ec-23_003500.1	Aspartate Aminotransferase	GO:0006520;GO:0004069;GO:0003824;GO:0030170
comp12494_c0_seq1.p1	Ec-23_003510.1	Cyclophilin-like domain	GO:0003755;n/a
comp12028_c0_seq1.p1	Ec-23_003530.1	Endo-1,3-beta-glucanase, family GH17	GO:0005975
comp32220_c0_seq3.p4	Ec-23_003540.1	cupin-like protein	GO:0045735;GO:0030145
comp27756_c0_seq5.p1	Ec-23_003595.1	hypothetical protein	NA
comp21111_c0_seq1.p1	Ec-23_003610.1	Bromodomain	GO:0005515
comp12211_c0_seq1.p1	Ec-23_003620.1	Ribosomal protein L2 domain 2	GO:0003735;GO:0005622;GO:0005840;GO:0006412
comp19852_c0_seq2.p1	Ec-23_003630.1	4-hydroxyphenylpyruvate dioxygenase, plastid precursor	GO:0003868;GO:0009072
comp32736_c0_seq4.p1	Ec-23_003720.1	UBA-like	GO:0005515
comp27423_c1_seq1.p1	Ec-23_003730.1	Thioredoxin-like fold	n/a;GO:0045454
comp30057_c0_seq4.p2	Ec-23_003750.2	Notch domain	GO:0016020;GO:0030154
comp30057_c0_seq4.p1	Ec-23_003770.1	Sulfotransferase	GO:0001733;GO:0005794;GO:0009058;GO:0016021
comp21301_c0_seq1.p1	Ec-23_003780.1	Small RNA degrading nuclease	NA
comp20440_c0_seq2.p1	Ec-23_003800.2	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a
comp20014_c0_seq1.p1	Ec-23_003880.1	minichromosome maintenance protein, a family of eukaryotic DNA replication proteins	GO:0003677;GO:0003678;GO:0005524;GO:0005634;GO:0006270;GO:0042555
comp57565_c0_seq1.p1	Ec-23_003890.2	Intraflagellar transpot 52, osm-6-like protein	n/a;n/a;n/a
comp31587_c4_seq2.p1	Ec-23_003900.1	Protein kinase domain containing protein	GO:0004672;GO:0005524;GO:0006468
comp21247_c0_seq3.p1	Ec-23_003920.1	Sodium/calcium exchanger membrane region	GO:0055085;GO:0016021
comp27361_c0_seq1.p1	Ec-23_003940.1	putative: beta-tubulin folding cofactor E	n/a;n/a;n/a
comp27321_c0_seq1.p1	Ec-23_003950.1	START domain	GO:0008289
comp32840_c2_seq8.p1	Ec-23_003960.1	SANT/Myb domain	GO:0003682
comp27695_c0_seq2.p1	Ec-23_003970.1	Phosphoribosyltransferase-like	GO:0000287;GO:0004749;GO:0009165
comp11060_c0_seq1.p1	Ec-23_004010.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777
comp13256_c0_seq1.p1	Ec-23_004010.2	Kinesin motor domain	GO:0003777;GO:0005524;GO:0007018;GO:0008017
comp61832_c0_seq1.p1	Ec-23_004020.1	Kinesin motor domain	GO:0007018;GO:0005524;GO:0008017;GO:0003777
comp31899_c0_seq7.p1	Ec-23_004030.1	expressed unknown protein	n/a;n/a;n/a
comp32873_c1_seq9.p1	Ec-23_004050.1	expressed unknown protein	n/a;n/a;n/a
comp29285_c0_seq2.p1	Ec-23_004060.1	Protein kinase-like domain	GO:0016772
comp85867_c0_seq1.p1	Ec-23_004070.1	component of dynein regulatory complex	GO:0048870;GO:0031514
comp26860_c0_seq1.p1	Ec-23_004080.1	hypothetical protein	n/a;n/a;n/a
comp25413_c0_seq1.p1	Ec-23_004100.1	Complex 1 LYR protein	n/a;n/a;n/a
comp32721_c4_seq9.p1	Ec-23_004120.1	conserved unknown protein	n/a;n/a;n/a
comp33994_c0_seq1.p1	Ec-23_004150.1	Glycine dehydrogenase (decarboxylating)	GO:0005960;GO:0003824;GO:0004375
comp21154_c0_seq1.p1	Ec-23_004160.1	CidB/LrgB family	GO:0004807;GO:0008152;GO:0016020
comp30869_c0_seq2.p1	Ec-24_000020.1	expressed unknown protein	n/a;n/a;n/a
comp20657_c0_seq1.p1	Ec-24_000030.1	Glycosyl transferase, family 31	GO:0016020;GO:0006486;GO:0008378
comp25932_c0_seq2.p1	Ec-24_000040.3	Immunoglobulin-like fold	NA
comp24283_c0_seq1.p2	Ec-24_000050.1	TspO/MBR-related protein	GO:0016021
comp24283_c0_seq1.p1	Ec-24_000060.1	Aromatic amino acid permease	GO:0016020;GO:0006865;GO:0003333
comp28787_c0_seq2.p1	Ec-24_000070.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp32333_c2_seq1.p1	Ec-24_000080.1	Mitochondrial substrate/solute carrier	GO:0005488;GO:0006810;GO:0016020
comp30829_c0_seq1.p1	Ec-24_000090.1	Patched	GO:0016020;GO:0008158;GO:0016021
comp30349_c1_seq1.p1	Ec-24_000110.1	Zinc carboxypeptidase family protein	GO:0004181;GO:0006508;GO:0008270;GO:0004182
comp25790_c0_seq2.p1	Ec-24_000130.1	hypothetical protein	n/a;n/a;n/a
comp27153_c0_seq1.p1	Ec-24_000150.1	Heat shock protein 70 - putative	n/a;n/a;n/a
comp32675_c2_seq16.p1	Ec-24_000160.2	DENND6	n/a;n/a;n/a
comp25506_c0_seq2.p1	Ec-24_000170.1	conserved unknown protein	n/a;n/a;n/a
comp27651_c0_seq1.p1	Ec-24_000190.1	Tetratricopeptide-like helical domain	GO:0005515
comp32124_c3_seq1.p1	Ec-24_000200.1	EF-hand domain pair	n/a;n/a;n/a
comp30349_c0_seq7.p1	Ec-24_000210.2	Putative heat Shock transcription factor	GO:0003700;GO:0005634;GO:0006355;GO:0043565
comp32922_c1_seq2.p1	Ec-24_000220.2	Domain of unknown function DUF1771	n/a;n/a;n/a
comp33169_c0_seq14.p1	Ec-24_000270.1	EsV-1-7 domain protein	NA
comp30000_c0_seq2.p1	Ec-24_000290.1	hypothetical protein	n/a;n/a;n/a
comp28291_c0_seq5.p1	Ec-24_000310.1	expressed unknown protein	n/a;n/a;n/a
comp28291_c0_seq5.p2	Ec-24_000320.1	hypothetical protein	n/a;n/a;n/a
comp33599_c0_seq1.p1	Ec-24_000330.1	expressed unknown protein	n/a;n/a;n/a
comp31244_c1_seq21.p1	Ec-24_000340.1	Similar to 3-Dehydroquinate Synthase	GO:0003856;GO:0055114;GO:0009073;GO:0016491
comp32562_c1_seq23.p1	Ec-24_000350.1	expressed unknown protein	n/a;n/a;n/a
comp20536_c0_seq2.p1	Ec-24_000360.1	Triosephosphate isomerase,	GO:0008152;GO:0004807
comp32484_c3_seq10.p1	Ec-24_000420.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003677;GO:0005524;GO:0005634;GO:0006270
comp31854_c0_seq3.p1	Ec-24_000450.1	expressed unknown protein	n/a;n/a;n/a
comp33018_c4_seq5.p1	Ec-24_000460.2	PAS domain	GO:0004871;GO:0007165
comp33955_c0_seq1.p2	Ec-24_000470.1	expressed unknown protein	n/a;n/a;n/a
comp27893_c1_seq1.p1	Ec-24_000500.1	CWC16 protein	GO:0005179;GO:0005576
comp34331_c0_seq1.p1	Ec-24_000510.1	EF-hand domain	GO:0005509
comp20965_c0_seq1.p1	Ec-24_000520.1	Histidine phosphatase superfamily	GO:0003993
comp33320_c0_seq1.p1	Ec-24_000540.1	Ankyrin repeat	GO:0005515
comp24498_c0_seq1.p1	Ec-24_000580.1	hypothetical protein	n/a;n/a;n/a
comp29785_c0_seq3.p1	Ec-24_000610.1	acetylglutamate kinase	GO:0008652
comp28692_c0_seq2.p1	Ec-24_000620.1	Uroporphyrinogen decarboxylase, chloroplast precursor	GO:0006779;GO:0004853
comp65116_c0_seq1.p1	Ec-24_000630.1	putative, Dynein intermediate chain	GO:0005515
comp27251_c0_seq2.p1	Ec-24_000640.1	expressed unknown protein	n/a;n/a;n/a
comp24232_c0_seq1.p1	Ec-24_000650.1	Uroporphyrinogen decarboxylase, chloroplast precursor	GO:0006779;GO:0004853
comp31486_c0_seq3.p3	Ec-24_000660.1	Nucleotidyltransferase	GO:0016779
comp32791_c0_seq62.p1	Ec-24_000670.1	Dynactin subunit 1	GO:0005869;GO:0010970;GO:0045502
comp32791_c0_seq62.p2	Ec-24_000680.2	DnaJ domain	GO:0031072
comp32791_c0_seq43.p4	Ec-24_000690.1	CMP/dCMP deaminase, zinc-binding	GO:0016787;GO:0008270
comp32683_c3_seq17.p1	Ec-24_000760.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp31999_c2_seq4.p3	Ec-24_000770.1	Pre-mRNA-splicing factor Cwf15/Cwc15	GO:0000398;GO:0005681
comp21510_c0_seq1.p1	Ec-24_000780.1	tRNA methyltransferase, Trm1	GO:0003723;GO:0004809;GO:0008033
comp21461_c0_seq2.p1	Ec-24_000790.1	Homeodomain-like	GO:0003677
comp28825_c0_seq2.p1	Ec-24_000800.1	conserved unknown protein	n/a;n/a;n/a
comp26650_c2_seq3.p1	Ec-24_000810.1	Rrp44 is a component of the exosome 3'->5' exoribonuclease complex, a complex that degrades mRNAs.	GO:0003723;GO:0004540
comp21089_c0_seq1.p1	Ec-24_000820.1	Tim22-like protein	GO:0005743;GO:0008565;GO:0015031
comp30265_c0_seq4.p1	Ec-24_000835.1	hypothetical protein	GO:0004112
comp30265_c0_seq11.p3	Ec-24_000840.1	Acetyltransferase (GNAT) domain protein	GO:0008080
comp30265_c0_seq11.p1	Ec-24_000850.1	Armadillo-like helical	GO:0005488
comp24874_c0_seq1.p1	Ec-24_000860.1	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	n/a;n/a;n/a
comp12880_c0_seq1.p1	Ec-24_000870.1	Acetyl-CoA acetyltransferase, putative mitochondrial precursor	GO:0008152;GO:0016747
comp31486_c0_seq3.p2	Ec-24_000920.1	SR RNA splicing protein	GO:0000166
comp34665_c0_seq1.p1	Ec-24_000950.1	Inosine triphosphate pyrophosphatase-like	n/a;GO:0005737
comp29648_c0_seq2.p1	Ec-24_000960.3	SANT/Myb domain	GO:0003682
comp26768_c0_seq1.p1	Ec-24_000970.1	DEAD box helicase	n/a;n/a;n/a
comp33983_c0_seq1.p1	Ec-24_000980.1	Elongator protein 3/MiaB/NifB	GO:0003824;GO:0051536;GO:0004076;GO:0009102
comp31760_c0_seq4.p1	Ec-24_000990.1	expressed unknown protein	n/a;n/a;n/a
comp21126_c0_seq1.p2	Ec-24_001000.1	expressed unknown protein	n/a;n/a;n/a
comp28597_c0_seq6.p1	Ec-24_001010.1	Glycine cleavage T-protein, C-terminal barrel domain	GO:0004047;GO:0005737;GO:0006546
comp26095_c0_seq1.p1	Ec-24_001040.1	beta-hydroxylase, aspartyl/asparaginyl family	GO:0018193
comp29204_c1_seq1.p1	Ec-24_001050.1	cAMP-dependent protein kinase catalytic subunit (PKA)-like	GO:0005524;GO:0006468;GO:0004672
comp31721_c0_seq2.p1	Ec-24_001060.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005524
comp26877_c0_seq2.p1	Ec-24_001070.1	Mitochondrial carrier protein	GO:0055085
comp26199_c0_seq2.p1	Ec-24_001080.1	Intraflagellar transport protein 140 putative	GO:0005515
comp33127_c0_seq5.p1	Ec-24_001110.1	Transient Receptor Potential Channel. Partial sequence	n/a;n/a;n/a
comp25635_c0_seq1.p1	Ec-24_001240.1	hypothetical protein	n/a;n/a;n/a
comp31349_c1_seq1.p1	Ec-24_001250.2	conserved unknown protein	GO:0031177
comp31801_c0_seq19.p1	Ec-24_001260.1	Phospholipid methyltransferase	n/a;n/a;n/a
comp32695_c3_seq2.p1	Ec-24_001270.1	conserved unknown protein	n/a;n/a;n/a
comp26080_c0_seq2.p1	Ec-24_001300.1	DNA-directed RNA polymerase III subunit RPC4	GO:0003677;GO:0003899;GO:0005666;GO:0006383
comp26596_c0_seq1.p1	Ec-24_001330.1	Glutathione reductase	GO:0050660;GO:0055114;GO:0016491
comp28922_c0_seq1.p1	Ec-24_001340.1	MEKK/MAPK-like	GO:0004672;GO:0005524;GO:0006468
comp30952_c0_seq1.p1	Ec-24_001370.1	Cyclophilin-like domain	GO:0003755;n/a
comp31370_c0_seq1.p1	Ec-24_001380.1	Calponin homology domain	GO:0005515
comp25758_c0_seq1.p1	Ec-24_001390.1	Isopenicillin N synthase-like	GO:0004597;GO:0018193;GO:0030176;GO:0055114
comp32594_c2_seq22.p2	Ec-24_001400.1	conserved unknown protein	n/a;n/a;n/a
comp114460_c0_seq1.p1	Ec-24_001410.2	Kinesin-associated protein	GO:0005871;GO:0019894
comp28749_c0_seq1.p1	Ec-24_001420.1	Peptidase M32, carboxypeptidase Taq metallopeptidase	GO:0004181;GO:0006508
comp30341_c0_seq1.p2	Ec-24_001430.1	LisH dimerisation motif	GO:0005515
comp29201_c0_seq5.p1	Ec-24_001440.1	Nitrogen permease regulator 3	n/a;n/a;n/a
comp22096_c1_seq2.p1	Ec-24_001460.1	Protein of unknown function DUF1751, integral membrane, eukaryotic	n/a;n/a;n/a
comp31925_c0_seq1.p1	Ec-24_001480.1	conserved unknown protein	n/a;n/a;n/a
comp27903_c0_seq1.p1	Ec-24_001490.1	conserved unknown protein	n/a;n/a;n/a
comp30602_c0_seq6.p1	Ec-24_001500.1	Amine oxidase	GO:0055114;GO:0016491
comp26646_c0_seq2.p1	Ec-24_001510.1	EF-hand domain pair	GO:0005509
comp31762_c1_seq3.p1	Ec-24_001520.1	translation factor	n/a;GO:0003725
comp19810_c0_seq1.p1	Ec-24_001540.1	Protein secE/sec61-gamma protein; Rhomboid-like protein	GO:0004252;GO:0006508;GO:0016021
comp29822_c0_seq3.p1	Ec-24_001550.1	hypothetical protein	n/a;n/a;n/a
comp34424_c0_seq1.p1	Ec-24_001570.1	expressed unknown protein	n/a;n/a;n/a
comp25180_c0_seq1.p1	Ec-24_001590.1	expressed unknown protein	n/a;n/a;n/a
comp32302_c1_seq5.p1	Ec-24_001600.1	CCT domain	GO:0005515
comp30703_c0_seq2.p1	Ec-24_001610.1	Hypothetical protein	n/a;GO:0046872
comp35323_c0_seq1.p1	Ec-24_001620.2	eukaryotic initiation factor eIF3 i subunit p36	GO:0005515
comp21440_c0_seq1.p1	Ec-24_001630.1	Rrp4 is a component of the exosome 3'->5' exoribonuclease complex, a complex that degrades mRNAs.	NA
comp21334_c0_seq1.p1	Ec-24_001650.1	Protein kinase-like domain	GO:0016772
comp19440_c0_seq1.p1	Ec-24_001670.1	expressed unknown protein	n/a;n/a;n/a
comp6467_c0_seq1.p1	Ec-24_001680.1	hypothetical protein	NA
comp12371_c0_seq1.p2	Ec-24_001700.1	Zinc finger C2H2-type/integrase DNA-binding domain	GO:0003676
comp12416_c0_seq1.p1	Ec-24_001710.1	NUC153 and WD40-repeat domain protein	n/a;GO:0005515
comp29001_c0_seq1.p1	Ec-24_001720.1	expressed unknown protein	n/a;n/a;n/a
comp32344_c0_seq22.p1	Ec-24_001740.1	Mitochondrial transcription termination factor	GO:0003690;GO:0005739;GO:0006355
comp34267_c0_seq1.p1	Ec-24_001780.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003700;GO:0005634;GO:0006355;GO:0030528;GO:0043565
comp15347_c0_seq1.p1	Ec-24_001820.1	expressed unknown protein	n/a;n/a;n/a
comp31033_c0_seq1.p1	Ec-24_001850.1	Amine oxidase and zinc finger domain protein	GO:0005515;GO:0008270;GO:0055114;GO:0016491
comp22046_c0_seq3.p1	Ec-24_001870.1	Similar to transporters, possibly for inorganic phosphate.	GO:0055085;GO:0016021
comp19749_c0_seq1.p1	Ec-24_001890.1	Bestrophin/UPF0187	n/a;n/a;n/a
comp26004_c0_seq2.p1	Ec-24_001900.1	P-loop containing nucleoside triphosphate hydrolase	GO:0006810;GO:0005524;GO:0042626;GO:0016021;GO:0016887
comp32699_c0_seq13.p1	Ec-24_001950.1	Major facilitator superfamily domain	n/a;n/a;n/a
comp29492_c0_seq1.p1	Ec-24_001970.2	Lrc5, mitochondrial YqeH-related GTPase	NA
comp12756_c0_seq2.p1	Ec-24_001990.1	chloroplast peptide deformylase	GO:0005506;GO:0006412;GO:0042586
comp29479_c0_seq2.p1	Ec-24_002000.1	Zinc finger, MIZ-type	GO:0008270
comp33750_c0_seq1.p1	Ec-24_002010.1	conserved unknown protein	n/a;n/a;n/a
comp32391_c0_seq1.p1	Ec-24_002090.1	Short-chain dehydrogenase/reductase SDR	GO:0008152;GO:0016491
comp28103_c1_seq1.p1	Ec-24_002170.1	conserved unknown protein	n/a;n/a;n/a
comp28103_c1_seq1.p3	Ec-24_002180.1	Dynein light chain-related	n/a;n/a;n/a
comp12469_c0_seq1.p1	Ec-24_002220.1	Regulatory factor, effector binding domain	n/a;n/a;n/a
comp27970_c0_seq2.p1	Ec-24_002230.1	EF-hand domain pair	GO:0005509
comp31914_c1_seq3.p1	Ec-24_002240.1	hypothetical protein	n/a;n/a;n/a
comp55617_c0_seq1.p1	Ec-24_002280.2	hypothetical protein	GO:0003700;GO:0005634;GO:0006355;GO:0043565;GO:0046983
comp27149_c0_seq1.p1	Ec-24_002290.1	Major facilitator superfamily	GO:0055085;GO:0016021
comp27644_c0_seq1.p1	Ec-24_002300.1	delta-6 fatty acid desaturase	GO:0020037
comp32882_c1_seq12.p1	Ec-24_002310.1	chloroplast dimethyladenosine synthase	GO:0000154;GO:0000179;GO:0008649
comp31487_c0_seq6.p1	Ec-24_002340.1	Ankyrin repeat-containing domain	n/a;n/a;n/a
comp29044_c0_seq1.p1	Ec-24_002390.2	Cation efflux protein	GO:0006812;GO:0008324;GO:0016021;GO:0055085
comp30766_c0_seq3.p1	Ec-24_002400.2	Peptidase M48	GO:0004222;GO:0006508;GO:0016020
comp20159_c0_seq1.p1	Ec-24_002410.1	Inosine-5'-monophosphate dehydrogenase	GO:0003938;GO:0006164;GO:0055114
comp20845_c0_seq1.p1	Ec-24_002470.1	Phosphoglucose isomerase (PGI)	GO:0004347;GO:0006094;GO:0006096
comp27074_c0_seq7.p1	Ec-24_002570.1	Pex, N-terminal	GO:0005515;GO:0008270
comp29900_c0_seq1.p1	Ec-24_002590.1	expressed unknown protein	n/a;n/a;n/a
comp15141_c0_seq2.p1	Ec-24_002600.1	Regulator of chromosome condensation, RCC1	n/a;n/a;n/a
comp32851_c1_seq19.p1	Ec-24_002650.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;GO:0008168;GO:0003676;GO:0032259
comp26855_c0_seq1.p1	Ec-24_002670.1	Histidine phosphatase superfamily, clade-1	GO:0006096;GO:0016868
comp28106_c0_seq3.p1	Ec-24_002680.1	Kelch-type beta propeller	GO:0005515
comp19548_c0_seq1.p1	Ec-24_002690.1	Serine palmitoyltransferase	GO:0003824;GO:0009058;GO:0030170
comp34361_c0_seq1.p1	Ec-24_002720.1	Domain of unknown function DUF4524	n/a;n/a;n/a
comp33078_c0_seq14.p1	Ec-24_002730.1	EsV-1-7 domain protein	NA
comp30226_c0_seq1.p1	Ec-24_002740.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp30226_c0_seq4.p1	Ec-24_002740.2	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp33012_c1_seq2.p1	Ec-24_002770.1	Protein-tyrosine phosphatase-like	GO:0004437;GO:0016311;GO:0016791;GO:0046839
comp33872_c0_seq1.p1	Ec-24_002800.1	G-patch domain	GO:0003676
comp28886_c0_seq1.p1	Ec-24_002900.1	expressed unknown protein	n/a;n/a;n/a
comp31847_c0_seq2.p1	Ec-24_002930.1	Heat shock protein 70	NA
comp32398_c1_seq22.p1	Ec-24_002960.1	RNA polymerase sigma factor, region 2	GO:0003677;GO:0003700;GO:0006352;GO:0006355;GO:0016987
comp31786_c0_seq7.p3	Ec-24_002970.1	PQ-loop repeat	NA
comp25117_c0_seq1.p1	Ec-24_002980.1	RNA polymerase sigma-70 region 3	GO:0003677;GO:0006355;GO:0016987;GO:0003700;GO:0006352
comp19670_c0_seq1.p1	Ec-24_002990.1	Signal recognition particle, SRP54 subunit, M-domain	GO:0048500;GO:0006614;GO:0008312
comp32565_c0_seq2.p1	Ec-24_003010.1	Lysocardiolipin acyltransferase	GO:0016746;GO:0008152
comp27548_c0_seq1.p1	Ec-24_003050.1	Metallo-dependent phosphatase-like and protein kinase-like domains	GO:0004672;GO:0005515;GO:0005524;GO:0006468;GO:0016772;GO:0016787
comp9493_c0_seq1.p1	Ec-24_003070.2	hypothetical protein	GO:0016671;GO:0019538;GO:0055114
comp33295_c0_seq2.p3	Ec-24_003080.2	ferric reductase	n/a;n/a;n/a
comp11822_c0_seq1.p1	Ec-24_003100.3	Aldolase-type TIM barrel	GO:0003824
comp24145_c0_seq1.p1	Ec-24_003110.1	Iron hydrogenase	GO:0005506;GO:0006118;GO:0008901;GO:0009055;GO:0042597;GO:0051536
comp12160_c0_seq1.p1	Ec-24_003200.1	Snf7 family	GO:0007034
comp28428_c0_seq2.p1	Ec-24_003210.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a
comp26017_c0_seq1.p2	Ec-24_003220.1	expressed unknown protein	n/a;n/a;n/a
comp12946_c0_seq1.p1	Ec-24_003230.1	RNA recognition motif domain	GO:0003676;GO:0000166
comp21374_c0_seq1.p1	Ec-24_003250.1	Secreted cupin superfamily protein	n/a;n/a;n/a
comp32154_c0_seq5.p1	Ec-24_003370.3	P-type ATPase, transmembrane domain	n/a;n/a;n/a
comp32154_c0_seq4.p1	Ec-24_003370.4	P-type ATPase, transmembrane domain	n/a;n/a;n/a
comp29984_c0_seq1.p1	Ec-24_003410.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0006470
comp27980_c0_seq1.p1	Ec-24_003430.1	Meiotic recombination protein DMC1/LIM15 homolog	GO:0003677;GO:0005524;GO:0008094;GO:0006259
comp31371_c0_seq5.p1	Ec-24_003440.1	Histone deacetylase complex subunit SAP30, Sin3 binding domain	GO:0005515
comp24396_c0_seq2.p1	Ec-24_003470.1	expressed unknown protein	n/a;n/a;n/a
comp34014_c0_seq1.p1	Ec-24_003480.1	EsV-1-7 domain protein	NA
comp32427_c0_seq7.p1	Ec-24_003490.1	Histone methylation DOT1	GO:0051726;GO:0034729;GO:0018024;GO:0031151
comp32839_c0_seq2.p1	Ec-24_003510.1	expressed unknown protein	n/a;n/a;n/a
comp31627_c1_seq3.p1	Ec-24_003520.1	Serine O-acetyltransferase	GO:0009001;GO:0009069;GO:0016740
comp30016_c0_seq2.p1	Ec-24_003550.1	Histone methylation DOT1	GO:0018024
comp31786_c0_seq7.p1	Ec-24_003560.2	Diphthamide biosynthesis protein 2, putative	NA
comp33973_c0_seq1.p1	Ec-24_003580.1	violaxanthin de-epoxidase, chloroplast precursor	GO:0009507;GO:0046422;GO:0055114
comp29125_c0_seq12.p1	Ec-24_003590.1	Histone deacetylase domain protein	n/a;n/a;n/a
comp29125_c0_seq10.p3	Ec-24_003600.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020
comp12235_c1_seq1.p1	Ec-24_003610.3	Alpha/Beta hydrolase fold	GO:0004806;GO:0006629
comp31786_c0_seq7.p2	Ec-24_003630.1	Rad1/Rec1/Rad17	GO:0005634;GO:0006281
comp34183_c0_seq1.p1	Ec-24_003640.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a
comp41448_c0_seq1.p1	Ec-24_003670.1	expressed unknown protein	n/a;n/a;n/a
comp33543_c0_seq1.p1	Ec-24_003680.1	Proteasome assembly chaperone 3	n/a;n/a;n/a
comp30284_c0_seq9.p1	Ec-24_003690.1	ku P80 DNA helicase, putative	GO:0003677;GO:0006303
comp30284_c0_seq3.p1	Ec-24_003700.1	Golgi apparatus membrane protein TVP15	n/a;n/a;n/a
comp28945_c0_seq1.p1	Ec-24_003720.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp30278_c0_seq8.p1	Ec-24_003780.1	Ankyrin repeat-containing domain	n/a;n/a;n/a
comp33074_c0_seq3.p1	Ec-24_003790.1	Ankyrin repeat-containing domain	n/a;GO:0005515
comp24248_c2_seq1.p1	Ec-24_003810.1	von Willebrand factor, type A	n/a;n/a;n/a
comp12436_c0_seq1.p1	Ec-24_003890.1	Putative lysophospholipase	n/a;n/a;n/a
comp24304_c0_seq1.p1	Ec-24_003900.3	acyl carrier protein	GO:0006633
comp32729_c0_seq6.p1	Ec-24_003910.2	UbiA prenyltransferase family	GO:0004659;GO:0016021
comp32729_c0_seq4.p2	Ec-24_003920.1	naphthoate synthase	GO:0008152;GO:0003824
comp25193_c0_seq1.p1	Ec-24_003940.1	putative ubiquitin activating enzyme	NA
comp32608_c0_seq6.p1	Ec-24_004030.1	Actin family	n/a;n/a;n/a
comp31829_c0_seq4.p1	Ec-24_004040.1	Protein of unknown function DUF1042	n/a;n/a;n/a
comp34853_c0_seq1.p2	Ec-24_004050.1	Mitochondrial protein import TIM8.13 complex subunit, Tim13 homolog	GO:0006626;GO:0042719;GO:0045039
comp32245_c0_seq24.p1	Ec-24_004090.1	Thioredoxin-like fold	n/a;n/a;n/a
comp30048_c1_seq7.p1	Ec-24_004100.1	conserved unknown protein	n/a;n/a;n/a
comp33074_c3_seq24.p1	Ec-24_004150.1	Phosphatidylinositol transfer protein PDR16	n/a;n/a;n/a
comp32608_c0_seq7.p1	Ec-24_004160.1	C2H2 zinc finger protein	GO:0046872;GO:0008270;GO:0005622;GO:0003676
comp32928_c0_seq8.p1	Ec-24_004170.1	ABC transporter-like	GO:0005524;GO:0016887
comp27100_c0_seq3.p1	Ec-24_004180.1	Ribose-phosphate diphosphokinase	GO:0000287;GO:0004749;GO:0009165
comp32484_c3_seq16.p1	Ec-24_004190.1	Globin, structural domain	GO:0015671;GO:0020037;GO:0005506;GO:0019825
comp32484_c1_seq1.p1	Ec-24_004200.1	Armadillo-type fold	GO:0005488
comp27100_c0_seq5.p1	Ec-24_004210.2	expressed unknown protein	n/a;n/a;n/a
comp24979_c0_seq4.p1	Ec-24_004250.1	Protein kinase-like domain	GO:0016772
comp26908_c0_seq1.p1	Ec-24_004260.1	AVL9/DENND6 domain	n/a;n/a;n/a
comp31800_c0_seq17.p1	Ec-24_004270.1	conserved unknown protein	n/a;n/a;n/a
comp26908_c0_seq1.p2	Ec-24_004300.1	Seryl-tRNA synthetase	GO:0016876;GO:0004828;GO:0003824;GO:0016875;GO:0016874;GO:0003674;GO:0006418;GO:0004812
comp35017_c0_seq1.p1	Ec-24_004310.1	Mitochondrial protein import TIM8.13 complex subunit, Tim8 homolog	GO:0042719;GO:0006626;GO:0045039
comp29732_c0_seq2.p1	Ec-24_004320.1	conserved unknown protein	n/a;n/a;n/a
comp12338_c0_seq1.p1	Ec-24_004360.1	Beta-1,6-glucan active enzyme, family GH16	NA
comp21352_c0_seq1.p1	Ec-24_004370.1	Acetyltransferase (GNAT) domain protein	GO:0008080;n/a
comp26925_c0_seq2.p1	Ec-24_004390.1	Trehalose 6-phosphate synthase, family GT20 / Trehalose 6-phosphate phosphatase	GO:0003824;GO:0005992
comp24805_c0_seq1.p1	Ec-24_004430.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0003676;GO:0008168;GO:0032259
comp33074_c3_seq35.p1	Ec-24_004440.1	putative; AAA family ATP ase	GO:0005524
comp35025_c0_seq1.p2	Ec-24_004450.1	Small nuclear ribonucleoprotein-associated protein D1	GO:0030529;GO:0016071
comp26987_c0_seq1.p1	Ec-24_004470.1	conserved unknown protein	n/a;n/a;n/a
comp25594_c0_seq1.p1	Ec-25_000010.1	Leucine carboxyl methyltransferase	GO:0008168;GO:0032259
comp33152_c1_seq20.p1	Ec-25_000020.1	dihydrolipoamide dehydrogenase	GO:0005960;GO:0004148;GO:0050660;GO:0005737;GO:0055114;GO:0045454;GO:0019464;GO:0016491
comp26670_c0_seq1.p1	Ec-25_000030.1	conserved unknown protein	n/a;n/a;n/a
comp33790_c0_seq1.p1	Ec-25_000040.1	Replication termination factor 2, RING-finger	GO:0005515;GO:0008270;n/a
comp28201_c0_seq9.p1	Ec-25_000060.1	mono-or diacylglycerol acyltransferase type 2	GO:0016747
comp90197_c0_seq1.p1	Ec-25_000070.1	Hypothetical leucine rich repeat calmodulin binding protein	GO:0005515
comp12818_c0_seq1.p1	Ec-25_000090.1	tRNA methyltransferase TRMD/TRM10-type domain	n/a;n/a;n/a
comp25631_c0_seq1.p1	Ec-25_000100.1	P-loop containing nucleoside triphosphate hydrolase	GO:0006810;GO:0005524;GO:0042626;GO:0016021;GO:0016887
comp31255_c0_seq2.p1	Ec-25_000110.8	NB-ARC and TPR repeat-containing protein	GO:0005524;GO:0006915
comp33984_c0_seq1.p1	Ec-25_000120.1	Bromodomain	GO:0005515
comp28115_c0_seq3.p1	Ec-25_000130.1	Maf-like protein	GO:0005737

comp11703_c0_seq1.p1	Ec-25_000140.2	Dihydrolipoamide acetyltransferase	GO:0008152;GO:0008415	PTHR23151: ; IPR006257: Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex; IPR004167: E3-binding domain; IPR000089: Biotin/lipoyl attachment; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; IPR001078: 2-oxoacid dehydrogenase acyltransferase, catalytic domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR023213: Chloramphenicol acetyltransferase-like domain; IPR011053: Single hybrid motif; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF52777: ; G3DSA:2.40.50.100: ; PTHR23151:SF9:	KOG0557
comp32109_c0_seq6.p1	Ec-25_000150.1	NADH:ubiquinone oxidoreductase intermediate-associated protein 30	n/a;n/a;n/a	SSF51735: ; IPR016040: NAD(P)-binding domain; IPR013857: NADH:ubiquinone oxidoreductase intermediate-associated protein 30; PF13460: NADH(P)-binding; IPR008979: Galactose-binding domain-like; PTHR13194:	NA
comp33059_c0_seq1.p1	Ec-25_000160.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33263_c0_seq11.p1	Ec-25_000180.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp28207_c0_seq1.p1	Ec-25_000210.1	Peptidase C26, gamma-glutamyl hydrolase	GO:0003824;GO:0006541;GO:0008242	IPR011697: Peptidase C26; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR029062: Class I glutamine amidotransferase-like; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015527: Peptidase C26, gamma-glutamyl hydrolase; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp34667_c0_seq1.p1	Ec-25_000260.1	Protein of unknown function UPF0301	n/a;n/a;n/a	IPR003774: Protein of unknown function UPF0301; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF143456: ; SignalP-noTM: ; G3DSA:3.40.1740.10: ; PTHR31984: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24539_c0_seq1.p1	Ec-25_000290.1	EsV-1-164	n/a;n/a;n/a	IPR013994: Carbohydrate-binding WSC, subgroup; PF13229: Right handed beta helix region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR19297: ; IPR002889: Carbohydrate-binding WSC; IPR012334: Pectin lyase fold; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR011050: Pectin lyase fold/virulence factor; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006626: Parallel beta-helix repeat	NA
comp21005_c0_seq1.p1	Ec-25_000300.1	Peptidase M76, ATP23	GO:0004222	IPR019165: Peptidase M76, ATP23; PTHR21711:	NA
comp20874_c0_seq1.p1	Ec-25_000310.1	Nucleoporin NSP1/NUP62	GO:0005643;GO:0017056	IPR026010: Nucleoporin NSP1/NUP62; IPR007758: Nucleoporin, NSP1-like, C-terminal; SignalP-noTM: ; Coil: ; SignalP-TM:	NA
comp27157_c0_seq2.p1	Ec-25_000320.1	Staphylococcal nuclease (SNase-like), OB-fold	GO:0003676;GO:0016788	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR12302: ; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR016071: Staphylococcal nuclease (SNase-like), OB-fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27909_c0_seq1.p1	Ec-25_000330.1	hypothetical protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29264_c0_seq3.p1	Ec-25_000390.1	GPI inositol-deacylase PGAP1-like	GO:0016788;GO:0006505;GO:0006886	IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012908: GPI inositol-deacylase PGAP1-like; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24794_c0_seq3.p1	Ec-25_000400.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32834_c0_seq17.p1	Ec-25_000410.1	Basic-leucine zipper domain	GO:0006355;GO:0043565;GO:0003700	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR004827: Basic-leucine zipper domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:1.20.5.170: ; SSF57959: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32698_c0_seq27.p1	Ec-25_000440.1	hypothetical protein	GO:0004190;GO:0006508;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32236_c1_seq4.p1	Ec-25_000450.1	Bystin	n/a;n/a;n/a	IPR007955: Bystin; Coil:	NA
comp31101_c0_seq4.p1	Ec-25_000470.2	WD40-repeat-containing domain	GO:0005515	PTHR13743: ; IPR000409: BEACH domain; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR011993: PH domain-like; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; IPR023362: PH-BEACH domain; IPR020472: G-protein beta WD-40 repeat	NA
comp26810_c0_seq1.p1	Ec-25_000490.1	Cytochrome b5-like heme/steroid binding domain	GO:0020037	IPR018506: Cytochrome b5, heme-binding site; PTHR19370: ; IPR001199: Cytochrome b5-like heme/steroid binding domain	NA
comp33130_c0_seq7.p1	Ec-25_000510.1	HECT	GO:0004842	IPR000408: Regulator of chromosome condensation, RCC1; PTHR11254: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13540: Regulator of chromosome condensation (RCC1) repeat; IPR000569: HECT; Coil: ; G3DSA:3.30.2160.10: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26243_c0_seq1.p1	Ec-25_000560.1	Clathrin heavy chain	GO:0005488	IPR016341: Clathrin, heavy chain; IPR016025: Clathrin, heavy chain, linker/propeller domain; IPR011990: Tetratricopeptide-like helical domain; IPR012331: Clathrin, heavy chain, linker; IPR001473: Clathrin, heavy chain, propeller, N-terminal; PTHR10292:SF1: ; IPR015348: Clathrin, heavy chain, linker, core motif; PF13838: Clathrin-H-link; Coil: ; IPR016024: Armadillo-type fold; PTHR10292: ; IPR000547: Clathrin, heavy chain/VPS, 7-fold repeat	KOG0985
comp25151_c0_seq1.p1	Ec-25_000570.1	RNase P subunit p30	GO:0008033;GO:0004540	IPR016195: Polymerase/histidinol phosphatase-like; IPR002738: RNase P subunit p30; G3DSA:3.20.20.140:	NA
comp31682_c1_seq10.p1	Ec-25_000590.1	Alpha/beta knot methyltransferases	GO:0005634;GO:0008168	IPR005304: Ribosomal biogenesis, methyltransferase, EMG1/NEP1; IPR029028: Alpha/beta knot methyltransferases	NA
comp34632_c0_seq1.p1	Ec-25_000600.1	Vps5 C-terminal	GO:0005515;GO:0007154;GO:0035091	PTHR10555: ; IPR011992: EF-hand domain pair; Coil: ; IPR001683: Phox homologous domain	NA
comp29815_c0_seq1.p2	Ec-25_000620.1	EF-hand domain pair	GO:0005509	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; SSF47473: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29815_c0_seq1.p1	Ec-25_000650.1	Nucleolar complex protein 4	GO:0042254	IPR005612: CCAAT-binding factor; PTHR12455: ; IPR027193: Nucleolar complex protein 4	NA
comp11737_c0_seq1.p1	Ec-25_000670.1	Lactoylglutathione lyase	NA	NA	NA
comp30484_c0_seq1.p1	Ec-25_000690.2	conserved unknown protein	n/a;n/a;n/a	PTHR12187:	NA
comp27126_c0_seq2.p1	Ec-25_000700.1	Ribosomal protein S1, RNA-binding domain	GO:0003676	IPR012340: Nucleic acid-binding, OB-fold; IPR003029: Ribosomal protein S1, RNA-binding domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR10724: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR022967: RNA-binding domain, S1; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31716_c0_seq1.p1	Ec-25_000710.1	Afadin/alpha-actinin-binding	n/a;n/a;n/a	Coil: ; IPR021622: Afadin/alpha-actinin-binding	NA
comp32006_c1_seq1.p1	Ec-25_000720.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34154_c0_seq1.p1	Ec-25_000730.1	Pre-mRNA splicing Prp18-interacting factor	GO:0003676;GO:0008270	PTHR12942: ; IPR001878: Zinc finger, CCHC-type; Coil: ; IPR021715: Pre-mRNA splicing Prp18-interacting factor	NA
comp20054_c0_seq1.p1	Ec-25_000740.1	DEAD box helicase	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR014014: RNA helicase, DEAD-box type, Q motif; IPR000629: ATP-dependent RNA helicase DEAD-box, conserved site; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR001650: Helicase, C-terminal; PTHR24031:	KOG0330
comp26454_c1_seq2.p1	Ec-25_000750.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	PTHR14614:SF2: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR019410: Lysine methyltransferase; PTHR14614:	NA
comp24821_c0_seq2.p1	Ec-25_000760.1	Endoribonuclease L-PSP/chorismate mutase-like	n/a;n/a;n/a	PTHR32332: ; IPR006175: YjgF/YER057c/UK114 family; IPR013785: Aldolase-type TIM barrel; IPR004136: 2-nitropropane dioxygenase, NPD; IPR013813: Endoribonuclease L-PSP/chorismate mutase-like; SSF51412:	NA
comp32691_c0_seq10.p1	Ec-25_000790.5	LRR-GTPase of the ROCO family	GO:0005525;GO:0005622;GO:0007264	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR020859: Roc domain; IPR032675: Leucine-rich repeat domain, L domain-like; IPR013684: Mitochondrial Rho-like; PTHR27000: ; IPR003591: Leucine-rich repeat, typical subtype; PR00449: Transforming protein P21 ras signature; G3DSA:3.30.70.1390: ; Coil:	NA
comp32551_c0_seq1.p1	Ec-25_000800.1	Hypothetical leucine rich repeat protein	GO:0005515	NA	NA
comp33497_c0_seq1.p1	Ec-25_000810.1	ATP binding protein MinD, bacterial-type	GO:0000918;GO:0006200;GO:0016887	IPR010223: ATP binding protein MinD, bacterial-type; PTHR13696: ; IPR002586: CobQ/CobB/MinD/ParA nucleotide binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase	NA
comp32675_c0_seq2.p1	Ec-25_000830.1	Calcineurin-like phosphoesterase domain, apaH type	GO:0016787	IPR029052: Metallo-dependent phosphatase-like; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; PTHR24032:	NA
comp19708_c0_seq1.p1	Ec-25_000840.1	Mpv17/PMP22	GO:0016021	IPR007248: Mpv17/PMP22	NA
comp33684_c0_seq1.p1	Ec-25_000850.1	Rab2A, RAB family GTPase	GO:0005622;GO:0007264;GO:0005525	IPR002041: Ran GTPase; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003578: Small GTPase superfamily, Rho type; IPR001806: Small GTPase superfamily; IPR005225: Small GTP-binding protein domain; IPR020849: Small GTPase superfamily, Ras type; PS51419: small GTPase Rab1 family profile.; IPR003579: Small GTPase superfamily, Rab type; PTHR24073:	NA
comp34060_c0_seq1.p1	Ec-25_000860.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp31987_c0_seq2.p1	Ec-25_000880.1	Plant homeodomain (PHD) finger domain	GO:0005515;GO:0008270	IPR017956: AT hook, DNA-binding motif; IPR019786: Zinc finger, PHD-type, conserved site; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR001965: Zinc finger, PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; IPR019787: Zinc finger, PHD-finger	NA
comp32687_c0_seq2.p1	Ec-25_000890.1	tRNA (guanine-N1-)-methyltransferase, N-terminal	GO:0003723;GO:0006396;GO:0008173	IPR029028: Alpha/beta knot methyltransferases; IPR029026: tRNA (guanine-N1-)-methyltransferase, N-terminal	NA
comp25982_c0_seq2.p1	Ec-25_000900.1	Casein kinase II, regulatory subunit	GO:0005956;GO:0019887	IPR016149: Casein kinase II, regulatory subunit, alpha-helical; PTHR11740:SF0: ; IPR016150: Casein kinase II, regulatory subunit, beta-sheet; IPR000704: Casein kinase II, regulatory subunit	NA
comp29826_c0_seq1.p1	Ec-25_000970.1	Armadillo-like helical	n/a;n/a;n/a	IPR011989: Armadillo-like helical	NA
comp34245_c0_seq1.p1	Ec-25_000980.1	Nucleophile aminohydrolases, N-terminal	GO:0004175;GO:0051603;GO:0004298;GO:0005839;GO:0006511	IPR029055: Nucleophile aminohydrolases, N-terminal; IPR000243: Peptidase T1A, proteasome beta-subunit; IPR001353: Proteasome, subunit alpha/beta; PTHR11599: ; IPR023333: Proteasome B-type subunit	NA
comp25194_c0_seq1.p2	Ec-25_000990.1	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	GO:0008685;GO:0016114	IPR020555: 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, conserved site; IPR003526: 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase; PTHR32125:	NA
comp25194_c0_seq1.p1	Ec-25_001000.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; SIGNAL_PEPTIDE: Signal peptide region; PTHR24015: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002885: Pentatricopeptide repeat; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27475_c0_seq2.p1	Ec-25_001010.1	Nicastrin	GO:0016485;GO:0016021	IPR008710: Nicastrin; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF53187: ; G3DSA:3.40.630.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp85755_c0_seq1.p1	Ec-25_001020.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp29177_c1_seq2.p1	Ec-25_001030.1	Similar to mitochondrial import receptor Tom70	GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; PTHR23083: ; IPR019734: Tetratricopeptide repeat; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG4234
comp30702_c0_seq1.p1	Ec-25_001070.1	Sulfotransferase domain	GO:0008146	IPR000863: Sulfotransferase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR10605:	NA
comp25972_c0_seq1.p1	Ec-25_001100.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020683: Ankyrin repeat-containing domain; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28289_c0_seq1.p1	Ec-25_001110.1	ATPase, AAA-type, core	GO:0005524	IPR003959: ATPase, AAA-type, core; IPR003593: AAA+ ATPase domain; IPR003960: ATPase, AAA-type, conserved site; G3DSA:1.10.8.60: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR23077:	NA
comp27586_c0_seq3.p1	Ec-25_001120.1	Choline transporter-like	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007603: Choline transporter-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29918_c0_seq1.p1	Ec-25_001140.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26193_c0_seq1.p1	Ec-25_001150.2	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp18261_c0_seq1.p1	Ec-25_001190.1	Putative tyrosine phosphatase	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; IPR007482: Protein-tyrosine phosphatase-like, PTPLA; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3187
comp30767_c0_seq3.p1	Ec-25_001230.2	WD40-repeat-containing domain	GO:0005515	IPR030545: WD repeat-containing protein 62; PTHR22847: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp21308_c0_seq1.p1	Ec-25_001250.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp33292_c1_seq1.p1	Ec-25_001280.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp12518_c0_seq1.p1	Ec-25_001290.1	Thioredoxin-like fold	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR13871: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012336: Thioredoxin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30220_c0_seq3.p1	Ec-25_001310.1	meiotic recombination 11	GO:0004527;GO:0006259	PTHR10139: ; IPR029052: Metallo-dependent phosphatase-like; PTHR10139:SF1: ; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; IPR003701: DNA double-strand break repair protein Mre11; Coil: ; IPR007281: Mre11, DNA-binding	NA
comp3408_c0_seq1.p1	Ec-25_001360.1	Fe-S hydro-lyase, tartrate dehydratase beta-type, catalytic domain	GO:0006091;GO:0004333;GO:0016836	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR30389: ; IPR011167: Iron-dependent fumarate hydratase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004647: Fe-S hydro-lyase, tartrate dehydratase beta-type, catalytic domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR004646: Fe-S hydro-lyase, tartrate dehydratase alpha-type, catalytic domain	NA
comp28814_c0_seq1.p1	Ec-25_001370.1	IAP100 protein	NA	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp32675_c6_seq1.p1	Ec-25_001400.1	Vacuolar protein sorting-associated protein 13A N-terminal domain	n/a;n/a;n/a	IPR011989: Armadillo-like helical; IPR026854: Vacuolar protein sorting-associated protein 13A N-terminal domain	NA
comp26887_c0_seq2.p1	Ec-25_001430.1	Peptidase M41	GO:0004222;GO:0005524;GO:0006508	PTHR23076: ; IPR003959: ATPase, AAA-type, core; IPR000642: Peptidase M41; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SSF140990: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003593: AAA+ ATPase domain; G3DSA:1.10.8.60: ; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12363_c0_seq1.p1	Ec-25_001450.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp29363_c0_seq1.p1	Ec-25_001470.1	NADP-dependent oxidoreductase domain	GO:0016491;GO:0055114;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001395: Aldo/keto reductase/potassium channel subunit beta; PTHR11732:SF7: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR023210: NADP-dependent oxidoreductase domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp34789_c0_seq1.p1	Ec-25_001480.1	Peroxin-3 domain	GO:0007031;GO:0005779	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; IPR006966: Peroxin-3; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26677_c0_seq2.p1	Ec-25_001490.1	NADP-dependent oxidoreductase domain	GO:0016491;GO:0055114	IPR001395: Aldo/keto reductase; IPR023210: NADP-dependent oxidoreductase domain	NA
comp25406_c0_seq1.p1	Ec-25_001500.1	Quinoprotein alcohol dehydrogenase-like domain	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027295: Quinoprotein alcohol dehydrogenase-like domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp24792_c0_seq2.p1	Ec-25_001530.1	Glycoside-hydrolase family GH114, TIM-barrel domain	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR017853: Glycoside hydrolase superfamily; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR004352: Glycoside-hydrolase family GH114, TIM-barrel domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32275_c0_seq6.p1	Ec-25_001540.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13432: Tetratricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat	NA
comp30454_c0_seq2.p1	Ec-25_001550.1	N-acetyltransferase ESCO, acetyl-transferase domain	GO:0003684;GO:0003887;GO:0006281;n/a	IPR028005: N-acetyltransferase ESCO, zinc-finger; IPR028009: N-acetyltransferase ESCO, acetyl-transferase domain; PTHR11076: ; SignalP-TM:	NA
comp30593_c0_seq1.p1	Ec-25_001570.1	Pectin lyase fold/virulence factor	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR003368: Polymorphic outer membrane protein repeat; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR11319:SF28: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR012334: Pectin lyase fold; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR011050: Pectin lyase fold/virulence factor; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR11319: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32244_c0_seq4.p1	Ec-25_001580.2	hypothetical protein	n/a;n/a;n/a	NA	NA
comp34189_c0_seq1.p1	Ec-25_001620.1	expressed unknown protein	n/a;n/a;n/a	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32504_c1_seq25.p1	Ec-25_001640.1	expressed unknown protein	n/a;n/a;n/a	G3DSA:1.20.1000.10: ; Coil:	NA
comp19970_c0_seq1.p1	Ec-25_001660.1	DnaJ domain containing protein - likely pseudogene	GO:0031072	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001623: DnaJ domain; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32672_c1_seq2.p2	Ec-25_001670.1	PDZ domain	GO:0005515	IPR001041: 2Fe-2S ferredoxin-type domain; SIGNAL_PEPTIDE: Signal peptide region; IPR001478: PDZ domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012675: Beta-grasp domain; PTHR23426: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28611_c0_seq1.p1	Ec-25_001690.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp34167_c0_seq1.p1	Ec-25_001710.1	Thioredoxin-like fold	n/a;GO:0045454	Coil: ; PTHR21148: ; IPR013766: Thioredoxin domain; IPR012336: Thioredoxin-like fold	NA
comp21471_c0_seq1.p1	Ec-25_001730.1	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34294_c0_seq1.p1	Ec-25_001750.1	eukaryotic initiation factor 4E	GO:0003723;GO:0003743;GO:0005737;GO:0006413	IPR023398: Translation Initiation factor eIF- 4e-like domain; IPR001040: Translation Initiation factor eIF- 4e	NA
comp30718_c0_seq4.p1	Ec-25_001800.1	DnaJ domain containing protein	GO:0006457;GO:0051082;GO:0031072	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24078:SF166: ; IPR001623: DnaJ domain; IPR018253: DnaJ domain, conserved site; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR24078: ; IPR026894: DNAJ-containing protein, X-domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp44898_c0_seq1.p1	Ec-25_001810.1	conserved unknown protein	GO:0005515;GO:0008270	Coil:	NA
comp25606_c0_seq1.p1	Ec-25_001820.2	NLI interacting factor	GO:0005515	PTHR12210: ; PTHR12210:SF13: ; IPR004274: FCP1 homology domain; IPR023214: HAD-like domain	NA
comp20089_c0_seq3.p1	Ec-25_001830.1	Protein of unknown function DUF227	GO:0004674;GO:0006468	IPR004119: Protein of unknown function DUF227; G3DSA:3.90.1200.10: ; Coil: ; IPR011009: Protein kinase-like domain	NA
comp27679_c0_seq2.p1	Ec-25_001840.1	ssDNA-binding transcriptional regulator	GO:0003677;GO:0006355	PTHR13215: ; IPR009044: ssDNA-binding transcriptional regulator; IPR003173: Transcriptional coactivator p15 (PC4); IPR009057: Homeodomain-like; Coil:	NA
comp17813_c0_seq1.p1	Ec-25_001870.1	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32600_c0_seq1.p1	Ec-25_001900.1	Formate-tetrahydrofolate ligase, FTHFS	GO:0005524;GO:0009396;GO:0004329	G3DSA:3.10.410.10: ; PTHR10025: ; IPR020628: Formate-tetrahydrofolate ligase, FTHFS, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:3.30.1510.10: ; IPR000559: Formate-tetrahydrofolate ligase, FTHFS	NA
comp31592_c0_seq7.p1	Ec-25_001910.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp31119_c0_seq5.p1	Ec-25_001920.1	LanC lantibiotic synthetase component C-like 2	NA	PTHR12736: ; IPR007822: Lanthionine synthetase C-like; SSF158745:	NA
comp30368_c0_seq5.p1	Ec-25_001930.1	Per1-like	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007217: Per1-like; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24479_c0_seq1.p1	Ec-25_001940.2	Putative Heat Shock transcription factor	GO:0003700;GO:0005634;GO:0006355;GO:0043565	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR000232: Heat shock factor (HSF)-type, DNA-binding; Coil: ; IPR027725: Heat shock transcription factor family	NA
comp32703_c1_seq1.p1	Ec-25_001970.1	Association with the SNF1 complex (ASC) domain	GO:0005515	IPR014756: Immunoglobulin E-set; IPR006828: Association with the SNF1 complex (ASC) domain; PTHR10343: ; SSF160219:	NA
comp32175_c0_seq27.p1	Ec-25_001990.1	Ribonuclease H-like domain	GO:0003676	IPR012337: Ribonuclease H-like domain	NA
comp21674_c0_seq2.p1	Ec-25_002000.1	Nicotinamide N-methyltransferase-like	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR019410: Nicotinamide N-methyltransferase-like; PTHR14614:	NA
comp32392_c0_seq9.p1	Ec-25_002020.3	Ubiquitin-specific protease 16	GO:0004221;GO:0006511	IPR018200: Ubiquitin specific protease, conserved site; SSF54001: ; IPR028889: Ubiquitin specific protease domain; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase; PTHR24006:	NA
comp24140_c0_seq1.p1	Ec-25_002030.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; IPR004142: NDRG; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31598_c2_seq1.p1	Ec-25_002070.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp21454_c0_seq4.p1	Ec-25_002080.1	Cwf19-like protein, C-terminal domain-2	n/a;n/a;n/a	PTHR12072: ; IPR011146: HIT-like domain; IPR006768: Cwf19-like, C-terminal domain-1; IPR006767: Cwf19-like protein, C-terminal domain-2	NA
comp34220_c0_seq1.p1	Ec-25_002110.1	UbiA prenyltransferase family	GO:0004659;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11048: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR000537: UbiA prenyltransferase family; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31838_c0_seq12.p1	Ec-25_002120.1	Rab-GTPase-TBC domain	GO:0005097;GO:0032313	PTHR22957:SF212: ; G3DSA:1.10.8.270: ; PTHR22957: ; IPR000195: Rab-GTPase-TBC domain; Coil:	NA
comp27845_c0_seq2.p1	Ec-25_002240.1	NAD(P)-binding domain	GO:0008152;GO:0016491	SSF51735: ; PTHR24316: ; IPR016040: NAD(P)-binding domain; IPR002347: Glucose/ribitol dehydrogenase; IPR002198: Short-chain dehydrogenase/reductase SDR	NA
comp31562_c0_seq1.p2	Ec-25_002250.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR14614:	NA
comp33214_c0_seq4.p1	Ec-25_002260.1	Hydrolase, alpha/beta fold family	n/a;n/a;n/a	IPR029058: Alpha/Beta hydrolase fold; PTHR11614: ; IPR022742: Serine aminopeptidase, S33	KOG1455
comp31562_c0_seq1.p1	Ec-25_002290.1	Quinoprotein alcohol dehydrogenase-like superfamily	n/a;n/a;n/a	PTHR13129: ; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily	NA
comp20726_c0_seq1.p1	Ec-25_002310.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	IPR024936: Cyclophilin-type peptidyl-prolyl cis-trans isomerase; IPR002130: Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain; IPR000504: RNA recognition motif domain; PTHR11071:SF156: ; IPR029000: Cyclophilin-like domain; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp28023_c0_seq2.p2	Ec-25_002370.1	Zinc finger, RanBP2-type	GO:0008270	SSF90209: ; PR01228: Eggshell protein signature; PTHR23111: ; IPR001876: Zinc finger, RanBP2-type	NA
comp27854_c0_seq1.p1	Ec-25_002380.1	FAD/NAD-linked reductase, dimerisation domain	GO:0050660;GO:0055114;GO:0016491	PR00368: FAD-dependent pyridine nucleotide reductase signature; IPR004099: Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain; PTHR22912: ; PR00411: Pyridine nucleotide disulphide reductase class-I signature; IPR016156: FAD/NAD-linked reductase, dimerisation domain; IPR001327: Pyridine nucleotide-disulphide oxidoreductase, NAD-binding domain; G3DSA:3.50.50.60: ; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	NA
comp30244_c0_seq2.p1	Ec-25_002400.1	Quinolinate synthetase A	GO:0008987;GO:0051539;GO:0009435	PTHR30573: ; IPR003473: Quinolinate synthetase A; SSF142754:	NA
comp26341_c0_seq2.p1	Ec-25_002440.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp21427_c0_seq1.p1	Ec-25_002450.1	IRC6, uncharacterised protein interacting with AP adaptor complexes	n/a;n/a;n/a	PTHR14659: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR019341: Alpha/gamma-adaptin-binding protein p34	NA
comp23800_c0_seq1.p1	Ec-25_002460.1	Dynein light chain 4, axonemal	GO:0005875;GO:0007017	SSF54648: ; IPR001372: Dynein light chain, type 1/2	NA
comp31154_c0_seq4.p1	Ec-25_002470.3	Notch domain	GO:0016020;GO:0030154	SSF81631: ; IPR002934: Polymerase, nucleotidyl transferase domain; IPR002058: PAP/25A-associated; PTHR23092: ; PTHR23092:SF1: ; G3DSA:3.30.460.10: ; SSF81301:	NA
comp12299_c0_seq1.p1	Ec-25_002480.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp21519_c0_seq1.p1	Ec-25_002490.1	U box domain	GO:0000151;GO:0004842;GO:0006511;GO:0016567;GO:0034450	IPR019474: Ubiquitin conjugation factor E4, core; SSF57850: ; IPR003613: U box domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; PTHR13931:SF2: ; PTHR13931:	NA
comp15786_c0_seq1.p1	Ec-25_002510.1	Ribosomal protein S8e/ribosomal biogenesis NSA2	GO:0003735;GO:0005622;GO:0005840;GO:0006412	IPR001047: Ribosomal protein S8e; IPR022309: Ribosomal protein S8e/ribosomal biogenesis NSA2	NA
comp29717_c0_seq1.p1	Ec-25_002530.1	Phox homologous domain	GO:0035091	IPR001683: Phox homologous domain	NA
comp24536_c0_seq2.p2	Ec-25_002540.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp24536_c0_seq2.p1	Ec-25_002550.1	Nucleotide-binding alpha-beta plait domain	GO:0003676;GO:0000166	SSF54928: ; PF13893: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain); IPR000504: RNA recognition motif domain; PF14259: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain); IPR012677: Nucleotide-binding alpha-beta plait domain; IPR003954: RNA recognition motif domain, eukaryote; PTHR23139:	NA
comp13124_c0_seq1.p1	Ec-25_002560.1	Ribonuclease H-like domain	GO:0004523;GO:0003676	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SSF68906: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR003034: SAP domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR012337: Ribonuclease H-like domain; IPR002156: Ribonuclease H domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PF13456: Reverse transcriptase-like	NA
comp11718_c0_seq1.p2	Ec-25_002570.1	40S ribosomal protein S12	NA	IPR029064: 50S ribosomal protein L30e-like; IPR000530: Ribosomal protein S12e; PTHR11843:SF0: ; IPR004038: Ribosomal protein L7Ae/L30e/S12e/Gadd45	NA
comp21236_c0_seq2.p1	Ec-25_002590.1	Nucleoporin Nup54, alpha-helical domain	n/a;n/a;n/a	IPR024864: Nucleoporin Nup54/Nup57/Nup44; IPR025712: Nucleoporin Nup54, alpha-helical domain; Coil: ; SignalP-TM:	NA
comp33079_c2_seq14.p1	Ec-25_002600.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	IPR020683: Ankyrin repeat-containing domain; Coil: ; SignalP-TM: ; IPR002110: Ankyrin repeat	NA
comp33079_c2_seq5.p1	Ec-25_002610.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp30205_c0_seq3.p1	Ec-25_002640.1	Zinc finger, PHD-type	GO:0005515;GO:0008270	IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR001965: Zinc finger, PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; IPR019787: Zinc finger, PHD-finger; G3DSA:3.90.10.10:	NA
comp27356_c0_seq2.p1	Ec-25_002650.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp26930_c1_seq1.p1	Ec-25_002670.1	Protein of unknown function DUF775	n/a;n/a;n/a	IPR008493: Protein of unknown function DUF775	NA
comp33646_c0_seq1.p1	Ec-25_002680.2	Protein of unknown function DUF583	n/a;n/a;n/a	PTHR35024: ; PTHR35024:SF2: ; IPR007607: Protein of unknown function DUF583	NA
comp31277_c1_seq6.p1	Ec-25_002700.1	DExx box DNA helicase domain	GO:0003677;GO:0004003;GO:0005524;GO:0006281	IPR014016: UvrD-like Helicase, ATP-binding domain; IPR013986: DExx box DNA helicase domain; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR014017: DNA helicase, UvrD-like, C-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR000212: DNA helicase, UvrD/REP type; G3DSA:1.10.486.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24216_c0_seq1.p1	Ec-25_002730.1	boron transporter 1	GO:0005452;GO:0006820;GO:0016020	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; IPR011531: Bicarbonate transporter, C-terminal; IPR003020: Bicarbonate transporter, eukaryotic; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:1.10.287.570: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27044_c0_seq2.p1	Ec-25_002740.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp27113_c0_seq1.p1	Ec-25_002750.1	Aminotransferase	GO:0003824;GO:0030170	SIGNAL_PEPTIDE: Signal peptide region; IPR000653: DegT/DnrJ/EryC1/StrS aminotransferase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR015424: Pyridoxal phosphate-dependent transferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR30244: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR015421: Pyridoxal phosphate-dependent transferase, major region, subdomain 1	NA
comp20510_c0_seq1.p1	Ec-25_002760.1	hydroxymethylbilane synthase, putative chloroplast precursor	GO:0004418;GO:0033014	IPR022419: Porphobilinogen deaminase, dipyrromethane cofactor binding site; IPR000860: Porphobilinogen deaminase; SIGNAL_PEPTIDE: Signal peptide region; IPR022418: Porphobilinogen deaminase, C-terminal; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; G3DSA:3.40.190.10: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR022417: Porphobilinogen deaminase, N-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SSF53850:	KOG2892
comp31985_c0_seq3.p1	Ec-25_002770.1	Enhancer of polycomb-like, N-terminal	n/a;n/a;n/a	IPR019542: Enhancer of polycomb-like, N-terminal	NA
comp24778_c0_seq1.p1	Ec-25_002780.1	Rab-GTPase-TBC domain	GO:0005097;GO:0032313	G3DSA:1.10.8.270: ; IPR000195: Rab-GTPase-TBC domain; Coil: ; PTHR20913:	NA
comp30031_c0_seq4.p2	Ec-25_002790.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32728_c0_seq29.p2	Ec-25_002800.3	LETM1-like	NA	IPR018247: EF-Hand 1, calcium-binding site; PTHR14009:SF1: ; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR011685: LETM1-like; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR14009: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24800_c0_seq2.p1	Ec-25_002810.1	Armadillo-like helical	GO:0005488	IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold; PTHR12609:	NA
comp38440_c0_seq1.p1	Ec-25_002820.2	hypothetical protein	n/a;n/a;n/a	NA	NA
comp30668_c1_seq8.p1	Ec-25_002870.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR12189: ; IPR004971: mRNA (guanine-N(7))-methyltransferase domain	NA
comp26220_c1_seq1.p1	Ec-25_002880.1	Tetratricopeptide TPR1	GO:0005515	SSF48452: ; IPR006636: Heat shock chaperonin-binding; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; PF13414: TPR repeat; IPR013026: Tetratricopeptide repeat-containing domain; PTHR22904: ; IPR019734: Tetratricopeptide repeat	NA
comp29061_c0_seq2.p2	Ec-25_002890.1	conserved unknown protein	NA	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR009915: NnrU domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR35988: ; PTHR35988:SF2: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29061_c1_seq1.p1	Ec-25_002900.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp12067_c0_seq1.p1	Ec-25_002910.1	Phosphomevalonate kinase	n/a;n/a;n/a	PTHR31814: ; IPR020568: Ribosomal protein S5 domain 2-type fold; IPR006204: GHMP kinase N-terminal domain; IPR014721: Ribosomal protein S5 domain 2-type fold, subgroup; IPR013750: GHMP kinase, C-terminal domain	NA
comp31968_c0_seq4.p1	Ec-25_002930.1	RNA helicase	n/a;GO:0003677;GO:0005524;GO:0000184;GO:0004386;GO:0005737;GO:0008270	PTHR10887: ; PF13086: AAA domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR018999: RNA helicase UPF1, UPF2-interacting domain; PF13087: AAA domain	KOG1802
comp30823_c3_seq1.p2	Ec-25_002940.1	Hpt domain protein	GO:0000160;GO:0004871	IPR008207: Signal transduction histidine kinase, phosphotransfer (Hpt) domain	NA
comp30185_c0_seq3.p1	Ec-25_002950.1	CBS domain	n/a;n/a;n/a	PTHR13780: ; IPR013785: Aldolase-type TIM barrel; PTHR13780:SF35: ; G3DSA:3.10.580.10: ; SSF54631: ; IPR000644: CBS domain	NA
comp30307_c0_seq3.p1	Ec-25_002960.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26684_c0_seq1.p1	Ec-25_002980.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;GO:0051726;GO:0034729;GO:0018024;GO:0031151	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR030445: Histone H3-K79 methyltransferase; IPR013110: Histone methylation DOT1	NA
comp30176_c0_seq1.p1	Ec-25_002990.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp32610_c0_seq11.p1	Ec-25_002990.2	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp31731_c2_seq3.p1	Ec-25_003000.1	Ran binding domain	GO:0046907	IPR000156: Ran binding domain; SSF50729: ; IPR011993: Pleckstrin homology-like domain; PTHR23138:	NA
comp24279_c0_seq1.p1	Ec-25_003010.1	CS domain	n/a;n/a;n/a	IPR007052: CS domain; IPR025934: NudC N-terminal domain; PTHR12356: ; Coil: ; IPR008978: HSP20-like chaperone	NA
comp31167_c4_seq1.p1	Ec-25_003020.1	Mitochondrial Processing Peptidase alpha subunit	GO:0003824;GO:0046872	PTHR11851: ; IPR007863: Peptidase M16, C-terminal domain; IPR011765: Peptidase M16, N-terminal; IPR011249: Metalloenzyme, LuxS/M16 peptidase-like; IPR011237: Peptidase M16 domain	KOG2067
comp29339_c0_seq3.p1	Ec-25_003030.1	snRNA-activating protein complex, subunit 3	GO:0031177	IPR022042: snRNA-activating protein complex, subunit 3; Coil:	NA
comp32270_c1_seq11.p1	Ec-25_003070.1	RNA polymerase III, largest subunit	GO:0003677;GO:0006351;GO:0003899;GO:0006350	IPR006592: RNA polymerase, N-terminal; SSF64484: ; IPR000722: RNA polymerase, alpha subunit; IPR007066: RNA polymerase Rpb1, domain 3; IPR007080: RNA polymerase Rpb1, domain 1; IPR015700: DNA-directed RNA polymerase III subunit RPC1; PTHR19376: ; IPR007083: RNA polymerase Rpb1, domain 4; G3DSA:2.40.40.20: ; IPR007081: RNA polymerase Rpb1, domain 5; G3DSA:3.30.1490.180:	NA
comp26705_c0_seq3.p1	Ec-25_003100.1	protoporphyrinogen oxidase, putative chloroplast precursor	GO:0004729;GO:0006118;GO:0006779;GO:0055114	G3DSA:1.10.3110.10: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10742: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR027418: Protoporphyrinogen oxidase, C-terminal domain; SSF54373: ; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.50.50.60: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002937: Amine oxidase; SignalP-noTM: ; IPR004572: Protoporphyrinogen oxidase; SSF51905:	NA
comp30011_c0_seq4.p1	Ec-25_003130.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; PTHR24343:	NA
comp28642_c0_seq3.p1	Ec-25_003140.1	expressed unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31917_c0_seq1.p1	Ec-25_003160.1	P-type ATPase, subfamily IV	GO:0000287;GO:0004012;GO:0005524;GO:0015914;GO:0016021	PTHR24092:SF8: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023299: P-type ATPase, cytoplasmic domain N; IPR008250: P-type ATPase, A domain; SSF81653: ; IPR032631: P-type ATPase, N-terminal; IPR023214: HAD-like domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006539: P-type ATPase, subfamily IV; SSF81665: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR018303: P-type ATPase, phosphorylation site; PF13246: Cation transport ATPase (P-type)	NA
comp31917_c0_seq1.p2	Ec-25_003180.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp20686_c0_seq1.p1	Ec-25_003210.3	DEAD box helicase DEAD/DEAH box helicase-like protein	n/a;n/a;n/a	IPR014014: RNA helicase, DEAD-box type, Q motif; IPR011545: DEAD/DEAH box helicase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014001: Helicase superfamily 1/2, ATP-binding domain; PTHR24031:SF330: ; IPR001650: Helicase, C-terminal; PTHR24031: ; SignalP-TM:	KOG0331
comp20181_c0_seq1.p1	Ec-25_003220.1	Zinc finger, RING/FYVE/PHD-type	n/a;GO:0008270	IPR001841: Zinc finger, RING-type; SSF57850: ; IPR004170: WWE domain; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR018123: WWE domain, subgroup; PTHR12622: ; SSF117839:	NA
comp34845_c0_seq1.p1	Ec-25_003230.1	GMP phosphodiesterase, delta subunit	n/a;n/a;n/a	PTHR12951: ; IPR008015: GMP phosphodiesterase, delta subunit; IPR014756: Immunoglobulin E-set	NA
comp19442_c0_seq1.p2	Ec-25_003240.1	RNA-binding	GO:0005622;GO:0008270	SSF54928: ; SSF90209: ; PF14259: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain); IPR000504: RNA recognition motif domain; PR01228: Eggshell protein signature; IPR012677: Nucleotide-binding alpha-beta plait domain; IPR001876: Zinc finger, RanBP2-type; PTHR23238:	NA
comp30092_c0_seq1.p1	Ec-25_003320.1	Protein phosphatase 2A, regulatory B subunit, B56	GO:0008601;GO:0007165;GO:0005488;GO:0000159	IPR002554: Protein phosphatase 2A, regulatory B subunit, B56; IPR016024: Armadillo-type fold	NA
comp24127_c0_seq1.p2	Ec-25_003330.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp20116_c0_seq1.p1	Ec-25_003360.1	Alpha/beta hydrolase fold-1	n/a;n/a;n/a	IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000073: Alpha/beta hydrolase fold-1; PTHR10992:	NA
comp31531_c1_seq9.p1	Ec-25_003370.2	LRR-GTPase of the ROCO family	GO:0005515	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR020859: Roc domain; IPR001611: Leucine-rich repeat; IPR032675: Leucine-rich repeat domain, L domain-like; IPR013684: Mitochondrial Rho-like; IPR009003: Peptidase S1, PA clan; IPR003591: Leucine-rich repeat, typical subtype; PTHR24365: ; Coil: ; G3DSA:2.40.10.10:	NA
comp29917_c0_seq3.p1	Ec-25_003380.1	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp31023_c0_seq4.p1	Ec-23_000490.1	Mannuronan C-5-epimerase N-terminal fragment	NA	IPR011050: Pectin lyase fold/virulence factor; IPR007742: Periplasmic copper-binding protein NosD, beta helix domain; IPR006626: Parallel beta-helix repeat; IPR012334: Pectin lyase fold	NA
comp28701_c0_seq1.p2	Ec-25_003540.2	Protein of unknown function DUF3411, plant	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR31620:SF8: ; SignalP-noTM: ; IPR021825: Protein RETICULATA-related; PTHR31620: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25112_c0_seq1.p1	Ec-25_003550.1	Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain	GO:0016620;GO:0055114	IPR020831: Glyceraldehyde/Erythrose phosphate dehydrogenase family; SSF51735: ; IPR006424: Glyceraldehyde-3-phosphate dehydrogenase, type I; IPR020830: Glyceraldehyde 3-phosphate dehydrogenase, active site; SSF55347: ; IPR020829: Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain; G3DSA:3.30.360.10: ; IPR016040: NAD(P)-binding domain; IPR020828: Glyceraldehyde 3-phosphate dehydrogenase, NAD(P) binding domain	NA
comp12025_c0_seq1.p1	Ec-25_003560.1	Eukaryotic translation initiation factor 3 subunit a (subunit 10)	GO:0006810;n/a;GO:0005488;GO:0005852;GO:0005215	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR000717: Proteasome component (PCI) domain; IPR027512: Eukaryotic translation initiation factor 3 subunit A; PR01228: Eggshell protein signature; PTHR14005: ; Coil:	NA
comp34487_c0_seq1.p1	Ec-25_003580.1	Transcription elongation factor, TFIIS/CRSP70, N-terminal, sub-type	GO:0005634;GO:0006351	IPR017923: Transcription factor IIS, N-terminal; IPR001222: Zinc finger, TFIIS-type; IPR017890: Transcription elongation factor S-IIM; IPR003617: Transcription elongation factor, TFIIS/CRSP70, N-terminal, sub-type; IPR016492: Transcription elongation factor, TFIIS-related; PTHR11477: ; IPR003618: Transcription elongation factor S-II, central domain; SSF57783: ; G3DSA:2.20.25.10:	NA
comp30366_c0_seq14.p1	Ec-25_003590.1	Flavin monooxygenase-like	GO:0050660;GO:0055114;GO:0050661;GO:0004499	PR00419: Adrenodoxin reductase family signature; G3DSA:3.50.50.60: ; PTHR23023: ; IPR020946: Flavin monooxygenase-like; SSF51905:	NA
comp26957_c0_seq2.p1	Ec-25_003630.2	expressed unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31993_c0_seq4.p1	Ec-25_003680.1	RGS domain	GO:0038032	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016137: RGS domain; G3DSA:1.10.167.10: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32408_c3_seq1.p1	Ec-25_003710.1	Plastid lipid-associated protein/fibrillin conserved domain	GO:0005198	SIGNAL_PEPTIDE: Signal peptide region; PTHR31906: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR006843: Plastid lipid-associated protein/fibrillin conserved domain	NA
comp30296_c0_seq4.p1	Ec-25_003720.2	Uncharacterised protein family UPF0139	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR13193:SF0: ; IPR005351: Uncharacterised protein family UPF0139; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20814_c0_seq1.p1	Ec-25_003730.1	Putative dehydroascorbate reductase	n/a;n/a;n/a	IPR010987: Glutathione S-transferase, C-terminal-like	NA
comp21363_c0_seq2.p1	Ec-25_003740.1	putative ATP-dependent proteinase, possible LON protease	GO:0004176;GO:0006508	IPR003111: Peptidase S16, lon N-terminal; IPR015947: PUA-like domain; PTHR23327:	NA
comp32349_c1_seq27.p1	Ec-25_003760.1	Amino acid transporter, transmembrane	n/a;n/a;n/a	PTHR16189: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29936_c0_seq2.p1	Ec-25_003770.1	Strawberry notch, helicase C domain	GO:0003676;GO:0004386;GO:0005524	IPR026741: Protein strawberry notch; PF13872: P-loop containing NTP hydrolase pore-1; IPR026937: Strawberry notch, helicase C domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil:	NA
comp29747_c0_seq1.p1	Ec-25_003790.1	Pentatricopeptide repeat	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; IPR002885: Pentatricopeptide repeat; PTHR24015:	NA
comp34672_c0_seq1.p1	Ec-25_003800.1	Light harvesting complex protein	GO:0016020;GO:0009765	SIGNAL_PEPTIDE: Signal peptide region; IPR022796: Chlorophyll A-B binding protein; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023329: Chlorophyll a/b binding protein domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001344: Chlorophyll A-B binding protein, plant; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26956_c0_seq1.p1	Ec-25_003810.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp31662_c0_seq2.p1	Ec-26_000010.1	Armadillo-type fold	GO:0005488	IPR011989: Armadillo-like helical; IPR019442: Domain of unknown function DUF2428, death-receptor-like; PTHR14387: ; IPR016024: Armadillo-type fold	NA
comp29262_c0_seq1.p1	Ec-26_000080.1	MULE transposase domain	n/a;n/a;n/a	IPR018289: MULE transposase domain	NA
comp29029_c0_seq1.p1	Ec-26_000120.1	Ketose-bisphosphate aldolase, class-II	GO:0016832;GO:0008270;GO:0005975	IPR013785: Aldolase-type TIM barrel; IPR000771: Ketose-bisphosphate aldolase, class-II; SSF51569: ; PTHR30304: ; SSF142764:	NA
comp12860_c0_seq1.p1	Ec-26_000130.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;GO:0031515;GO:0030488;GO:0016429	G3DSA:3.10.330.20: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR014816: tRNA (1-methyladenosine) methyltransferase catalytic subunit Gcd14; PTHR12133:	NA
comp19816_c0_seq1.p1	Ec-26_000140.1	Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain	GO:0006457;GO:0003755;GO:0000413	SIGNAL_PEPTIDE: Signal peptide region; IPR029000: Cyclophilin-like domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR024936: Cyclophilin-type peptidyl-prolyl cis-trans isomerase; IPR002130: Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR020892: Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp19816_c0_seq1.p2	Ec-26_000150.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp28948_c0_seq1.p1	Ec-26_000170.1	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a	PTHR11200:SF152: ; IPR000300: Inositol polyphosphate-related phosphatase; PTHR11200: ; IPR005135: Endonuclease/exonuclease/phosphatase; Coil:	NA
comp24555_c0_seq1.p1	Ec-26_000190.1	Glycosyl transferase, family 31	GO:0006486;GO:0008378;GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002659: Glycosyl transferase, family 31; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33131_c0_seq7.p1	Ec-26_000200.1	Myosin head, motor domain	GO:0003774;GO:0005524;GO:0016459	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000644: CBS domain; PTHR13140: ; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF54277: ; IPR000270: PB1 domain; G3DSA:3.10.20.240: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SSF54631: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:3.10.580.10: ; IPR006141: Intein N-terminal splicing region; IPR001609: Myosin head, motor domain; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32921_c1_seq4.p1	Ec-26_000220.1	Triose-phosphate transporter domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF103481: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004853: Triose-phosphate transporter domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11132: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20801_c0_seq1.p1	Ec-26_000240.1	putative serine protease inhibitor	GO:0009611;GO:0004867	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; G3DSA:3.30.10.10: ; IPR000864: Proteinase inhibitor I13, potato inhibitor I; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31373_c0_seq2.p2	Ec-26_000250.1	Zinc finger, RING-type	GO:0005515;GO:0008270	PTHR11210: ; IPR001841: Zinc finger, RING-type; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR024766: Zinc finger, RING-H2-type	NA
comp20627_c0_seq1.p1	Ec-26_000280.1	Alpha/beta hydrolase fold-1	n/a;n/a;n/a	IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR029059: Alpha/beta hydrolase fold-5; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12641_c0_seq1.p1	Ec-26_000290.1	Prolyl 4-hydroxylase, alpha subunit	GO:0005506;GO:0031418;GO:0055114;GO:0016705;GO:0016706;GO:0016491	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006620: Prolyl 4-hydroxylase, alpha subunit; IPR005123: Oxoglutarate/iron-dependent dioxygenase; PTHR14650: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28548_c0_seq3.p1	Ec-26_000330.1	GAF domain	GO:0005515	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR019537: Transmembrane protein 65; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029016: GAF domain-like; PTHR21706: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR003018: GAF domain	NA
comp31239_c0_seq2.p1	Ec-26_000340.3	Nucleotide-binding alpha-beta plait domain	GO:0000166	PTHR24012: ; PTHR24012:SF348: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp22048_c0_seq1.p1	Ec-26_000350.1	Carbon-nitrogen hydrolase	GO:0006807;GO:0016810	IPR003010: Carbon-nitrogen hydrolase; PTHR23088:	NA
comp12758_c0_seq1.p1	Ec-26_000370.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005634;GO:0030163;GO:0005737;GO:0016787	IPR003959: ATPase, AAA-type, core; IPR003960: ATPase, AAA-type, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR005937: 26S proteasome subunit P45; PTHR23073: ; IPR003593: AAA+ ATPase domain; G3DSA:1.10.8.60: ; Coil:	NA
comp33132_c0_seq7.p1	Ec-26_000380.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp33132_c0_seq9.p1	Ec-26_000390.1	Bromodomain	GO:0005515	G3DSA:2.30.30.270: ; IPR018359: Bromodomain, conserved site; IPR001487: Bromodomain; IPR016197: Chromo domain-like; IPR022702: DNA (cytosine-5)-methyltransferase 1, replication foci domain; Coil: ; IPR028935: WHIM3 domain; IPR010525: Auxin response factor; IPR028941: WHIM2 domain; PTHR13900:	NA
comp11878_c0_seq1.p1	Ec-26_000400.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003676	IPR003593: AAA+ ATPase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR012337: Ribonuclease H-like domain; Coil: ; PTHR20953:	NA
comp34731_c0_seq1.p1	Ec-26_000410.1	EsV-1-7	GO:0016491;GO:0055114	IPR023210: NADP-dependent oxidoreductase domain	NA
comp11707_c0_seq1.p1	Ec-26_000480.1	PYchF, plastid YchF-like GTPase	n/a;n/a;n/a	SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR012675: Beta-grasp domain; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013029: Domain of unknown function DUF933; IPR004396: Ribosome-binding ATPase YchF/Obg-like ATPase 1; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR031167: OBG-type guanine nucleotide-binding (G) domain; SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR23305: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR012676: TGS-like; IPR006073: GTP binding domain; SignalP-noTM: ; IPR023192: TGS-like domain; Coil:	NA
comp19629_c0_seq2.p1	Ec-26_000490.1	Protein of unknown function DUF1499	n/a;n/a;n/a	IPR010865: Protein of unknown function DUF1499; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12176_c0_seq1.p1	Ec-26_000500.1	PYlqF, plastid YlqF/RbgA-like GTPase	GO:0005525;GO:0005622	PTHR11089: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006073: GTP binding domain; IPR023179: GTP-binding protein, orthogonal bundle domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR019991: GTP-binding protein, ribosome biogenesis	NA
comp32311_c0_seq3.p1	Ec-26_000540.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	SSF54928: ; IPR000571: Zinc finger, CCCH-type; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain; Coil: ; SSF90229:	NA
comp33208_c0_seq5.p1	Ec-26_000560.2	Centrosomal protein of 290kDa	GO:0005634;GO:0005813;GO:0060271	Coil: ; IPR026201: Centrosomal protein of 290kDa	NA
comp33027_c0_seq42.p2	Ec-26_000570.1	Ribosomal L11 methyltransferase, PrmA	GO:0008168;GO:0008276;GO:0006479;GO:0005737	PF06325: Ribosomal protein L11 methyltransferase (PrmA); IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR025799: Protein arginine N-methyltransferase	NA
comp33027_c0_seq59.p1	Ec-26_000580.1	membrane acyl-CoA binding protein	GO:0005515	IPR029058: Alpha/Beta hydrolase fold; IPR013761: Sterile alpha motif/pointed domain; IPR001660: Sterile alpha motif domain; IPR021129: Sterile alpha motif, type 1; PTHR24193: ; IPR000048: IQ motif, EF-hand binding site; IPR020683: Ankyrin repeat-containing domain; IPR024743: Dynein heavy chain, coiled coil stalk; Coil: ; IPR002110: Ankyrin repeat	NA
comp31985_c0_seq1.p1	Ec-26_000600.1	PSP1, C-terminal	n/a;n/a;n/a	PTHR21600: ; Coil: ; PTHR21600:SF3: ; IPR007557: PSP1, C-terminal	NA
comp28190_c0_seq2.p1	Ec-26_000610.2	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR16266:SF17: ; PTHR16266: ; IPR019775: WD40 repeat, conserved site; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat	NA
comp20433_c0_seq1.p1	Ec-26_000720.1	Pleckstrin homology domain	NA	SSF50729: ; IPR011993: Pleckstrin homology-like domain; Coil: ; IPR001849: Pleckstrin homology domain	NA
comp19546_c0_seq1.p1	Ec-26_000730.1	Nucleolar complex protein 2	n/a;n/a;n/a	IPR005343: Nucleolar complex protein 2; Coil: ; SignalP-TM:	NA
comp31855_c1_seq1.p1	Ec-26_000740.1	SET domain protein	GO:0005515	NA	NA
comp68087_c0_seq1.p1	Ec-26_000770.1	Kelch-type beta propeller	GO:0005515	SSF117281: ; PF13418: Galactose oxidase, central domain; IPR000742: Epidermal growth factor-like domain; PF13415: Galactose oxidase, central domain; PTHR23244: ; IPR013032: EGF-like, conserved site; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:2.170.300.10: ; IPR015915: Kelch-type beta propeller; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp122980_c0_seq1.p3	Ec-26_000770.2	Kelch-type beta propeller	GO:0005515	PTHR23244:SF297: ; SSF117281: ; PF13418: Galactose oxidase, central domain; PTHR23244: ; IPR015915: Kelch-type beta propeller	NA
comp29219_c0_seq1.p1	Ec-26_000790.1	Zinc finger, RING/FYVE/PHD-type	GO:0005515;GO:0008270	SSF57850: ; IPR001841: Zinc finger, RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; Coil: ; PTHR32002:	NA
comp27291_c1_seq2.p1	Ec-26_000800.1	3-Phosphoshikimate 1-Carboxyvinyltransferase	GO:0003866;GO:0003824	IPR001986: Enolpyruvate transferase domain; SIGNAL_PEPTIDE: Signal peptide region; IPR006264: 3-phosphoshikimate 1-carboxyvinyltransferase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023193: 3-phosphoshikimate 1-carboxyvinyltransferase, conserved site; SignalP-noTM: ; PTHR21090: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013792: RNA 3'-terminal phosphate cyclase/enolpyruvate transferase, alpha/beta	KOG0692
comp24565_c0_seq1.p1	Ec-26_000810.1	Zinc finger, RanBP2-type	GO:0008270	SSF90209: ; SignalP-noTM: ; PTHR23111: ; IPR001876: Zinc finger, RanBP2-type; SignalP-TM:	NA
comp20532_c0_seq3.p1	Ec-26_000840.1	Peroxisomal biogenesis factor 11	GO:0005779;GO:0016559	PTHR12652: ; IPR008733: Peroxisomal biogenesis factor 11	NA
comp26617_c0_seq3.p1	Ec-26_000850.1	Protein of unknown function DUF3593	NA	IPR019634: Uncharacterised protein family Ycf49; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR021995: Protein of unknown function DUF3593; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33280_c0_seq2.p1	Ec-26_000860.1	Transcriptional coactivator Hfi1/Transcriptional adapter 1	GO:0070461	IPR024738: Transcriptional coactivator Hfi1/Transcriptional adapter 1	NA
comp33280_c0_seq2.p2	Ec-26_000880.1	Translation initiation factor IF6	GO:0043022;GO:0042256	SSF55909: ; G3DSA:3.75.10.10: ; IPR002769: Translation initiation factor IF6	KOG3185
comp12035_c0_seq1.p1	Ec-26_000890.1	Peptidase M24, structural domain	GO:0006508;GO:0008235;GO:0009987	IPR000994: Peptidase M24, structural domain; PTHR10804:	NA
comp88249_c0_seq1.p1	Ec-26_000910.1	MORN motif	n/a;n/a;n/a	G3DSA:2.20.110.10: ; PTHR23084: ; IPR003409: MORN motif; SSF82185:	NA
comp26000_c0_seq1.p1	Ec-26_000920.1	Aldehyde dehydrogenase	GO:0008152;GO:0016491;GO:0055114	IPR029510: Aldehyde dehydrogenase, glutamic acid active site; IPR016161: Aldehyde/histidinol dehydrogenase; IPR015590: Aldehyde dehydrogenase domain; IPR016162: Aldehyde dehydrogenase N-terminal domain; IPR016160: Aldehyde dehydrogenase, cysteine active site; PTHR11699: ; IPR016163: Aldehyde dehydrogenase, C-terminal	KOG2450
comp32503_c0_seq8.p2	Ec-26_000950.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32503_c0_seq8.p1	Ec-26_000960.1	Alpha/beta knot methyltransferases	GO:0003723;GO:0006396;GO:0008173	IPR029028: Alpha/beta knot methyltransferases; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR12029: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR001537: tRNA/rRNA methyltransferase, SpoU type; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR029026: tRNA (guanine-N1-)-methyltransferase, N-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30241_c0_seq9.p1	Ec-26_000990.1	putative myo-inositol monophosphatase	GO:0046854	G3DSA:3.30.540.10: ; IPR020550: Inositol monophosphatase, conserved site; IPR000760: Inositol monophosphatase; SSF56655: ; G3DSA:3.40.190.80: ; IPR020583: Inositol monophosphatase, metal-binding site	NA
comp21780_c0_seq1.p1	Ec-26_001000.3	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR13018: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR13018:SF40: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24781_c0_seq1.p1	Ec-26_001070.2	hypothetical protein	n/a;n/a;n/a	NA	NA
comp21258_c1_seq1.p1	Ec-26_001080.1	tRNA/rRNA methyltransferase, SpoU type	GO:0006396;GO:0003723;GO:0008168;GO:0008173	IPR001537: tRNA/rRNA methyltransferase, SpoU type; IPR029028: Alpha/beta knot methyltransferases; IPR029064: 50S ribosomal protein L30e-like; IPR013123: RNA 2-O ribose methyltransferase, substrate binding; IPR029026: tRNA (guanine-N1-)-methyltransferase, N-terminal; PTHR12029:	NA
comp24696_c0_seq1.p1	Ec-26_001090.2	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp34018_c0_seq1.p1	Ec-26_001100.1	GroEL-like apical domain	GO:0006457;GO:0005524;GO:0005737;GO:0051082;GO:0042026	IPR002423: Chaperonin Cpn60/TCP-1 family; IPR027409: GroEL-like apical domain; SSF54849: ; IPR027413: GroEL-like equatorial domain; IPR001844: Chaperonin Cpn60; SSF48592:	NA
comp32858_c2_seq5.p1	Ec-26_001130.1	Zinc/iron permease	GO:0016020;GO:0055085;GO:0046873;GO:0030001	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR16950: ; SignalP-noTM: ; IPR003689: Zinc/iron permease; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29430_c1_seq1.p1	Ec-26_001140.1	Mitochondrial ubiquitin ligase activator of NFKB 1	GO:0007005;GO:0004842	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR022170: Mitochondrial ubiquitin ligase activator of NFKB 1; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29482_c0_seq1.p1	Ec-26_001150.1	Pentatricopeptide repeat	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24015: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002885: Pentatricopeptide repeat; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12254_c0_seq1.p1	Ec-26_001160.2	Zn(2)-C6 fungal-type DNA-binding domain	GO:0000981;GO:0005634;GO:0006355;GO:0008270	IPR001138: Zn(2)-C6 fungal-type DNA-binding domain	NA
comp31776_c0_seq19.p1	Ec-26_001170.1	P-loop containing nucleoside triphosphate hydrolase	GO:0003677;GO:0004003;GO:0005524;GO:0006281	IPR000212: DNA helicase, UvrD/REP type; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR027785: UvrD-like helicase C-terminal domain	NA
comp31776_c0_seq4.p1	Ec-26_001170.3	P-loop containing nucleoside triphosphate hydrolase	GO:0003677;GO:0004003;GO:0005524;GO:0006281	PTHR11070:SF2: ; IPR014016: UvrD-like Helicase, ATP-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR000212: DNA helicase, UvrD/REP type	NA
comp31776_c0_seq4.p3	Ec-26_001170.4	P-loop containing nucleoside triphosphate hydrolase	GO:0003677;GO:0004003;GO:0005524;GO:0006281	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR000212: DNA helicase, UvrD/REP type; IPR027785: UvrD-like helicase C-terminal domain	NA
comp20886_c0_seq2.p1	Ec-26_001190.2	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp28101_c0_seq2.p1	Ec-26_001200.1	Plastid lipid-associated protein/fibrillin conserved domain	GO:0005198;n/a	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR006843: Plastid lipid-associated protein/fibrillin conserved domain	NA
comp19674_c0_seq1.p1	Ec-26_001210.1	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28303_c1_seq3.p1	Ec-26_001240.1	Radical SAM	GO:0003824;GO:0051536	SSF102114: ; IPR013785: Aldolase-type TIM barrel; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR007197: Radical SAM; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004383: Ribosomal RNA large subunit methyltransferase RlmN/Cfr; G3DSA:3.80.30.10: ; PF13394: 4Fe-4S single cluster domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26809_c0_seq4.p3	Ec-26_001250.1	Ovarian tumour, otubain	n/a;n/a;n/a	IPR003323: OTU domain; SSF54001: ; PTHR12419: ; Coil:	NA
comp26809_c0_seq4.p1	Ec-26_001260.1	expressed unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24706_c0_seq2.p2	Ec-26_001290.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24706_c0_seq2.p1	Ec-26_001300.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp25069_c1_seq2.p1	Ec-26_001320.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33934_c0_seq1.p1	Ec-26_001350.1	tRNAHis guanylyltransferase Thg1	GO:0000287;GO:0006400;GO:0008193	IPR007537: tRNAHis guanylyltransferase Thg1; IPR024956: tRNAHis guanylyltransferase catalytic domain; IPR025845: Thg1 C-terminal domain	NA
comp12838_c0_seq1.p1	Ec-26_001370.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp12568_c0_seq2.p1	Ec-26_001380.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29526_c0_seq3.p1	Ec-26_001430.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;GO:0008168	PF12847: Methyltransferase domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR024160: Bin3-type S-adenosyl-L-methionine binding domain; IPR010675: Bicoid-interacting 3; PTHR12315:	NA
comp11847_c0_seq1.p1	Ec-26_001440.1	conserved unknown protein	NA	PTHR23029: ; IPR029033: Histidine phosphatase superfamily; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR013078: Histidine phosphatase superfamily, clade-1; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20264_c0_seq4.p1	Ec-26_001460.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp27559_c0_seq4.p1	Ec-26_001470.1	Plastid lipid-associated protein/fibrillin conserved domain	GO:0005198	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR31906: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR006843: Plastid lipid-associated protein/fibrillin conserved domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp11925_c0_seq1.p1	Ec-26_001480.1	hypothetical protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20822_c0_seq2.p1	Ec-26_001500.1	SNF1-related protein kinase	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; PTHR24343:	NA
comp11890_c0_seq1.p1	Ec-26_001520.1	N-terminal acetyltransferase A, auxiliary subunit	n/a;GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; IPR013105: Tetratricopeptide TPR2; Coil: ; IPR013026: Tetratricopeptide repeat-containing domain; PTHR22767: ; IPR021183: N-terminal acetyltransferase A, auxiliary subunit; IPR019734: Tetratricopeptide repeat	NA
comp31117_c2_seq1.p1	Ec-26_001560.1	Nucleotide-diphospho-sugar transferase	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR005069: Nucleotide-diphospho-sugar transferase	NA
comp25541_c0_seq1.p1	Ec-26_001570.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32512_c0_seq1.p1	Ec-26_001610.2	expressed unknown protein	n/a;n/a;n/a	NA	NA

comp32110_c0_seq8.p1	Ec-26_001650.1	ABC transporter-like	GO:0005524;GO:0016887	IPR003439: ABC transporter-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:1.20.1560.10: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011527: ABC transporter type 1, transmembrane domain; PTHR24223: ; IPR017871: ABC transporter, conserved site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20930_c0_seq2.p2	Ec-26_001680.1	hypothetical protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; Coil: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp31372_c0_seq6.p1	Ec-26_001690.1	conserved unknown protein	n/a;n/a;n/a	NA	NA

comp19881_c0_seq1.p1	Ec-26_006490.1	Histone H4	GO:0003677;GO:0005634;GO:0046982;GO:0000786	NA	NA
comp12382_c0_seq1.p1	Ec-26_006500.1	Histone H2A.Z	GO:0003677;GO:0046982	NA	NA
comp33290_c0_seq1.p1	Ec-26_006510.1	Bromodomain	GO:0005515	PTHR22880: ; Coil: ; IPR001487: Bromodomain; SignalP-TM: ; PTHR22880:SF150:	NA
comp31053_c0_seq1.p1	Ec-26_006520.1	Ribosomal RNA-processing protein 14/surfeit locus protein 6, C-terminal domain	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR029190: Ribosomal RNA-processing protein 14/surfeit locus protein 6, C-terminal domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029188: Ribosomal RNA-processing protein 14, N-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR007019: Surfeit locus 6	NA
comp27419_c0_seq1.p1	Ec-26_006540.1	Rab-GTPase-TBC domain	GO:0005097;GO:0032313	G3DSA:1.10.8.270: ; IPR000195: Rab-GTPase-TBC domain; PTHR22957:	NA
comp28307_c0_seq1.p1	Ec-26_006550.1	Vacuolar sorting protein 9, subgroup	n/a;n/a;n/a	SSF109993: ; IPR003123: VPS9 domain; PTHR23101:	NA
comp35003_c0_seq1.p1	Ec-26_006570.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21175_c0_seq1.p1	Ec-26_006580.1	YEATS	GO:0005634;GO:0006355	IPR005033: YEATS; Coil:	NA
comp24832_c0_seq1.p2	Ec-26_006620.1	Ankyrin repeat-containing domain	n/a;n/a;n/a	IPR020683: Ankyrin repeat-containing domain	NA
comp33654_c0_seq1.p1	Ec-26_006630.1	Winged helix-turn-helix DNA-binding domain	n/a;n/a;n/a	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR011993: PH domain-like; PTHR13128:SF12: ; IPR007286: EAP30; PTHR13128: ; IPR021648: Vacuolar protein sorting protein 36, GLUE domain	NA
comp12131_c0_seq1.p1	Ec-26_006650.2	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp31905_c0_seq5.p1	Ec-27_000020.1	Tyrosyl-DNA phosphodiesterase I	GO:0005634;GO:0006281;GO:0008081	IPR010347: Tyrosyl-DNA phosphodiesterase I; PTHR12415:SF0: ; IPR027415: Tyrosyl-DNA phosphodiesterase C-terminal domain; G3DSA:3.30.870.10: ; SSF56024:	NA
comp32192_c0_seq1.p1	Ec-27_000030.1	poly(L-malate)-hydrolase precursor	GO:0006508;GO:0008233	IPR007365: Transferrin receptor-like, dimerisation domain; IPR007484: Peptidase M28; SSF52025: ; PTHR10404: ; G3DSA:3.50.30.30: ; IPR003137: Protease-associated domain, PA; IPR031054: Glutamate carboxypeptidase 2 homologue; SSF53187: ; G3DSA:3.40.630.10:	NA
comp31410_c0_seq2.p1	Ec-27_000060.1	Major facilitator superfamily domain	n/a;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR015414: Transmembrane protein Tvp38/TMEM64-like; IPR020846: Major facilitator superfamily domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR12677: ; PF09335: SNARE associated Golgi protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG3140
comp32575_c0_seq6.p1	Ec-27_000070.1	Elongated TPR repeat-containing domain	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; IPR023114: Elongated TPR repeat-containing domain	NA
comp32575_c0_seq6.p2	Ec-27_000080.1	Protein-tyrosine phosphatase-like	n/a;n/a;n/a	IPR029021: Protein-tyrosine phosphatase-like; IPR016130: Protein-tyrosine phosphatase, active site; IPR020428: Protein-tyrosine phosphatase, dual specificity phosphatase, eukaryotic; IPR004861: Protein-tyrosine phosphatase, SIW14-like; PTHR31126:	NA
comp32648_c3_seq8.p1	Ec-27_000090.1	ERCC4 domain containing protein	GO:0003677;GO:0006259;GO:0004518	PTHR13451: ; IPR006166: ERCC4 domain; IPR011335: Restriction endonuclease type II-like; IPR020819: DNA repair nuclease, XPF-type/Helicase	KOG2379
comp32648_c3_seq4.p1	Ec-27_000110.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR002885: Pentatricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; PF13374: Tetratricopeptide repeat; PTHR24015:	NA
comp13098_c0_seq2.p1	Ec-27_000130.1	Kinesin-like protein	GO:0003777;GO:0005871;GO:0007018	IPR019821: Kinesin motor domain, conserved site; IPR027640: Kinesin-like protein; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR001752: Kinesin motor domain	NA
comp12638_c0_seq1.p1	Ec-27_000150.1	Sar1B, Ras superfamily GTPase	GO:0005525	IPR024156: Small GTPase superfamily, ARF type; PTHR11711: ; IPR005225: Small GTP-binding protein domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR006687: Small GTPase superfamily, SAR1-type; IPR006689: Small GTPase superfamily, ARF/SAR type	NA
comp24867_c0_seq3.p1	Ec-27_000160.1	Nicotinamide N-methyltransferase-like	n/a;n/a;n/a	IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; Coil: ; IPR019410: Nicotinamide N-methyltransferase-like; PTHR14614:	NA
comp12151_c0_seq1.p1	Ec-27_000170.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp24378_c0_seq1.p1	Ec-27_000190.1	Cathepsin L-like proteinase	GO:0008234;GO:0006508;GO:0004197	SSF54001: ; IPR014756: Immunoglobulin E-set; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; IPR013128: Peptidase C1A; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.90.70.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:2.70.220.10: ; IPR003172: MD-2-related lipid-recognition domain; SIGNAL_PEPTIDE: Signal peptide region; IPR000169: Cysteine peptidase, cysteine active site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR013201: Proteinase inhibitor I29, cathepsin propeptide; IPR025660: Cysteine peptidase, histidine active site; IPR000668: Peptidase C1A, papain C-terminal; SignalP-noTM:	KOG1543
comp31911_c0_seq1.p1	Ec-27_000210.1	Raptor	GO:0031929;GO:0005488;GO:0031931	IPR011989: Armadillo-like helical; IPR004083: Regulatory associated protein of TOR; PR01547: Saccharomyces cerevisiae 175.8kDa hypothetical protein signature; IPR016024: Armadillo-type fold; IPR029347: Raptor N-terminal CASPase-like domain; Coil:	KOG1517
comp30704_c0_seq2.p1	Ec-27_000220.1	WD40/YVTN repeat-like-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR004083: Regulatory associated protein of TOR; IPR001680: WD40 repeat; Coil:	NA
comp29257_c0_seq1.p1	Ec-27_000230.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31714_c0_seq8.p1	Ec-27_000240.1	C2 domain	GO:0005515	PTHR10024: ; IPR000008: C2 domain; IPR002765: Uncharacterised protein family UPF0145	NA
comp31755_c0_seq7.p1	Ec-27_000260.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp32597_c0_seq15.p4	Ec-27_000270.1	Zinc finger, RING/FYVE/PHD-type	GO:0004221;GO:0006511	SSF54001: ; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase; PTHR24006: ; SignalP-TM: ; IPR001607: Zinc finger, UBP-type; SSF57850: ; IPR018200: Ubiquitin specific protease, conserved site; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR028889: Ubiquitin specific protease domain; Coil:	NA
comp32597_c0_seq15.p3	Ec-27_000280.1	Chitobiosyldiphosphodolichol beta-mannosyltransferase, family GT33	GO:0009058	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF53756: ; IPR026051: Asparagine-linked glycosylation protein 1-like; PF13692: Glycosyl transferases group 1; IPR028098: Glycosyltransferase subfamily 4, N-terminal domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2941
comp30765_c0_seq5.p1	Ec-27_000290.1	conserved unknown protein	GO:0005515;GO:0008270;GO:0030414	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29627_c0_seq2.p1	Ec-27_000310.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp14087_c0_seq1.p1	Ec-27_000320.1	SCO1 homolog, cytochrome c oxidase copper chaperone	NA	IPR003782: Copper chaperone SCO1/SenC; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR12151:SF5: ; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; cd02968: SCO; IPR012336: Thioredoxin-like fold; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	KOG2792
comp30516_c0_seq6.p4	Ec-27_000330.1	Histidine phosphatase superfamily, clade-1	GO:0006096;GO:0016868	IPR013078: Histidine phosphatase superfamily, clade-1; IPR029033: Histidine phosphatase superfamily; IPR005952: Phosphoglycerate mutase 1	NA
comp30516_c0_seq8.p1	Ec-27_000340.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0004672;GO:0005524;GO:0006468	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; PTHR24353: ; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR000961: AGC-kinase, C-terminal; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10:	NA
comp12066_c0_seq1.p1	Ec-27_000360.1	YL1 nuclear, C-terminal	n/a;GO:0003677;GO:0005634;GO:0006355;GO:0045449;GO:0003700	PTHR13275: ; IPR013272: YL1 nuclear, C-terminal; IPR008895: YL1 nuclear	NA
comp33075_c0_seq3.p1	Ec-27_000370.1	P-loop containing nucleoside triphosphate hydrolase	GO:0007018;GO:0005524;GO:0008017;GO:0005875;GO:0003777	IPR019821: Kinesin motor domain, conserved site; IPR005613: Actin interacting protein 3; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR027640: Kinesin-like protein; Coil: ; IPR001752: Kinesin motor domain	NA
comp29915_c0_seq1.p1	Ec-27_000380.1	Kinesin-like protein	GO:0007018;GO:0005524;GO:0008017;GO:0003777;GO:0005871	IPR019821: Kinesin motor domain, conserved site; IPR027640: Kinesin-like protein; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR001752: Kinesin motor domain	NA
comp31567_c0_seq2.p1	Ec-27_000400.1	microsomal Glutathione S-transferase	n/a;n/a;n/a	SSF161084: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10250: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR023352: Membrane associated eicosanoid/glutathione metabolism-like domain; IPR001129: Membrane-associated, eicosanoid/glutathione metabolism (MAPEG) protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30608_c0_seq5.p1	Ec-27_000430.1	Calcium/proton exchanger CAX	GO:0006816;GO:0015369	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004837: Sodium/calcium exchanger membrane region; IPR004798: Calcium/proton exchanger CAX; PTHR31503: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34248_c0_seq1.p1	Ec-27_000450.1	Hypothetical leucine rich repeat protein	GO:0005515	PTHR10588: ; G3DSA:3.80.10.10: ; IPR003591: Leucine-rich repeat, typical subtype; SSF52058: ; IPR001611: Leucine-rich repeat; IPR025875: Leucine rich repeat 4; Coil:	NA
comp12402_c0_seq1.p1	Ec-27_000470.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27995_c0_seq1.p1	Ec-27_000480.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp19445_c0_seq2.p1	Ec-27_000500.1	Alpha/beta knot methyltransferases	GO:0005737;GO:0006364;GO:0008168;n/a	IPR029028: Alpha/beta knot methyltransferases; IPR003742: SPOUT methyltransferase, predicted; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR029026: tRNA (guanine-N1-)-methyltransferase, N-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp19445_c0_seq2.p2	Ec-27_000510.1	Prp18	GO:0005681;GO:0008380	IPR014906: Pre-mRNA processing factor 4 (PRP4)-like; Coil: ; PTHR13007: ; IPR004098: Prp18; SSF158230:	NA
comp13131_c0_seq1.p1	Ec-27_000520.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp16056_c0_seq1.p1	Ec-27_000530.1	Pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor (PDHE1-A)	GO:0008152;GO:0016624	Coil: ; IPR001017: Dehydrogenase, E1 component; IPR029061: Thiamin diphosphate-binding fold; PTHR11516:	NA
comp32623_c5_seq7.p1	Ec-27_000540.1	Aldolase-type TIM barrel	GO:0003824	IPR013785: Aldolase-type TIM barrel; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SSF51569: ; IPR007570: Uncharacterised protein family Ycf23; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp11917_c0_seq1.p1	Ec-27_000570.1	Putative deacetylase LmbE-like domain	n/a;n/a;n/a	IPR003737: N-acetylglucosaminyl phosphatidylinositol deacetylase-related; IPR024078: Putative deacetylase LmbE-like domain	NA
comp32145_c2_seq9.p1	Ec-27_000580.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR001440: Tetratricopeptide TPR1; IPR011990: Tetratricopeptide-like helical domain; PF13414: TPR repeat; Coil: ; IPR013026: Tetratricopeptide repeat-containing domain; PTHR22904: ; IPR019734: Tetratricopeptide repeat	NA
comp30513_c0_seq2.p1	Ec-27_000590.1	Winged helix-turn-helix DNA-binding domain	GO:0003700;GO:0005634;GO:0006355;GO:0043565	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR000232: Heat shock factor (HSF)-type, DNA-binding; Coil:	NA
comp30814_c0_seq1.p1	Ec-27_000610.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13414: TPR repeat; SignalP-noTM: ; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR23083:	NA
comp27292_c0_seq1.p1	Ec-27_000650.1	Protein arginine N-methyltransferase	GO:0008168;GO:0006479	NA	NA
comp28739_c0_seq4.p1	Ec-27_000660.1	POT1 protection of telomeres 1 homolog	GO:0000723;GO:0000784;GO:0003677	IPR028389: Protection of telomeres protein 1; IPR012340: Nucleic acid-binding, OB-fold; PTHR14513:SF0: ; IPR011564: Telomeric single stranded DNA binding POT1/Cdc13	NA
comp20106_c0_seq1.p1	Ec-27_000670.2	Oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR017595: 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase, type 2; IPR018020: Oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase; SSF158694: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33399_c0_seq1.p1	Ec-27_000680.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp20775_c0_seq2.p1	Ec-27_000690.1	GTPBP1, EF1alpha-like GTPase	GO:0005525	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR009001: Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal; IPR000795: Transcription factor, GTP-binding domain; G3DSA:2.40.30.10: ; PTHR23115: ; PTHR23115:SF180: ; PF00009: Elongation factor Tu GTP binding domain; IPR009000: Translation protein, beta-barrel domain	NA
comp19448_c0_seq2.p1	Ec-27_000720.2	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29865_c0_seq2.p1	Ec-27_000730.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0005524;GO:0006468;GO:0004672	PTHR24349: ; IPR018247: EF-Hand 1, calcium-binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR002048: EF-hand domain; IPR011992: EF-hand domain pair; SSF47473: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR000719: Protein kinase domain; G3DSA:1.10.510.10:	KOG0032
comp26359_c0_seq1.p1	Ec-27_000740.1	Hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp32274_c0_seq1.p1	Ec-27_000750.2	WD40-repeat-containing domain	GO:0005515	PTHR13743: ; IPR031570: Domain of unknown function DUF4704; IPR000409: BEACH domain; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; Coil:	NA
comp30964_c0_seq9.p1	Ec-27_000760.1	PDZ domain	GO:0035091;GO:0005515	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF109993: ; IPR001478: PDZ domain; IPR003123: VPS9 domain; IPR001683: Phox homologous domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28322_c0_seq3.p1	Ec-27_000770.1	Aldo/keto reductase	GO:0016491;GO:0055114	IPR001395: Aldo/keto reductase; IPR023210: NADP-dependent oxidoreductase domain	NA
comp31723_c0_seq6.p1	Ec-27_000780.1	HBS1, eRF3-like GTPase involved in mRNA "no-go decay"	n/a;n/a;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR009001: Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal; IPR000795: Transcription factor, GTP-binding domain; G3DSA:2.40.30.10: ; IPR004160: Translation elongation factor EFTu/EF1A, C-terminal; IPR004161: Translation elongation factor EFTu/EF1A, domain 2; PTHR23115: ; Coil: ; PF00009: Elongation factor Tu GTP binding domain; IPR009000: Translation protein, beta-barrel domain	NA
comp26679_c0_seq1.p1	Ec-27_000790.1	expressed unknown protein	n/a;n/a;n/a	PTHR13257: ; Coil: ; SignalP-TM:	NA
comp27218_c0_seq2.p1	Ec-27_000820.3	RNA-binding protein Lupus La	GO:0003676	IPR011991: Winged helix-turn-helix DNA-binding domain; IPR006630: RNA-binding protein Lupus La; IPR000504: RNA recognition motif domain; PTHR22792:SF63: ; IPR012677: Nucleotide-binding alpha-beta plait domain; PTHR22792:	NA
comp20924_c0_seq1.p1	Ec-27_000830.1	Zinc finger, RING-type	GO:0005515;GO:0008270	IPR001841: Zinc finger, RING-type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SSF52025: ; G3DSA:3.50.30.30: ; IPR003137: Protease-associated domain, PA; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; PTHR22765: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31723_c0_seq9.p2	Ec-27_000840.1	HAD-like domain	n/a;n/a;n/a	PTHR12725: ; SIGNAL_PEPTIDE: Signal peptide region; IPR006439: HAD hydrolase, subfamily IA; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023214: HAD-like domain; IPR026870: Zinc-ribbon domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26239_c1_seq2.p1	Ec-27_000860.1	expressed unknown protein	NA	SIGNAL_PEPTIDE: Signal peptide region; IPR006614: Peroxin/Ferlin domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; IPR010482: Peroxin domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31851_c1_seq5.p1	Ec-27_000880.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR026741: Protein strawberry notch; PF13872: P-loop containing NTP hydrolase pore-1; PTHR12706:SF13: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil:	NA
comp31825_c0_seq2.p3	Ec-27_000910.1	Homeodomain-like	GO:0003677	IPR009057: Homeodomain-like; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR011011: Zinc finger, FYVE/PHD-type; IPR017877: Myb-like domain; IPR019787: Zinc finger, PHD-finger	NA
comp27801_c0_seq2.p1	Ec-27_000940.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp25049_c0_seq3.p1	Ec-27_000950.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp31851_c0_seq3.p1	Ec-27_000980.1	terbinafine resistance locus protein (yip1)	GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR006977: Yip1 domain; PTHR21236: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34152_c0_seq1.p2	Ec-27_000990.1	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	n/a;n/a;n/a	PTHR22870: ; IPR009091: Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II; IPR000408: Regulator of chromosome condensation, RCC1; PF13540: Regulator of chromosome condensation (RCC1) repeat	NA
comp34152_c0_seq1.p1	Ec-27_001000.1	Histone-binding protein RBBP4, N-terminal	n/a;n/a;n/a	IPR022052: Histone-binding protein RBBP4, N-terminal; IPR017986: WD40-repeat-containing domain; PTHR22850: ; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain; IPR020472: G-protein beta WD-40 repeat	NA
comp25301_c0_seq3.p2	Ec-27_001010.1	Thioredoxin-like fold	GO:0045454;n/a	IPR005746: Thioredoxin; IPR012336: Thioredoxin-like fold; IPR013766: Thioredoxin domain	NA
comp28614_c0_seq1.p1	Ec-27_001020.1	Retinoic acid induced 16-like protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; PTHR21705: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR019384: Retinoic acid induced 16-like protein; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp29571_c0_seq1.p1	Ec-27_001030.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31265_c0_seq2.p1	Ec-27_001040.3	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp28920_c0_seq3.p1	Ec-27_001060.1	Zinc finger, C2HC5-type	GO:0005634;GO:0006355;GO:0008270	IPR009349: Zinc finger, C2HC5-type; PTHR12963:	NA
comp28920_c0_seq3.p2	Ec-27_001070.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34370_c0_seq1.p1	Ec-27_001080.1	Rubredoxin	GO:0005506	SSF57802: ; IPR024935: Rubredoxin domain; IPR024934: Rubredoxin-like domain; IPR004039: Rubredoxin-type fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29193_c0_seq1.p1	Ec-27_001100.1	Trimeric LpxA-like	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; G3DSA:2.160.10.10: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011004: Trimeric LpxA-like; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31933_c0_seq3.p1	Ec-27_001110.3	P-type ATPase, A domain	GO:0000166;GO:0046872	IPR023298: P-type ATPase, transmembrane domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PF12710: haloacid dehalogenase-like hydrolase; IPR008250: P-type ATPase, A domain; IPR023214: HAD-like domain; IPR032630: P-type ATPase, C-terminal; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR006539: P-type ATPase, subfamily IV; SSF81665: ; IPR001757: P-type ATPase; IPR018303: P-type ATPase, phosphorylation site; IPR023299: P-type ATPase, cytoplasmic domain N; IPR032631: P-type ATPase, N-terminal; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32954_c5_seq5.p1	Ec-27_001130.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp32954_c1_seq2.p1	Ec-27_001130.3	conserved unknown protein	n/a;n/a;n/a	Coil:	NA
comp32947_c0_seq5.p1	Ec-27_001150.5	expressed unknown protein	NA	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20890_c0_seq1.p1	Ec-27_001170.1	Endo-1,3-beta-glucanase N-terminal fragment, family GH16	GO:0004553;GO:0005975	NA	NA
comp31351_c0_seq2.p1	Ec-27_001190.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp104024_c0_seq1.p1	Ec-27_001210.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp19504_c0_seq1.p1	Ec-27_001230.1	Ribosomal protein L22/L17, eukaryotic/archaeal	GO:0005840;GO:0015934;GO:0005622;GO:0006412;GO:0003735	IPR001063: Ribosomal protein L22/L17; IPR005721: Ribosomal protein L22/L17, eukaryotic/archaeal; IPR018260: Ribosomal protein L22/L17, conserved site	NA
comp32682_c2_seq1.p1	Ec-27_001280.1	Uncharacterised conserved protein UCP023322, transmembrane eukaryotic	GO:0016020	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR008559: Uncharacterised conserved protein UCP023322, transmembrane eukaryotic; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002809: Protein of unknown function DUF106, transmembrane; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26951_c0_seq1.p1	Ec-27_001290.1	MIF4-like, type 1/2/3	n/a;n/a;n/a	IPR003891: Initiation factor eIF-4 gamma, MA3; PTHR12626: ; IPR016024: Armadillo-type fold; IPR016021: MIF4-like, type 1/2/3	NA
comp31082_c0_seq1.p1	Ec-27_001300.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR007052: CS domain; IPR011990: Tetratricopeptide-like helical domain; Coil: ; IPR008978: HSP20-like chaperone; IPR019734: Tetratricopeptide repeat	NA
comp31082_c0_seq1.p2	Ec-27_001310.1	conserved unknown protein	GO:0003676	G3DSA:2.30.30.140: ; SSF63748: ; Coil: ; IPR002999: Tudor domain; PTHR12664:	NA
comp26578_c0_seq2.p1	Ec-27_001320.1	CAAX amino terminal protease	GO:0016020	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; PTHR10794: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003675: CAAX amino terminal protease; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp25600_c0_seq1.p1	Ec-27_001360.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33641_c0_seq1.p1	Ec-27_001370.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27578_c0_seq1.p1	Ec-27_001390.1	Intraflagellar transport protein 81	GO:0030992;GO:0042384;GO:0015631;GO:0042073	IPR029600: Intraflagellar transport protein 81; Coil:	NA
comp31839_c0_seq3.p1	Ec-27_001420.1	DNA-directed DNA polymerase X	GO:0003677;GO:0003887	IPR029398: DNA polymerase beta, thumb domain; IPR010996: DNA polymerase beta-like, N-terminal domain; SSF81301: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; G3DSA:3.30.460.10: ; IPR028207: DNA polymerase beta, palm domain; SSF81585: ; IPR002008: DNA polymerase family X, beta-like; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR018944: DNA polymerase lambda, fingers domain; PTHR11276: ; IPR027421: DNA polymerase family X lyase domain; G3DSA:1.10.150.20: ; PF14716: Helix-hairpin-helix domain; IPR019843: DNA polymerase family X, binding site; IPR022312: DNA polymerase family X; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR002054: DNA-directed DNA polymerase X	NA
comp26570_c0_seq1.p1	Ec-27_001430.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp23462_c0_seq1.p1	Ec-27_001440.1	Alpha/beta hydrolase fold-1	GO:0016787	IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; IPR000073: Alpha/beta hydrolase fold-1; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR10992: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000639: Epoxide hydrolase-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33981_c0_seq1.p1	Ec-27_001450.1	conserved unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SignalP-noTM: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp30272_c0_seq1.p1	Ec-27_001480.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp21261_c0_seq1.p1	Ec-27_001500.1	Ubiquitin-associated domain/translation elongation factor EF-Ts, N-terminal	GO:0005515	IPR000449: Ubiquitin-associated domain/translation elongation factor EF-Ts, N-terminal; IPR021109: Aspartic peptidase domain; IPR019103: Aspartic peptidase, DDI1-type; G3DSA:3.10.20.90: ; IPR015940: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote; G3DSA:1.10.8.10: ; IPR029071: Ubiquitin-related domain; IPR000626: Ubiquitin-like; PTHR12917: ; IPR009060: UBA-like	NA
comp28323_c0_seq1.p1	Ec-27_001510.1	membrane alanyl aminopeptidase	GO:0006508	IPR001930: Peptidase M1, alanine aminopeptidase/leukotriene A4 hydrolase; IPR014782: Peptidase M1, membrane alanine aminopeptidase, N-terminal; G3DSA:1.10.390.10: ; SSF55486: ; IPR024571: ERAP1-like C-terminal domain; SSF63737:	NA
comp24470_c0_seq1.p1	Ec-27_001530.1	Eukaryotic translation initiation factor 3 subunit l eukaryotic translation initiation factor eIF3 s	GO:0005737;GO:0003743;GO:0005852	IPR019382: Translation initiation factor 3 complex subunit L	NA
comp33133_c0_seq17.p1	Ec-27_001540.1	Bromodomain	GO:0005515	PTHR22880: ; IPR018359: Bromodomain, conserved site; IPR010405: Cofactor of BRCA1; IPR001487: Bromodomain	NA
comp32587_c1_seq8.p1	Ec-27_001550.1	AAA+ ATPase domain	GO:0005524;GO:0016887	IPR003439: ABC transporter-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR026082: ABC transporter A, ABCA; PF12698: ABC-2 family transporter protein; IPR017871: ABC transporter, conserved site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31823_c0_seq1.p1	Ec-27_001590.2	similar to Calcium-independent phospholipase A2-gamma, C terminal part.	GO:0006629	IPR016035: Acyl transferase/acyl hydrolase/lysophospholipase; PTHR24185: ; Coil: ; IPR002641: Patatin/Phospholipase A2-related; PTHR24185:SF1: ; G3DSA:3.40.1090.10:	NA
comp26907_c0_seq2.p1	Ec-27_001600.1	Glutaredoxin	n/a;n/a;n/a	IPR002109: Glutaredoxin; PTHR10168: ; IPR014025: Glutaredoxin subgroup; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR012336: Thioredoxin-like fold; IPR010488: Zeta toxin domain	KOG1752
comp12349_c0_seq1.p1	Ec-27_001700.1	NADP-dependent oxidoreductase domain	GO:0016491;GO:0055114;n/a	IPR001395: Aldo/keto reductase; IPR023210: NADP-dependent oxidoreductase domain	NA
comp28805_c0_seq1.p1	Ec-27_001730.1	flagellar associated protein	GO:0005524;GO:0016887	PTHR19211: ; IPR003593: AAA+ ATPase domain; IPR003439: ABC transporter-like; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; PF12848: ABC transporter; IPR017871: ABC transporter, conserved site	NA
comp28273_c0_seq3.p1	Ec-27_001750.1	YjeF N-terminal domain	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR13232: ; IPR004443: YjeF N-terminal domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp21328_c0_seq2.p1	Ec-27_001760.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp20333_c0_seq1.p1	Ec-27_001780.1	Kinesin motor domain containing protein	GO:0007018;GO:0005524;GO:0008017;GO:0005875;GO:0003777	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR019821: Kinesin motor domain, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR027640: Kinesin-like protein; Coil: ; IPR001752: Kinesin motor domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28133_c1_seq2.p1	Ec-27_001800.1	Vesicle coat complex COPI, alpha subunit	GO:0030126;GO:0016192;GO:0006886;GO:0005515;GO:0005198	PTHR19876: ; IPR006692: Coatomer, WD associated region; IPR019775: WD40 repeat, conserved site; IPR001680: WD40 repeat; IPR020472: G-protein beta WD-40 repeat; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR016391: Coatomer alpha subunit; IPR010714: Coatomer, alpha subunit, C-terminal	KOG0292
comp32682_c0_seq2.p1	Ec-27_001810.1	P-loop containing nucleoside triphosphate hydrolase	GO:0000166;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; IPR030231: GPN-loop GTPase 2; IPR004130: GPN-loop GTPase	NA
comp23917_c0_seq2.p1	Ec-27_001830.1	B9 domain	n/a;n/a;n/a	IPR010796: B9 domain; PTHR12968: ; Coil:	NA
comp21342_c0_seq1.p2	Ec-27_001840.1	small ubiquitin-like modifier	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; G3DSA:3.10.20.90: ; PTHR10562: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029071: Ubiquitin-related domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27173_c0_seq2.p1	Ec-27_001860.1	Protein kinase-like domain	GO:0016772	IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR24362: ; IPR011009: Protein kinase-like domain; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26534_c0_seq1.p1	Ec-27_001900.1	Phenylalanine--tRNA ligase	GO:0006432;GO:0005524;GO:0009328;GO:0005737;GO:0004826;GO:0000166;GO:0006418;GO:0006412;GO:0004812	SSF55681: ; IPR004529: Phenylalanyl-tRNA synthetase, class IIc, alpha subunit; G3DSA:3.30.930.10: ; PTHR11538: ; IPR002319: Phenylalanyl-tRNA synthetase; IPR006195: Aminoacyl-tRNA synthetase, class II	KOG2784
comp25928_c1_seq2.p1	Ec-27_001910.1	RNA polymerase sigma-70 region 2	GO:0003677;GO:0006355;GO:0006352;GO:0016987;GO:0003700	G3DSA:1.10.601.10: ; PTHR30603: ; IPR007624: RNA polymerase sigma-70 region 3; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007627: RNA polymerase sigma-70 region 2; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013325: RNA polymerase sigma factor, region 2; IPR011991: Winged helix-turn-helix DNA-binding domain; SIGNAL_PEPTIDE: Signal peptide region; IPR014284: RNA polymerase sigma-70 like domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR013324: RNA polymerase sigma factor, region 3/4; IPR000943: RNA polymerase sigma-70; IPR007630: RNA polymerase sigma-70 region 4	NA
comp27725_c0_seq1.p1	Ec-27_001940.1	Enhancer of polycomb protein	GO:0032777;GO:0035267	IPR024943: Enhancer of polycomb protein; IPR019542: Enhancer of polycomb-like, N-terminal	NA
comp24468_c0_seq1.p1	Ec-27_001950.1	Tryptophan synthase (alpha / beta chains)	GO:0004834;GO:0006568	IPR013785: Aldolase-type TIM barrel; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011060: Ribulose-phosphate binding barrel; SignalP-TM: ; IPR006654: Tryptophan synthase, beta chain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:3.40.50.1100: ; SIGNAL_PEPTIDE: Signal peptide region; IPR002028: Tryptophan synthase, alpha chain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR006653: Tryptophan synthase, beta chain, conserved site; IPR001926: Tryptophan synthase beta subunit-like PLP-dependent enzyme; SignalP-noTM: ; IPR023026: Tryptophan synthase beta chain/beta chain-like; PTHR10314:	KOG1395
comp29003_c0_seq1.p1	Ec-27_001960.1	Winged helix-turn-helix DNA-binding domain	GO:0003700;GO:0005634;GO:0006355;GO:0043565	IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; IPR000232: Heat shock factor (HSF)-type, DNA-binding; IPR027725: Heat shock transcription factor family	NA
comp27981_c0_seq5.p1	Ec-27_001990.1	Plastid lipid-associated protein/fibrillin conserved domain	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR006843: Plastid lipid-associated protein/fibrillin conserved domain	NA
comp30481_c0_seq3.p1	Ec-27_002000.1	Deoxyhypusine synthase	GO:0008612	IPR029035: DHS-like NAD/FAD-binding domain; IPR002773: Deoxyhypusine synthase	NA
comp30481_c0_seq1.p1	Ec-27_002010.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp26534_c0_seq1.p2	Ec-27_002020.2	Tail specific protease	GO:0006508;GO:0008236	PTHR32060: ; IPR029045: ClpP/crotonase-like domain; G3DSA:3.30.750.44: ; IPR001478: PDZ domain; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR005151: Tail specific protease; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30881_c0_seq4.p1	Ec-27_002040.1	Serine/threonine-protein kinase CTR1	GO:0004672;GO:0005524;GO:0006468	PTHR23257: ; IPR000719: Protein kinase domain; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; G3DSA:1.10.510.10: ; IPR011009: Protein kinase-like domain	NA
comp29811_c0_seq3.p1	Ec-27_002070.1	MEKK and related serine/threonine protein kinases amardillo repeat-containing protein	GO:0016772	IPR017441: Protein kinase, ATP binding site; IPR011989: Armadillo-like helical; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; PTHR24361: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; IPR016024: Armadillo-type fold; Coil: ; PTHR24361:SF129:	KOG0198
comp20931_c0_seq2.p1	Ec-27_002090.1	beta-ketoacyl synthase	GO:0003824;GO:0008152	IPR014031: Beta-ketoacyl synthase, C-terminal; IPR017568: 3-oxoacyl-[acyl-carrier-protein] synthase 2; PTHR11712: ; IPR014030: Beta-ketoacyl synthase, N-terminal; IPR016038: Thiolase-like, subgroup; IPR018201: Beta-ketoacyl synthase, active site; IPR016039: Thiolase-like; IPR020841: Polyketide synthase, beta-ketoacyl synthase domain	KOG1394
comp20114_c0_seq1.p1	Ec-27_002100.1	HAT (Half-A-TPR) repeat	GO:0006396;GO:0005622;GO:0005515	SSF48452: ; IPR003107: HAT (Half-A-TPR) repeat; IPR011990: Tetratricopeptide-like helical domain; PTHR11246: ; IPR013026: Tetratricopeptide repeat-containing domain	NA
comp29872_c0_seq1.p1	Ec-27_002110.1	Heat Shock transcription factor	GO:0005634;GO:0006355;GO:0043565;GO:0003700	NA	NA
comp28529_c1_seq9.p1	Ec-27_002130.1	Anoctamin	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007632: Anoctamin; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34411_c0_seq1.p1	Ec-27_002140.1	6,7-dimethyl-8-ribityllumazine synthase	GO:0009231;GO:0009349	IPR002180: 6,7-dimethyl-8-ribityllumazine synthase; SIGNAL_PEPTIDE: Signal peptide region; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp33771_c0_seq1.p1	Ec-27_002150.1	Low temperature viability protein	n/a;n/a;n/a	PTHR21531: ; Coil: ; IPR007307: Low temperature viability protein	NA
comp32794_c0_seq7.p1	Ec-27_002180.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp28533_c0_seq1.p1	Ec-27_002200.1	UAS	n/a;n/a;n/a	G3DSA:3.10.20.90: ; IPR006577: UAS; PF13899: Thioredoxin-like; IPR029071: Ubiquitin-related domain; IPR001012: UBX domain; PTHR23322: ; IPR012336: Thioredoxin-like fold	NA
comp32863_c0_seq21.p1	Ec-27_002260.1	ABC transporter-like	GO:0005524;GO:0016887	PTHR11384: ; IPR003439: ABC transporter-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027417: P-loop containing nucleoside triphosphate hydrolase; G3DSA:1.20.1560.10: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR003593: AAA+ ATPase domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011527: ABC transporter type 1, transmembrane domain; IPR017871: ABC transporter, conserved site; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31296_c0_seq1.p1	Ec-27_002270.2	putative PKG-Ib	GO:0005515	PTHR12442:SF5: ; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; PTHR12442: ; Coil:	KOG1587
comp31296_c0_seq15.p2	Ec-27_002280.1	Cupin-like domain protein	n/a;n/a;n/a	NA	NA
comp31296_c0_seq15.p4	Ec-27_002290.1	conserved unknown protein	n/a;n/a;n/a	SSF54427: ; G3DSA:3.10.450.50:	NA
comp13122_c0_seq1.p1	Ec-27_002300.1	Tetratricopeptide-like helical domain	GO:0005515	PTHR21581:SF6: ; PTHR21581: ; IPR011990: Tetratricopeptide-like helical domain	NA
comp19458_c0_seq1.p1	Ec-27_002310.1	CobW/HypB/UreG domain	n/a;n/a;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR003495: CobW/HypB/UreG domain; PTHR13748: ; Coil:	NA
comp27317_c0_seq5.p1	Ec-27_002350.2	Nicotinate phosphoribosyltransferase pncB type	GO:0004516;GO:0019358	IPR007229: Nicotinate phosphoribosyltransferase family; IPR006405: Nicotinate phosphoribosyltransferase pncB-type; IPR002638: Quinolinate phosphoribosyl transferase, C-terminal; G3DSA:3.20.140.10: ; SSF54675: ; PTHR11098:SF1:	NA
comp28752_c0_seq1.p3	Ec-27_002360.1	Coatomer protein complex, gamma sub-unit	GO:0005488;GO:0016192;GO:0006886;GO:0030117	IPR017106: Coatomer gamma subunit; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold; IPR002553: Clathrin/coatomer adaptor, adaptin-like, N-terminal	Vesicle
comp24607_c0_seq1.p1	Ec-27_002370.1	Major facilitator superfamily domain	n/a;GO:0055085;GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PTHR11360: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011701: Major facilitator superfamily; G3DSA:1.20.1250.20: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19919_c0_seq1.p1	Ec-27_002390.1	gluconolactonase (precursor)	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR10907: ; IPR013658: SMP-30/Gluconolaconase/LRE-like region; SSF63829: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011042: Six-bladed beta-propeller, TolB-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32585_c0_seq8.p1	Ec-27_002410.1	kinesin (KAR3 subfamily)	GO:0007018;GO:0005524;GO:0008017;GO:0003777	IPR019821: Kinesin motor domain, conserved site; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR027640: Kinesin-like protein; Coil: ; IPR001752: Kinesin motor domain; SignalP-TM:	KOG0239
comp24725_c0_seq1.p1	Ec-27_002420.1	Putative: similar to kinetochore associated 2	NA	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR005550: Kinetochore protein Ndc80; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0995
comp12767_c0_seq2.p1	Ec-27_002450.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp30803_c0_seq8.p1	Ec-27_002460.3	UbiB domain	n/a;n/a;n/a	IPR004147: UbiB domain; PTHR10566: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR10566:SF58: ; IPR011009: Protein kinase-like domain	NA
comp12536_c0_seq1.p1	Ec-27_002470.1	enoyl-(acyl carrier protein) reductase	GO:0008152;GO:0016491	PTHR24322: ; SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR002347: Glucose/ribitol dehydrogenase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13561: Enoyl-(Acyl carrier protein) reductase; IPR016040: NAD(P)-binding domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG0725
comp32964_c1_seq8.p1	Ec-27_002520.1	hypothetical protein	GO:0005515	IPR001202: WW domain; G3DSA:2.20.70.10:	NA
comp32686_c2_seq10.p4	Ec-27_002540.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0006457;GO:0031072;GO:0051082	PTHR24077: ; IPR001623: DnaJ domain; IPR018253: DnaJ domain, conserved site	NA
comp30021_c0_seq3.p1	Ec-27_002550.1	Helicase, C-terminal	n/a;n/a;n/a	IPR011545: DEAD/DEAH box helicase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal; IPR018973: DEAD/DEAH-box helicase, putative; PTHR24031:	NA
comp30892_c1_seq2.p1	Ec-27_002580.1	hypothetical protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp27233_c1_seq2.p1	Ec-27_002590.1	G-patch domain protein	GO:0003676	NA	NA
comp30009_c0_seq1.p1	Ec-27_002610.1	IMMEDIATE UPRIGHT	NA	NA	NA
comp24535_c0_seq1.p1	Ec-27_002630.1	similar to centromere protein E	n/a;n/a;n/a	Coil:	NA
comp24560_c0_seq1.p1	Ec-27_002640.1	Zinc finger, RING/FYVE/PHD-type	GO:0005634;GO:0007049	IPR001841: Zinc finger, RING-type; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; IPR004575: Cdk-activating kinase assembly factor MAT1/Tfb3; Coil: ; IPR015877: Cdk-activating kinase assembly factor MAT1, centre	NA
comp12897_c0_seq1.p1	Ec-27_002650.2	similarity to cobalamin synthesis protein	NA	PTHR13748:SF43: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR13748: ; IPR003495: CobW/HypB/UreG domain; IPR011629: Cobalamin (vitamin B12) biosynthesis CobW-like, C-terminal	NA
comp22113_c0_seq1.p1	Ec-27_002660.1	MHCK/EF2 kinase	GO:0004674;GO:0005524;GO:0006468	PTHR14187: ; IPR004166: MHCK/EF2 kinase; PF13519: von Willebrand factor type A domain; IPR002035: von Willebrand factor, type A; IPR011009: Protein kinase-like domain	NA
comp11961_c0_seq1.p1	Ec-27_002670.1	Serine Carboxypeptidase	GO:0006508;GO:0004185	IPR001563: Peptidase S10, serine carboxypeptidase; IPR029058: Alpha/Beta hydrolase fold; IPR018202: Peptidase S10, serine carboxypeptidase, active site	KOG1282
comp32898_c0_seq7.p1	Ec-27_002690.1	AAA+ ATPase domain	GO:0005515;GO:0005524;n/a	cd00009: AAA; IPR030513: Dehydrin, conserved site; IPR003959: ATPase, AAA-type, core; IPR003960: ATPase, AAA-type, conserved site; PTHR23069: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR23069:SF0: ; IPR003593: AAA+ ATPase domain; G3DSA:1.10.8.60: ; Coil:	NA
comp25881_c0_seq3.p2	Ec-27_002710.1	D-aminoacyl-tRNA deacylase	GO:0016788;GO:0051499	SSF142535: ; G3DSA:3.40.50.10700: ; PTHR34667:SF1: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR34667: ; G3DSA:3.40.630.50: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR007508: D-aminoacyl-tRNA deacylase DtdA; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp25881_c0_seq3.p1	Ec-27_002720.1	Molybdate-anion transporter MOT2	GO:0015098;GO:0015689;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR008509: Molybdate-anion transporter MOT2; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR020846: Major facilitator superfamily domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR24003: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26884_c0_seq1.p1	Ec-27_002740.1	Light harvesting complex protein	GO:0009765;GO:0016020	IPR022796: Chlorophyll A-B binding protein; IPR001344: Chlorophyll A-B binding protein, plant; IPR023329: Chlorophyll a/b binding protein domain	NA
comp32686_c2_seq10.p2	Ec-27_002750.3	RBEL1, Ras superfamily GTPase	NA	PTHR14932: ; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil:	NA
comp27411_c0_seq1.p1	Ec-27_002760.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp24975_c0_seq1.p1	Ec-27_002780.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp19680_c0_seq2.p1	Ec-27_002790.1	Methyltransferase type 11	GO:0008152;GO:0008168	PTHR10108:SF711: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR10108: ; IPR013216: Methyltransferase type 11	NA
comp12525_c0_seq1.p1	Ec-27_002800.1	ThiJ/PfpI	n/a;n/a;n/a	PTHR11019: ; PF13587: N-terminal domain of DJ-1_PfpI family; IPR029062: Class I glutamine amidotransferase-like; IPR002818: ThiJ/PfpI	NA
comp28729_c0_seq2.p1	Ec-27_002810.2	Arfaptin homology (AH) domain/BAR domain	n/a;n/a;n/a	SSF103657: ; IPR027267: Arfaptin homology (AH) domain/BAR domain; Coil:	NA
comp25863_c0_seq1.p1	Ec-27_002820.1	Arf GTPase activating protein	GO:0032312;GO:0008060;GO:0008270;GO:0005096	IPR001164: Arf GTPase activating protein; Coil: ; SSF57863: ; PTHR23180:	NA
comp26755_c0_seq1.p1	Ec-27_002830.1	Ankyrin repeat-containing domain	n/a;GO:0005515	SSF90209: ; IPR020683: Ankyrin repeat-containing domain; IPR011989: Armadillo-like helical; IPR001876: Zinc finger, RanBP2-type; IPR002110: Ankyrin repeat; PTHR24193:	NA
comp30639_c2_seq2.p1	Ec-27_002840.2	HECT	GO:0004842	PTHR11254:SF73: ; IPR000569: HECT domain; PTHR11254:	NA
comp31000_c0_seq1.p1	Ec-27_002900.1	eukaryotic translation initiation factor 2 alpha kinase PEK	GO:0016772	IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR011009: Protein kinase-like domain; IPR008271: Serine/threonine-protein kinase, active site; IPR000719: Protein kinase domain; PTHR11042: ; G3DSA:1.10.510.10: ; Coil:	KOG1035
comp30021_c0_seq8.p1	Ec-27_002910.1	hypothetical protein	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain	NA
comp32772_c0_seq21.p1	Ec-27_002920.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13424: Tetratricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; IPR019734: Tetratricopeptide repeat	NA
comp30821_c0_seq2.p1	Ec-27_002930.1	Translation protein SH3-like domain	GO:0043022;n/a;GO:0003723;GO:0003746;GO:0045905;GO:0006452;GO:0045901	IPR008991: Translation protein SH3-like domain; IPR012340: Nucleic acid-binding, OB-fold; IPR019769: Translation elongation factor, IF5A, hypusine site; IPR001884: Translation elongation factor IF5A; IPR014722: Ribosomal protein L2 domain 2; IPR020189: Translation elongation factor, IF5A C-terminal	NA
comp31844_c2_seq2.p2	Ec-27_002960.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp31844_c2_seq2.p1	Ec-27_002970.2	hypothetical protein	n/a;n/a;n/a	IPR001876: Zinc finger, RanBP2-type	NA
comp27702_c0_seq1.p1	Ec-27_002980.1	Rab-GTPase-TBC domain	GO:0005097;GO:0032313	G3DSA:1.10.8.270: ; IPR000195: Rab-GTPase-TBC domain; PTHR22957:	NA
comp28725_c0_seq1.p1	Ec-27_002990.1	Vesicle coat complex COPII, subunit SEC31	GO:0005515	PTHR13923: ; IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; IPR024298: Ancestral coatomer element 1, Sec16/Sec31	KOG0307
comp31000_c1_seq1.p1	Ec-27_003000.1	Peptidase M17, leucyl aminopeptidase, C-terminal	GO:0005622;GO:0005737;GO:0008235;GO:0006508;GO:0004177;GO:0019538;GO:0030145	PTHR11963: ; IPR000819: Peptidase M17, leucyl aminopeptidase, C-terminal; G3DSA:3.40.50.10590: ; IPR011356: Leucine aminopeptidase/peptidase B; SSF53187: ; G3DSA:3.40.630.10:	NA
comp31033_c1_seq4.p1	Ec-27_003010.1	Sas10 C-terminal domain	GO:0005634;GO:0006364;GO:0016458;GO:0032040	IPR007146: Sas10/Utp3/C1D; PTHR13237: ; IPR018972: Sas10 C-terminal domain	NA
comp28779_c0_seq2.p1	Ec-27_003020.1	mitogen-activated protein kinase	GO:0006468;GO:0004672;GO:0016772	PTHR24055: ; IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; G3DSA:3.30.200.20: ; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; Coil:	KOG0660
comp26781_c0_seq5.p1	Ec-27_003040.1	Zinc finger, RING/FYVE/PHD-type	GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011016: Zinc finger, RING-CH-type; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR13145:	NA
comp26981_c0_seq4.p1	Ec-27_003060.1	tRNA endonuclease-like domain	GO:0004518;GO:0003676	IPR006677: tRNA intron endonuclease, catalytic domain-like; IPR011856: tRNA endonuclease-like domain	NA
comp32798_c0_seq8.p2	Ec-27_003080.1	Bromodomain	GO:0005515	PTHR22880: ; IPR001487: Bromodomain	NA
comp32544_c0_seq2.p1	Ec-27_003100.3	probable pseudogene to fused with Esi0000_0588	NA	IPR005331: Sulfotransferase	NA
comp32798_c0_seq10.p1	Ec-27_003130.1	Trifunctional Chorismate Mutase/Prephenate Dehydratase/Prephenate Dehydrogenase	GO:0004664;GO:0009094;GO:0008152;GO:0003824;GO:0005488	IPR003099: Prephenate dehydrogenase; SSF51735: ; IPR001086: Prephenate dehydratase; IPR002912: ACT domain; SSF55021: ; G3DSA:3.30.70.260: ; G3DSA:3.40.190.10: ; IPR016040: NAD(P)-binding domain; PTHR21022: ; IPR018528: Prephenate dehydratase, conserved site; Coil: ; SSF53850:	KOG2380
comp33873_c0_seq1.p1	Ec-27_003160.1	peroxisomal enoyl-coenzyme A hydratase	GO:0008152;GO:0003824	IPR029045: ClpP/crotonase-like domain; IPR014748: Crotonase, C-terminal; IPR001753: Crotonase superfamily; PTHR11941:	KOG1681
comp34460_c0_seq1.p1	Ec-27_003180.1	NUDIX hydrolase domain-like	GO:0016787	IPR015797: NUDIX hydrolase domain-like; IPR020476: NUDIX hydrolase; IPR020084: NUDIX hydrolase, conserved site; PTHR13994: ; IPR000086: NUDIX hydrolase domain; IPR003293: Nudix hydrolase 6-like	NA
comp28367_c0_seq2.p2	Ec-27_003190.1	RNA recognition motif domain	GO:0003676;GO:0005515	IPR012816: Conserved hypothetical protein CHP02464; IPR008984: SMAD/FHA domain; IPR000253: Forkhead-associated (FHA) domain; PTHR24622: ; SSF54928: ; IPR000504: RNA recognition motif domain; PF14259: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain); SSF143990: ; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp28367_c0_seq2.p1	Ec-27_003200.1	Tetratricopeptide-like helical domain	GO:0016020;GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PF13414: TPR repeat; Coil: ; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; IPR003416: MgtC/SapB/SrpB transporter; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31117_c1_seq6.p1	Ec-27_003210.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28266_c0_seq3.p1	Ec-27_003220.1	Armadillo-like helical	n/a;GO:0005488	PTHR12363: ; IPR001494: Importin-beta, N-terminal domain; IPR013598: Exportin-1/Importin-beta-like; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold	NA
comp26333_c0_seq1.p1	Ec-27_003260.1	Zinc finger, RING/FYVE/PHD-type	n/a;GO:0005515	IPR018247: EF-Hand 1, calcium-binding site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; IPR003961: Fibronectin type III; SSF47473: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013783: Immunoglobulin-like fold; PTHR15136: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12409_c0_seq1.p1	Ec-27_003270.1	NAD(P)-binding domain	GO:0003824;GO:0005488;GO:0008152	SSF51735: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR005097: Saccharopine dehydrogenase / Homospermidine synthase; IPR016040: NAD(P)-binding domain; PTHR12286: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp19875_c0_seq1.p1	Ec-27_003280.1	expressed unknown protein	n/a;n/a;n/a	SSF81995: ; Coil:	NA
comp24399_c0_seq1.p1	Ec-27_003300.2	RmlC-like jelly roll fold	GO:0047800;GO:0055114;n/a	PTHR22966: ; IPR011051: RmlC-like cupin domain; IPR014710: RmlC-like jelly roll fold; IPR012864: Cysteine oxygenase/2-aminoethanethiol dioxygenase	NA
comp25616_c0_seq1.p1	Ec-27_003310.1	Zinc finger, AN1-type	GO:0005515;GO:0008270	G3DSA:3.10.20.90: ; IPR000058: Zinc finger, AN1-type; SSF118310: ; IPR029071: Ubiquitin-related domain; IPR000626: Ubiquitin-like	NA
comp21249_c0_seq1.p1	Ec-27_003320.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12435_c0_seq1.p1	Ec-27_003330.1	WD40/YVTN repeat-like-containing domain	GO:0005515	PTHR10241: ; IPR015943: WD40/YVTN repeat-like-containing domain; Coil: ; IPR011047: Quinoprotein alcohol dehydrogenase-like superfamily	NA
comp25271_c0_seq1.p1	Ec-27_003340.1	NRDE protein domains	GO:0008152;GO:0003824	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR016038: Thiolase-like, subgroup; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR008551: Protein of unknown function DUF833; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32288_c0_seq4.p1	Ec-27_003350.1	CRAL-TRIO domain	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR001251: CRAL-TRIO domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR23324: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29453_c0_seq1.p1	Ec-27_003360.1	MEra, mitochondrial Era GTPase	GO:0005525	IPR009019: K homology domain, prokaryotic type; IPR005225: Small GTP-binding protein domain; IPR006073: GTP binding domain; IPR015946: K homology domain-like, alpha/beta; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; PTHR11649:	NA
comp24158_c0_seq2.p1	Ec-27_003370.1	expressed unknown protein	GO:0005525;GO:0005874;GO:0007017	NA	NA
comp12523_c0_seq1.p1	Ec-27_003380.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp24158_c0_seq2.p2	Ec-27_003390.1	mitochondrial phosphate carrier protein	GO:0016020;GO:0005488;GO:0006810	PTHR24089: ; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR023395: Mitochondrial carrier domain; IPR018108: Mitochondrial substrate/solute carrier; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24627_c0_seq1.p1	Ec-27_003400.1	lipase	GO:0003824;GO:0004806;GO:0006629	IPR002921: Fungal lipase-like domain; IPR029058: Alpha/Beta hydrolase fold; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR21493: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG4569
comp19530_c1_seq1.p1	Ec-27_003410.1	Nucleophile aminohydrolases, N-terminal	n/a;GO:0051603;GO:0004298;GO:0005839	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR001353: Proteasome, subunit alpha/beta; IPR023332: Proteasome A-type subunit; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000426: Proteasome alpha-subunit, N-terminal domain; IPR029055: Nucleophile aminohydrolases, N-terminal; SignalP-noTM: ; PTHR11599: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28892_c0_seq6.p1	Ec-27_003420.1	SH2 domain	GO:0005515	SSF48452: ; IPR000980: SH2 domain; IPR011990: Tetratricopeptide-like helical domain	NA
comp26792_c0_seq6.p1	Ec-27_003430.1	Triose-phosphate transporter domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004853: Triose-phosphate transporter domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11132: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30242_c1_seq5.p1	Ec-27_003470.1	6-pyruvoyl tetrahydropterin synthase/QueD family protein	n/a;n/a;n/a	SSF55620: ; G3DSA:3.30.479.10: ; IPR007115: 6-pyruvoyl tetrahydropterin synthase/QueD family protein	NA
comp30098_c1_seq1.p1	Ec-27_003490.1	Clathrin assembly complex, small subunit	GO:0006810;GO:0008565;GO:0015031	IPR016635: Adaptor protein complex, sigma subunit; G3DSA:3.30.450.60: ; Coil: ; IPR011012: Longin-like domain; IPR022775: AP complex, mu/sigma subunit	KOG0934
comp29198_c0_seq1.p1	Ec-27_003510.1	Hypothetical leucine rich repeat protein	NA	PTHR24110: ; G3DSA:3.80.10.10: ; SSF52047: ; IPR003590: Leucine-rich repeat, ribonuclease inhibitor subtype	NA
comp29464_c0_seq2.p1	Ec-27_003520.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp29464_c0_seq2.p2	Ec-27_003530.1	putative Rab geranylgeranyl transferase type II beta subunit	GO:0018344;GO:0003824;GO:0004663	IPR026873: Geranylgeranyl transferase type-2 subunit beta; PTHR11774: ; IPR008930: Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid; IPR001330: Prenyltransferase/squalene oxidase; PF13249: Prenyltransferase-like	NA
comp11879_c0_seq2.p1	Ec-27_003540.1	expressed unknown protein	n/a;n/a;n/a	SignalP-TM:	NA
comp25022_c0_seq2.p1	Ec-27_003550.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	PF13489: Methyltransferase domain; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase	NA
comp31095_c1_seq8.p2	Ec-27_003560.1	Peptide chain release factor	GO:0006415;GO:0005737;GO:0016149	SSF75620: ; IPR014720: Double-stranded RNA-binding domain; PTHR11075: ; IPR000352: Peptide chain release factor class I/class II; Coil: ; IPR005139: Peptide chain release factor	NA
comp31095_c1_seq8.p1	Ec-27_003570.2	Fibronectin type III	GO:0005515	IPR000884: Thrombospondin type-1 (TSP1) repeat; G3DSA:2.10.25.10: ; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:2.20.100.10: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR003961: Fibronectin type III; IPR000742: EGF-like domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR013032: EGF-like, conserved site; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013783: Immunoglobulin-like fold; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20353_c0_seq2.p1	Ec-27_003590.1	molybdopterin hydrolase / adenylyltransferase	GO:0006777	IPR008284: Molybdenum cofactor biosynthesis, conserved site; IPR005110: MoeA, N-terminal and linker domain; G3DSA:2.170.190.11: ; IPR001453: MoaB/Mog domain; IPR005111: MoeA, C-terminal, domain IV; PTHR10192: ; G3DSA:3.90.105.10:	NA
comp30416_c1_seq2.p1	Ec-27_003620.1	Ribonuclease H-like domain	GO:0003676	IPR008906: HAT dimerisation domain, C-terminal; IPR012337: Ribonuclease H-like domain; PTHR23272:	NA
comp30374_c0_seq2.p1	Ec-27_003640.1	SH3 domain	GO:0035091;GO:0005515	IPR001452: SH3 domain; IPR011511: Variant SH3 domain; G3DSA:2.30.30.40: ; Coil: ; IPR001683: Phox homologous domain	NA
comp31480_c0_seq1.p1	Ec-27_003670.1	Bromodomain	GO:0005515	PTHR22880:SF145: ; IPR003888: FY-rich, N-terminal; IPR001487: Bromodomain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; PTHR22880: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; IPR028935: WHIM3 domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR028941: WHIM2 domain	NA
comp24316_c0_seq1.p1	Ec-27_003690.1	Hpc2-related domain	GO:0005840;GO:0006412;GO:0005622;GO:0003735	NA	NA
comp31159_c0_seq10.p1	Ec-27_003720.2	RINT-1/TIP-20	GO:0005783;GO:0048193	PTHR13520: ; PTHR13520:SF0: ; IPR007528: RINT-1/TIP-20	NA
comp31159_c0_seq8.p1	Ec-27_003730.1	aspartate/glutamate/uridylate kinase	n/a;n/a;n/a	NA	NA
comp31159_c0_seq3.p1	Ec-27_003730.2	aspartate/glutamate/uridylate kinase	n/a;n/a;n/a	IPR001048: Aspartate/glutamate/uridylate kinase	NA
comp35802_c0_seq1.p1	Ec-27_003740.1	conserved unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29965_c0_seq1.p1	Ec-27_003770.1	Peptidase C19, ubiquitin carboxyl-terminal hydrolase	GO:0036459;GO:0006511	G3DSA:2.20.210.10: ; PTHR24619: ; IPR018200: Ubiquitin specific protease, conserved site; SSF54001: ; IPR001394: Peptidase C19, ubiquitin carboxyl-terminal hydrolase; IPR028889: Ubiquitin specific protease domain; Coil:	NA
comp28158_c0_seq1.p1	Ec-27_003790.1	putative plastidic ribulosamine/erythrulosamine 3-kinase	GO:0016772	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PTHR12149: ; G3DSA:3.90.1200.10: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011009: Protein kinase-like domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR016477: Fructosamine/Ketosamine-3-kinase; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp20782_c0_seq2.p1	Ec-27_003800.1	HSP20-like chaperone	n/a;n/a;n/a	IPR007052: CS domain; PTHR12356: ; IPR008978: HSP20-like chaperone	NA
comp26709_c1_seq2.p1	Ec-27_003810.1	Fimbrin	GO:0005515	IPR018247: EF-Hand 1, calcium-binding site; IPR001715: Calponin homology domain; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; SSF47473: ; IPR001589: Actinin-type actin-binding domain, conserved site; PTHR19961: ; Coil:	KOG0046
comp30950_c0_seq4.p1	Ec-27_003830.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp33760_c0_seq1.p1	Ec-27_003850.1	CS domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007052: CS domain; IPR008978: HSP20-like chaperone; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21223_c0_seq1.p2	Ec-27_003860.3	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp30451_c0_seq5.p1	Ec-27_003870.1	Iron/zinc purple acid phosphatase-like C-terminal domain	GO:0003993;GO:0046872	IPR029052: Metallo-dependent phosphatase-like; IPR015914: Purple acid phosphatase, N-terminal; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR008963: Purple acid phosphatase-like, N-terminal; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR025733: Iron/zinc purple acid phosphatase-like C-terminal domain; PTHR22953: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31056_c0_seq5.p2	Ec-27_003880.1	Tim50 homolog, mitochondrial inner membrane protein of TIM23 complex	NA	PTHR12210: ; IPR004274: NLI interacting factor; IPR023214: HAD-like domain	KOG2832
comp31285_c0_seq1.p2	Ec-27_003890.1	Acyl carrier protein-like	GO:0008152;GO:0003824	G3DSA:3.40.50.980: ; IPR000873: AMP-dependent synthetase/ligase; G3DSA:2.30.38.10: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR009081: Acyl carrier protein-like; IPR020845: AMP-binding, conserved site; PTHR22754: ; G3DSA:3.30.300.30: ; SSF56801: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31056_c0_seq5.p1	Ec-27_003900.1	expressed unknown protein	n/a;n/a;n/a	SignalP-TM:	NA
comp29259_c0_seq1.p1	Ec-27_003910.1	Phosphoribulokinase	GO:0005524;GO:0008152;GO:0016301	SIGNAL_PEPTIDE: Signal peptide region; IPR027417: P-loop containing nucleoside triphosphate hydrolase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR006082: Phosphoribulokinase; IPR006083: Phosphoribulokinase/uridine kinase; PTHR10285: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12861_c0_seq2.p1	Ec-27_003920.2	Ankyrin repeat-containing domain	n/a;n/a;n/a	IPR011990: Tetratricopeptide-like helical domain; IPR020683: Ankyrin repeat-containing domain; IPR013026: Tetratricopeptide repeat-containing domain; PTHR22904: ; IPR019734: Tetratricopeptide repeat; IPR002110: Ankyrin repeat	NA
comp35007_c0_seq1.p1	Ec-27_003930.1	ribulose-phosphate 3-epimerase	GO:0005975;GO:0016857	IPR013785: Aldolase-type TIM barrel; IPR000056: Ribulose-phosphate 3-epimerase-like; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011060: Ribulose-phosphate binding barrel; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR026019: Ribulose-phosphate 3-epimerase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; PTHR11749:SF7: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG3111
comp31362_c0_seq1.p1	Ec-27_003940.1	chitin synthase 1, chs-1	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PR00833: Pollen allergen Poa pI signature; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26284_c0_seq1.p1	Ec-27_003950.1	Sterol methyltransferase	GO:0006694;GO:0008168	IPR030384: SAM-dependent methyltransferase SMT-type; IPR013705: Sterol methyltransferase C-terminal; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR10108:SF908: ; PTHR10108: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013216: Methyltransferase type 11	NA
comp24571_c0_seq2.p2	Ec-27_003960.1	JAB1/MPN/MOV34 metalloenzyme domain	GO:0005515	IPR000555: JAB1/MPN/MOV34 metalloenzyme domain; IPR024969: Rpn11/EIF3F C-terminal domain; PTHR10540:	NA
comp31652_c0_seq7.p3	Ec-27_003970.1	conserved unknown protein	GO:0005515	IPR018392: LysM domain; IPR001478: PDZ domain	NA
comp31652_c0_seq4.p1	Ec-27_003980.1	Asparaginase, c-terminal	GO:0016787	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000246: Peptidase T2, asparaginase 2; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029055: Nucleophile aminohydrolases, N-terminal; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1593
comp31652_c0_seq1.p1	Ec-27_003990.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp12130_c0_seq1.p1	Ec-27_004010.1	Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain	GO:0055114;GO:0016491	PTHR11938: ; PR00419: Adrenodoxin reductase family signature; IPR016040: NAD(P)-binding domain; G3DSA:3.50.50.60: ; SSF51971: ; IPR021163: Ferredoxin-NADP+ reductase, adrenodoxin-type; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain	NA
comp26886_c0_seq1.p1	Ec-27_004020.1	Indole-3-glycerol-phosphate synthase	n/a;n/a;n/a	IPR013785: Aldolase-type TIM barrel; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PTHR22854:SF2: ; IPR019494: FIST C domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR22854: ; IPR013702: FIST domain, N-terminal; IPR011060: Ribulose-phosphate binding barrel; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR013798: Indole-3-glycerol phosphate synthase	KOG4201
comp10506_c0_seq1.p1	Ec-27_004030.1	conserved unknown protein	GO:0004197;GO:0006508	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31173_c0_seq16.p1	Ec-27_004040.1	3,4-dihydroxy-2-butanone 4-phosphate synthase, RibB	GO:0009231;GO:0008686	IPR000926: GTP cyclohydrolase II, RibA; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF142695: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR21327: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR000422: 3,4-dihydroxy-2-butanone 4-phosphate synthase, RibB; IPR017945: DHBP synthase RibB-like alpha/beta domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31173_c0_seq13.p1	Ec-27_004050.1	spermidine/spermine synthase	GO:0003824	PF01564: Spermine/spermidine synthase; IPR006383: HAD-superfamily hydrolase, subfamily IB, PSPase-like; PTHR11558: ; PF12710: haloacid dehalogenase-like hydrolase; IPR030373: Polyamine biosynthesis domain, conserved site; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023214: HAD-like domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE: Signal peptide region; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR030374: Polyamine biosynthesis domain; G3DSA:2.30.140.10: ; SignalP-noTM: ; IPR001045: Spermidine/spermine synthases	KOG1562
comp28671_c0_seq2.p2	Ec-27_004060.1	KIAA1430 homologue	n/a;n/a;n/a	IPR029488: KIAA1430 homologue	NA
comp31173_c0_seq7.p2	Ec-27_004070.1	2-keto-3-deoxy-6-phosphogluconate aldolase	GO:0008152;GO:0016829	IPR013785: Aldolase-type TIM barrel; PTHR30246: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000887: KDPG/KHG aldolase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SSF51569: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp26978_c0_seq3.p1	Ec-27_004080.1	Exocyst complex component Sec5	n/a;n/a;n/a	PF15469: Exocyst complex component Sec5; IPR029175: Exocyst complex component EXOC2/Sec5; Coil:	NA
comp20111_c0_seq1.p2	Ec-27_004100.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp28390_c0_seq1.p1	Ec-27_004120.1	WD40-repeat-containing domain	GO:0005515	IPR017986: WD40-repeat-containing domain; IPR019775: WD40 repeat, conserved site; PTHR22850: ; IPR001680: WD40 repeat; IPR015943: WD40/YVTN repeat-like-containing domain	NA
comp21546_c0_seq2.p1	Ec-27_004130.1	Sterol methyltransferase	GO:0006694;GO:0008152;GO:0008168	IPR030384: SAM-dependent methyltransferase SMT-type; IPR013705: Sterol methyltransferase C-terminal; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PTHR10108:SF908: ; PTHR10108: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR013216: Methyltransferase type 11	NA
comp61243_c0_seq1.p1	Ec-27_004140.1	hypothetical protein	GO:0005515;n/a	Coil: ; IPR000048: IQ motif, EF-hand binding site	NA
comp31291_c0_seq7.p1	Ec-27_004160.1	dihydrolipoamide dehydrogenase	GO:0005506;GO:0050660;GO:0031418;GO:0005737;GO:0055114;GO:0045454;GO:0016705;GO:0019538;GO:0016706;GO:0016491	IPR012999: Pyridine nucleotide-disulphide oxidoreductase, class I, active site; PR00368: FAD-dependent pyridine nucleotide reductase signature; IPR004099: Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain; PTHR22912: ; PR00411: Pyridine nucleotide disulphide reductase class-I signature; IPR006258: Dihydrolipoamide dehydrogenase; IPR016156: FAD/NAD-linked reductase, dimerisation domain; IPR001327: Pyridine nucleotide-disulphide oxidoreductase, NAD-binding domain; G3DSA:3.50.50.60: ; PIRSF000350: ; IPR023753: Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain; SSF51905:	KOG1335
comp31291_c0_seq1.p2	Ec-27_004170.2	Hypothetical leucine rich repeat protein	NA	PTHR24106: ; SSF52047: ; IPR032675: Leucine-rich repeat domain, L domain-like; Coil: ; IPR003590: Leucine-rich repeat, ribonuclease inhibitor subtype	NA
comp14523_c0_seq1.p1	Ec-27_004180.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp12016_c0_seq1.p1	Ec-27_004200.1	ATP synthase gamma chain	GO:0015986;GO:0045261;GO:0046933;GO:0046961	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; G3DSA:1.10.287.80: ; IPR023633: ATPase, F1 complex, gamma subunit domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; G3DSA:3.40.1380.10: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000131: ATPase, F1 complex, gamma subunit; SignalP-noTM: ; IPR023632: ATPase, F1 complex, gamma subunit conserved site; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1531
comp32235_c1_seq5.p2	Ec-27_004220.2	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp32235_c1_seq5.p1	Ec-27_004230.1	Rrp44 is a component of the exosome 3'->5' exoribonuclease complex, a complex that degrades mRNAs.	GO:0003723;GO:0004540	SM00955: ; PF00773: RNB domain; IPR012340: Nucleic acid-binding, OB-fold; IPR022966: Ribonuclease II/R, conserved site; PTHR23355:	NA
comp26064_c0_seq2.p2	Ec-27_004240.1	Chaperonin Cpn10	GO:0006457;GO:0005524;GO:0005737	IPR020818: Chaperonin Cpn10; IPR011032: GroES (chaperonin 10)-like; IPR018369: Chaperonin Cpn10, conserved site	NA
comp26064_c0_seq2.p1	Ec-27_004250.1	Timeless related protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR22940: ; IPR006906: Timeless protein	KOG1974
comp32085_c0_seq2.p1	Ec-27_004260.1	FAD-binding, type 1	GO:0055114;GO:0016491	IPR017927: Ferredoxin reductase-type FAD-binding domain; IPR001094: Flavodoxin; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; G3DSA:2.40.30.10: ; IPR008254: Flavodoxin/nitric oxide synthase; IPR029039: Flavoprotein-like; IPR001433: Oxidoreductase FAD/NAD(P)-binding; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR003097: FAD-binding, type 1; IPR023173: NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3; PTHR19384: ; IPR001709: Flavoprotein pyridine nucleotide cytochrome reductase; SSF52343: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; G3DSA:3.40.50.80: ; SignalP-noTM: ; IPR017938: Riboflavin synthase-like beta-barrel; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32085_c0_seq3.p1	Ec-27_004270.1	Flavoprotein-like	GO:0009055;GO:0006118;GO:0055114;GO:0016491	IPR017927: Ferredoxin reductase-type FAD-binding domain; IPR001094: Flavodoxin; G3DSA:2.40.30.10: ; IPR008254: Flavodoxin/nitric oxide synthase; IPR029039: Flavoprotein-like; SSF52343: ; IPR001433: Oxidoreductase FAD/NAD(P)-binding; G3DSA:3.40.50.80: ; IPR017938: Riboflavin synthase-like beta-barrel; IPR023173: NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3; IPR003097: FAD-binding, type 1; PTHR19384: ; IPR001709: Flavoprotein pyridine nucleotide cytochrome reductase	NA

comp24828_c0_seq1.p1	Ec-27_004290.1	FtsH protease	GO:0006139;GO:0003676;GO:0003887;GO:0000166	[illegible]	KOG0731
comp24779_c0_seq1.p1	Ec-27_004300.1	Uncharacterised protein family UPF0272	n/a;n/a;n/a	IPR002822: Uncharacterised protein family UPF0272; G3DSA:3.30.70.1380: ; G3DSA:3.10.20.300:	NA
comp13117_c0_seq2.p2	Ec-27_004320.1	Mitochondrial matrix cochaperone	GO:0005515;GO:0006457	[illegible]	KOG3003
comp13117_c0_seq2.p1	Ec-27_004330.1	WD40 repeat	GO:0005515	[illegible]	NA
comp29818_c0_seq2.p1	Ec-27_004350.1	Acyl transferase/acyl hydrolase/lysophospholipase	GO:0008152	[illegible]	NA
comp32816_c1_seq7.p14	Ec-27_004360.1	Ribosome biogenesis factor, NIP7	GO:0005634;GO:0042255	[illegible]	NA
comp32816_c1_seq7.p1	Ec-27_004370.3	Vacuolar protein sorting-associated protein 13	n/a;n/a;n/a	[illegible]	NA
comp30901_c0_seq5.p1	Ec-27_004380.1	Putative mitochondrial carrier protein PET8	GO:0005488;GO:0006810;GO:0016020;GO:0055085	[illegible]	NA
comp30901_c0_seq5.p2	Ec-27_004390.1	WW domain	GO:0005515	IPR001202: WW domain; G3DSA:2.20.70.10:	NA
comp30901_c0_seq4.p1	Ec-27_004400.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp32609_c0_seq4.p1	Ec-27_004400.2	hypothetical protein	n/a;n/a;n/a	NA	NA
comp21457_c0_seq1.p1	Ec-27_004410.1	tRNA Pseudouridine Synthase	GO:0003723;GO:0001522;GO:0009451;GO:0009982	[illegible]	KOG4393
comp10573_c0_seq1.p1	Ec-27_004420.1	Tetratricopeptide TPR2	n/a;GO:0005515	[illegible]	NA
comp25043_c0_seq3.p2	Ec-27_004430.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp27097_c0_seq1.p1	Ec-27_004460.1	Alpha/Beta hydrolase fold	GO:0004197;GO:0006508;GO:0030693	PTHR12277: ; IPR029059: Alpha/beta hydrolase fold-5; IPR029058: Alpha/Beta hydrolase fold	NA
comp12919_c0_seq1.p1	Ec-27_004470.1	Ribosomal protein S4/S9, eukaryotic/archaeal	GO:0003723;GO:0015935;GO:0006412;GO:0003735	[illegible]	NA
comp12410_c0_seq1.p1	Ec-27_004480.1	conserved unknown protein	NA	[illegible]	NA
comp19536_c0_seq1.p1	Ec-27_004490.1	Protease-associated domain, PA	n/a;n/a;n/a	[illegible]	NA
comp25437_c0_seq2.p1	Ec-27_004500.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp31030_c0_seq4.p1	Ec-27_004520.2	Carnitine O-acyltransferase	GO:0008415	PTHR22589:SF29: ; SSF52777: ; IPR000542: Acyltransferase ChoActase/COT/CPT	KOG3719
comp32576_c0_seq8.p1	Ec-27_004530.1	Armadillo-type fold	GO:0005488	[illegible]	NA
comp28943_c0_seq4.p1	Ec-27_004560.1	CAP domain	n/a;n/a;n/a	IPR001480: Bulb-type lectin domain; IPR001283: Cysteine-rich secretory protein, allergen V5/Tpx-1-related; IPR014044: CAP domain	NA
comp24500_c0_seq1.p1	Ec-27_004570.1	Acyl-CoA N-acyltransferase	n/a;n/a;n/a	IPR016181: Acyl-CoA N-acyltransferase	NA
comp34357_c0_seq1.p1	Ec-27_004580.1	Domain of unknown function DUF1995	n/a;n/a;n/a	IPR018962: Domain of unknown function DUF1995	NA
comp32566_c1_seq24.p1	Ec-27_004600.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	NA
comp11868_c0_seq1.p1	Ec-27_004610.1	Chromosome segregation protein SMC	NA	G3DSA:1.20.1280.50: ; Coil:	NA
comp28856_c0_seq2.p1	Ec-27_004620.1	Nin one binding (NOB1) Zn-ribbon-like	n/a;n/a;n/a	PTHR12814:SF2: ; IPR014881: Nin one binding (NOB1) Zn-ribbon-like; PTHR12814:	NA
comp33157_c1_seq22.p1	Ec-27_004630.1	Dihydrofolate reductase domain	GO:0006231;GO:0009165;GO:0004799;GO:0055114;GO:0004146;GO:0006545	[illegible]	NA
comp17520_c0_seq1.p1	Ec-27_004640.1	Formiminotransferase, N-terminal subdomain	GO:0008152;GO:0005542;GO:0016740	[illegible]	NA
comp32562_c2_seq2.p1	Ec-27_004650.1	GPA4, alpha subunit of a heterotrimeric G protein	GO:0007186;GO:0007165;GO:0003924;GO:0031683;GO:0019001;GO:0004871	[illegible]	NA
comp25537_c0_seq3.p1	Ec-27_004660.1	conserved unknown protein	n/a;n/a;n/a	PTHR34649:SF1: ; PTHR34649: ; Coil:	NA
comp21312_c1_seq1.p1	Ec-27_004680.1	Alpha/Beta hydrolase fold	GO:0016787	IPR029058: Alpha/Beta hydrolase fold; IPR000073: Alpha/beta hydrolase fold-1; PTHR10992: ; SignalP-TM:	NA
comp20243_c0_seq1.p1	Ec-27_004690.1	Possible protein kinase	GO:0015629;GO:0005083;GO:0005515;GO:0006461;GO:0008154	[illegible]	NA
comp25348_c0_seq3.p1	Ec-27_004700.1	SR RNA splicing protein	GO:0003676;GO:0000166	NA	NA
comp12471_c0_seq1.p1	Ec-27_004710.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0006457;GO:0031072;GO:0051082	[illegible]	NA
comp26746_c0_seq2.p1	Ec-27_004720.1	Nucleotide-binding alpha-beta plait domain	GO:0000166	[illegible]	[illegible]
comp32172_c0_seq12.p1	Ec-27_004730.1	Domain of unknown function DUF4098	GO:0015078;GO:0015986;GO:0016469;GO:0016820;GO:0033178	[illegible]	[illegible]
comp33816_c0_seq1.p1	Ec-27_004740.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp28077_c0_seq1.p1	Ec-27_004750.1	conserved unknown protein	n/a;n/a;n/a	Coil:	[illegible]
comp19583_c0_seq1.p1	Ec-27_004760.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31035_c0_seq3.p1	Ec-27_004770.1	Tafazzin	GO:0006644;GO:0016746	[illegible]	[illegible]
comp12434_c0_seq1.p1	Ec-27_004780.1	HotDog domain	n/a;n/a;n/a	[illegible]	[illegible]
comp12434_c0_seq1.p2	Ec-27_004790.1	Dimeric alpha-beta barrel	n/a;n/a;n/a	[illegible]	[illegible]
comp31251_c0_seq1.p1	Ec-27_004810.1	EF-hand domain pair	GO:0005509	[illegible]	[illegible]
comp11774_c0_seq1.p1	Ec-27_004820.1	Retrieval of early ER protein Rer1	GO:0016021	[illegible]	[illegible]
comp12783_c0_seq1.p1	Ec-27_004830.1	Phospholipase/carboxylesterase/thioesterase	GO:0016787	[illegible]	[illegible]
comp34066_c0_seq1.p1	Ec-27_004840.2	WD40 repeat	GO:0005515	[illegible]	[illegible]
comp32139_c0_seq2.p1	Ec-27_004850.1	expressed unknown protein	GO:0003676;GO:0046872;GO:0008270	[illegible]	[illegible]
comp32139_c0_seq7.p1	Ec-27_004860.1	HI0933 family protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31808_c0_seq8.p1	Ec-27_004880.1	Protein arginine N-methyltransferase	GO:0008168;GO:0006479	[illegible]	[illegible]
comp31085_c0_seq4.p1	Ec-27_004900.1	WD40-repeat-containing domain	GO:0005515	[illegible]	[illegible]
comp32694_c1_seq8.p2	Ec-27_004910.1	Molybdopterin cofactor biosynthesis C (MoaC) domain	GO:0006777	[illegible]	[illegible]
comp32694_c1_seq8.p1	Ec-27_004930.1	Vacuolar protein sorting-associated protein 13	GO:0005509	[illegible]	[illegible]
comp21429_c0_seq3.p1	Ec-27_004960.1	protein of unknown function DUF399	NA	[illegible]	[illegible]
comp32621_c0_seq14.p1	Ec-27_004970.1	Glutamate synthase (ferredoxin-dependent)	GO:0015930;GO:0006537	[illegible]	[illegible]
comp31642_c0_seq6.p1	Ec-27_004990.1	P-loop containing nucleoside triphosphate hydrolase	GO:0004176;GO:0004252;GO:0005524;GO:0006508	[illegible]	[illegible]
comp21528_c0_seq2.p2	Ec-27_005020.1	Cyclin-like	n/a;n/a;n/a	[illegible]	[illegible]
comp21528_c0_seq2.p1	Ec-27_005030.1	Glucokinase	GO:0051156;GO:0005524;GO:0006096;GO:0004340	[illegible]	[illegible]
comp24651_c0_seq1.p1	Ec-27_005090.1	Ankyrin repeat-containing domain	n/a;GO:0005515	[illegible]	[illegible]
comp32406_c0_seq2.p1	Ec-27_005100.2	SET domain	GO:0005515	[illegible]	[illegible]
comp33152_c1_seq21.p2	Ec-27_005110.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp19862_c0_seq1.p1	Ec-27_005120.1	nodulin family protein	GO:0055085;GO:0016021	[illegible]	[illegible]
comp13085_c0_seq1.p2	Ec-27_005130.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp27040_c0_seq1.p1	Ec-27_005140.1	glyoxalase domain containing protein	NA	[illegible]	[illegible]
comp33488_c0_seq1.p1	Ec-27_005150.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp21275_c0_seq1.p1	Ec-27_005160.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp31576_c1_seq9.p3	Ec-27_005170.1	Putative glutamine amidotransferase type 2	GO:0008152	[illegible]	[illegible]
comp31576_c1_seq9.p1	Ec-27_005190.1	Amidohydrolase 1	GO:0016787	[illegible]	[illegible]
comp25131_c0_seq2.p1	Ec-27_005200.1	Tetratricopeptide-like helical domain	GO:0005515	[illegible]	[illegible]
comp27541_c0_seq1.p1	Ec-27_005220.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270	[illegible]	[illegible]
comp31285_c0_seq1.p1	Ec-27_005230.1	AAA+ ATPase domain	GO:0006810;GO:0005524;GO:0042626;GO:0016021;GO:0016887	[illegible]	[illegible]
comp24571_c0_seq2.p1	Ec-27_005240.1	Pseudouridine synthase	GO:0003723;GO:0001522;GO:0009451;GO:0009982	[illegible]	[illegible]
comp27690_c0_seq1.p1	Ec-27_005250.1	SNF2-related	GO:0003677;GO:0005524	[illegible]	[illegible]
comp12655_c0_seq1.p1	Ec-27_005260.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp20281_c0_seq1.p2	Ec-27_005270.2	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp21371_c0_seq1.p1	Ec-27_005280.1	Protein arginine N-methyltransferase	GO:0008168;GO:0006479	NA	[illegible]
comp30605_c0_seq3.p1	Ec-27_005300.1	protein tyrosine kinase	GO:0006468;GO:0004713;GO:0005515	[illegible]	[illegible]
comp32200_c0_seq3.p1	Ec-27_005310.1	conserved hypothetical protein	GO:0005524;GO:0006810;GO:0016021;GO:0016887;GO:0042626	[illegible]	[illegible]
comp27583_c0_seq6.p1	Ec-27_005330.1	conserved unknown protein	n/a;n/a;n/a	Coil:	[illegible]
comp29468_c0_seq3.p1	Ec-27_005350.1	Peptidase M24, structural domain	GO:0004177;GO:0004239;GO:0006508;GO:0008235	[illegible]	[illegible]
comp26287_c0_seq2.p1	Ec-27_005360.1	FAM175 family	n/a;n/a;n/a	[illegible]	[illegible]
comp30482_c0_seq1.p1	Ec-27_005430.1	chromosome 22 open reading frame 13, isoform CRA_c	NA	[illegible]	[illegible]
comp28843_c1_seq1.p1	Ec-27_005450.1	WD40 repeat	GO:0005515	[illegible]	[illegible]
comp32353_c2_seq9.p1	Ec-27_005480.1	Engulfment/cell motility, ELMO	GO:0005856;GO:0006909	[illegible]	[illegible]
comp17324_c0_seq2.p1	Ec-27_005500.1	Ovarian tumour, otubain	n/a;n/a;n/a	[illegible]	[illegible]
comp31834_c0_seq9.p1	Ec-27_005510.1	Heat shock protein 40 like protein/ DnaJ domain containing protein	GO:0006457;GO:0031072;GO:0051082	[illegible]	[illegible]
comp34172_c0_seq1.p1	Ec-27_005530.1	Tetratricopeptide-like helical domain	GO:0005515	[illegible]	[illegible]
comp24132_c0_seq2.p1	Ec-27_005560.1	calcium-dependent cytoplasmic cysteine proteinase, papain-like protein	GO:0004198;GO:0005622;GO:0006508	[illegible]	[illegible]
comp26564_c0_seq2.p1	Ec-27_005580.1	Zinc finger, RING-type	GO:0005515;GO:0008270	[illegible]	[illegible]
comp37054_c0_seq1.p1	Ec-27_005600.1	rRNA-processing protein Fcf1/Utp23	GO:0032040	[illegible]	[illegible]
comp32292_c0_seq6.p2	Ec-27_005650.4	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp34505_c0_seq1.p1	Ec-27_005660.1	Thioredoxin-like fold	n/a;GO:0045454	[illegible]	[illegible]
comp21323_c0_seq2.p1	Ec-27_005670.1	Dihydroorotate dehydrogenase, class 2	GO:0016020;GO:0004152;GO:0016627;GO:0055114;GO:0005737;GO:0006207	[illegible]	[illegible]
comp31984_c3_seq1.p1	Ec-27_005680.1	carbonic anhydrase alpha type	GO:0006730;GO:0008270;GO:0004089	[illegible]	[illegible]
comp20946_c0_seq1.p1	Ec-27_005710.1	Miro-related GTP-ase 1	GO:0015936;GO:0055114;GO:0007264;GO:0004420;GO:0005525;GO:0050662	[illegible]	[illegible]
comp31036_c0_seq2.p1	Ec-27_005740.1	Protein of unknown function DUF3651, TMEM131	n/a;n/a;n/a	[illegible]	[illegible]
comp31139_c1_seq4.p1	Ec-27_005750.1	Phospholipase C, phosphatidylinositol-specific, Y domain	GO:0007165;GO:0004435;GO:0035556;GO:0005515;GO:0006629	[illegible]	[illegible]
comp21156_c0_seq2.p1	Ec-27_005770.1	dTDP-glucose 4,6-dehydratase	GO:0008460;GO:0009225	[illegible]	[illegible]
comp12125_c0_seq1.p1	Ec-27_005780.1	Pentatricopeptide repeat	n/a;n/a;n/a	[illegible]	[illegible]
comp20338_c0_seq1.p1	Ec-27_005790.1	ATPase, V0 complex, c/d subunit	GO:0033179;GO:0016469;GO:0015986;GO:0015991;GO:0033177;GO:0015078;GO:0046961	[illegible]	[illegible]
comp19407_c0_seq1.p1	Ec-27_005820.1	Transcription initiation factor TAFII31	GO:0046982;GO:0006352	[illegible]	[illegible]
comp12264_c0_seq1.p1	Ec-27_005830.1	Exonuclease	GO:0004527	[illegible]	[illegible]
comp27476_c0_seq1.p1	Ec-27_005840.1	expressed unknown protein	n/a;n/a;n/a	Coil:	[illegible]
comp23170_c0_seq1.p2	Ec-27_005850.1	hypothetical protein	n/a;n/a;n/a	Coil:	[illegible]
comp31335_c0_seq4.p3	Ec-27_005860.1	Concanavalin A-like lectin/glucanase domain	n/a;n/a;n/a	[illegible]	[illegible]
comp14621_c0_seq1.p1	Ec-27_005870.1	conserved unknown protein	n/a;n/a;n/a	Coil:	[illegible]
comp31335_c0_seq4.p1	Ec-27_005880.1	conserved unknown protein	n/a;n/a;n/a	PTHR13251:	[illegible]
comp29629_c0_seq2.p1	Ec-27_005900.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp32304_c1_seq1.p1	Ec-27_005930.1	conserved unknown protein	GO:0004499;GO:0009055;GO:0016491;GO:0050660;GO:0050661;GO:0055114	[illegible]	[illegible]
comp21173_c0_seq1.p2	Ec-27_005950.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp26783_c0_seq1.p1	Ec-27_005970.1	Hypothetical leucine rich repeat protein	GO:0005515	[illegible]	[illegible]
comp12915_c0_seq1.p1	Ec-27_005980.1	DRG2, developmentally regulated GTPase 2	GO:0005622;GO:0005525	[illegible]	[illegible]
comp30349_c0_seq1.p1	Ec-27_005990.1	Ankyrin repeat-containing domain	n/a;GO:0005515	[illegible]	[illegible]
comp29000_c0_seq1.p1	Ec-27_006020.1	conserved unknown protein	n/a;n/a;n/a	NA	[illegible]
comp17347_c0_seq1.p1	Ec-27_006030.1	conserved unknown protein	n/a;n/a;n/a	NA	[illegible]
comp34746_c0_seq1.p1	Ec-27_006040.1	NYN domain, limkain-b1-type	n/a;n/a;n/a	[illegible]	[illegible]
comp21596_c0_seq1.p1	Ec-27_006050.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	[illegible]	[illegible]
comp32199_c1_seq3.p1	Ec-27_006070.1	Serine/threonine/dual specificity protein kinase, catalytic domain	GO:0005524;GO:0004672;GO:0006468	[illegible]	[illegible]
comp21255_c0_seq2.p1	Ec-27_006080.1	Scaffold protein Nfu/NifU, N-terminal	GO:0005506	[illegible]	[illegible]
comp12881_c0_seq1.p1	Ec-27_006090.1	PUG domain	GO:0005515	[illegible]	[illegible]
comp11617_c0_seq1.p1	Ec-27_006110.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp33865_c0_seq1.p1	Ec-27_006120.1	Peptide methionine sulphoxide reductase MsrB	GO:0033743;GO:0055114	[illegible]	[illegible]
comp76726_c0_seq1.p1	Ec-27_006130.2	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	[illegible]	[illegible]
comp31045_c0_seq4.p1	Ec-27_006140.1	Tetratricopeptide-like helical domain	GO:0005515	[illegible]	[illegible]
comp12608_c0_seq1.p1	Ec-27_006150.1	START domain	GO:0008289	[illegible]	[illegible]
comp32125_c0_seq9.p1	Ec-27_006160.1	conserved unknown protein	n/a;n/a;n/a	NA	[illegible]
comp32125_c0_seq7.p1	Ec-27_006170.1	hypothetical protein	n/a;GO:0005515	[illegible]	[illegible]
comp30976_c0_seq1.p1	Ec-27_006190.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp32847_c0_seq3.p1	Ec-27_006200.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31609_c1_seq1.p1	Ec-27_006200.2	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp25548_c0_seq1.p1	Ec-27_006210.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	[illegible]	[illegible]
comp22495_c0_seq3.p1	Ec-27_006220.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp21017_c0_seq1.p2	Ec-27_006240.1	Translation initiation factor SUI1	GO:0005840;GO:0005622;GO:0006413;GO:0003743;GO:0006412;GO:0003735	[illegible]	[illegible]
comp31019_c1_seq16.p1	Ec-27_006250.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp32197_c0_seq1.p1	Ec-27_006270.1	expressed unknown protein	n/a;n/a;n/a	Coil:	[illegible]
comp33902_c0_seq1.p1	Ec-27_006280.1	methylase-related	n/a;n/a;n/a	[illegible]	[illegible]
comp27561_c0_seq1.p1	Ec-27_006290.1	hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp28876_c0_seq1.p1	Ec-27_006300.1	Target SNARE coiled-coil domain	GO:0005515	[illegible]	[illegible]
comp21214_c0_seq2.p1	Ec-27_006310.1	conserved unknown protein	GO:0008168;GO:0003676;GO:0032259	[illegible]	[illegible]
comp12530_c0_seq1.p1	Ec-27_006320.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp26680_c0_seq1.p1	Ec-27_006330.1	c-myb-like transcription factor	GO:0003677	[illegible]	[illegible]
comp24367_c0_seq3.p1	Ec-27_006340.1	rRNA-processing protein EFG1	n/a;n/a;n/a	[illegible]	[illegible]
comp19698_c0_seq1.p1	Ec-27_006350.1	Peroxisomal biogenesis factor 11	GO:0005779;GO:0016559	[illegible]	[illegible]
comp28876_c1_seq4.p1	Ec-27_006360.1	Mediator complex, subunit Med7	GO:0016592;GO:0001104;GO:0006357	[illegible]	[illegible]
comp30087_c0_seq1.p1	Ec-27_006370.1	GC-rich sequence DNA-binding factor	GO:0005634;GO:0003677;GO:0006355;GO:0003700	[illegible]	[illegible]
comp33024_c1_seq31.p1	Ec-27_006390.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp19706_c0_seq1.p1	Ec-27_006410.1	NADP-dependent oxidoreductase domain	GO:0016491;GO:0055114	[illegible]	[illegible]
comp19505_c0_seq1.p1	Ec-27_006420.1	Snf7 family	GO:0007034	[illegible]	[illegible]
comp32561_c0_seq4.p1	Ec-27_006450.1	Rhodanese-like domain	n/a;n/a;n/a	[illegible]	[illegible]
comp23730_c0_seq3.p1	Ec-27_006460.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp30525_c0_seq2.p1	Ec-27_006470.1	expressed unknown protein	NA	NA	[illegible]
comp30525_c0_seq1.p1	Ec-27_006470.2	expressed unknown protein	NA	NA	[illegible]
comp32750_c0_seq35.p1	Ec-27_006480.1	expressed unknown protein	n/a;n/a;n/a	Coil:	[illegible]
comp34132_c0_seq1.p1	Ec-27_006490.1	Sphingosine kinase	GO:0004143;GO:0007205	[illegible]	[illegible]
comp26983_c0_seq1.p1	Ec-27_006520.1	Photosystem II Psp29, biogenesis	GO:0009523;GO:0010207;GO:0010027;GO:0015979	[illegible]	[illegible]
comp24462_c0_seq2.p1	Ec-27_006530.1	Flavin reductase-like, FMN-binding	GO:0042602;GO:0055114;GO:0010181;GO:0016491	[illegible]	[illegible]
comp20949_c0_seq2.p1	Ec-27_006560.1	NADH-dependent fumarate reductase	GO:0009055;GO:0016491;n/a	[illegible]	[illegible]
comp21426_c0_seq1.p1	Ec-27_006570.1	WD40/YVTN repeat-like-containing domain	GO:0005515	[illegible]	[illegible]
comp30902_c0_seq2.p1	Ec-27_006590.1	Glycosyl transferase, family 2	n/a;n/a;n/a	[illegible]	[illegible]
comp24709_c0_seq2.p1	Ec-27_006620.1	Heat shock protein 70	n/a;n/a;n/a	[illegible]	[illegible]
comp29217_c1_seq2.p1	Ec-27_006660.1	TALE homeobox domain transcription factor	GO:0003677;GO:0006355;GO:0045449	[illegible]	[illegible]
comp27338_c0_seq2.p1	Ec-27_006680.2	Tetratricopeptide-like helical domain	GO:0005515	[illegible]	[illegible]
comp32241_c1_seq1.p1	Ec-27_006690.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp32226_c0_seq11.p1	Ec-25_003400.1	Mannuronan C-5-epimerase N-terminal fragment	GO:0030170;GO:0006520	[illegible]	[illegible]
comp28564_c0_seq1.p1	Ec-27_006720.1	Armadillo-like helical	GO:0005488	[illegible]	[illegible]
comp24737_c0_seq1.p1	Ec-27_006730.1	Protein of unknown function DUF1295	n/a;n/a;n/a	[illegible]	[illegible]
comp33229_c0_seq8.p1	Ec-27_006740.1	UBA-like	GO:0005515	[illegible]	[illegible]
comp34641_c1_seq1.p1	Ec-27_006770.1	WD40 repeat	GO:0005515	[illegible]	[illegible]
comp27576_c0_seq2.p1	Ec-27_006780.1	Protein of unknown function DUF4336	n/a;n/a;n/a	[illegible]	[illegible]
comp11850_c0_seq1.p1	Ec-27_006790.1	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a	[illegible]	[illegible]
comp33264_c1_seq44.p1	Ec-27_006800.2	Hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp28248_c0_seq2.p1	Ec-27_006860.1	Aminoacyl-tRNA synthetase, class II (G/ H/ P/ S), conserved domain	GO:0005524;GO:0000166;GO:0006418;GO:0004812	[illegible]	[illegible]
comp19853_c0_seq1.p1	Ec-27_006870.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp19993_c0_seq1.p1	Ec-27_006880.1	Aryldialkylphosphatase	GO:0008270;GO:0009056	[illegible]	[illegible]
comp29372_c0_seq3.p1	Ec-27_006890.1	S-Adenosylmethionine decarboxylase	GO:0004014	[illegible]	[illegible]
comp29719_c0_seq3.p1	Ec-27_006900.1	Ankyrin repeat-containing domain	n/a;GO:0005515	[illegible]	[illegible]
comp31591_c0_seq4.p1	Ec-27_006910.1	Cytochrome b5-like heme/steroid binding domain	GO:0020037	[illegible]	[illegible]
comp12062_c0_seq1.p1	Ec-27_006920.1	WD40/YVTN repeat-like-containing domain	GO:0005515	[illegible]	[illegible]
comp30163_c0_seq2.p2	Ec-27_006930.1	Nucleophile aminohydrolases, N-terminal	GO:0051603;GO:0004298;GO:0005839;GO:0006511	[illegible]	[illegible]
comp30163_c0_seq1.p1	Ec-27_006940.1	ATP-grasp fold, subdomain 2	GO:0005524	[illegible]	[illegible]
comp22117_c0_seq2.p1	Ec-27_006960.1	Mitochondrial carrier domain	GO:0005488;GO:0006810;GO:0016020;GO:0055085	[illegible]	[illegible]
comp29322_c0_seq3.p1	Ec-27_006980.1	expressed unknown protein	n/a;n/a;n/a	Coil:	[illegible]
comp23432_c0_seq2.p1	Ec-27_006990.1	Glycerol-3-phosphate dehydrogenase	GO:0055114;GO:0004367;GO:0009331;GO:0006072	[illegible]	[illegible]
comp34352_c0_seq1.p1	Ec-27_007000.1	GTP cyclohydrolase I	GO:0005737;GO:0003934;GO:0046654	[illegible]	[illegible]
comp26266_c0_seq2.p1	Ec-27_007010.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	[illegible]	[illegible]
comp31841_c0_seq11.p1	Ec-27_007020.1	LMBR1-like membrane protein	n/a;n/a;n/a	[illegible]	[illegible]
comp27047_c0_seq4.p1	Ec-28_000010.1	DEP domain	GO:0035556	[illegible]	[illegible]
comp32810_c0_seq7.p1	Ec-28_000040.1	WD40 repeat	GO:0005515	[illegible]	[illegible]
comp32248_c1_seq4.p1	Ec-28_000050.1	Mannose-6-phosphate isomerase	n/a;GO:0004476	[illegible]	[illegible]
comp28991_c0_seq2.p1	Ec-28_000060.1	Armadillo-like helical	n/a;GO:0005488	[illegible]	[illegible]
comp30632_c0_seq3.p1	Ec-28_000110.2	Rieske [2Fe-2S] iron-sulphur domain	GO:0016491;GO:0051537;GO:0055114	[illegible]	[illegible]
comp25244_c0_seq1.p1	Ec-28_000120.1	MTIF2L, mitochondrial translation initiation factor 2-like	n/a;n/a;n/a	[illegible]	[illegible]
comp15012_c0_seq1.p1	Ec-28_000130.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp97470_c0_seq1.p1	Ec-28_000140.2	RmlC-like jelly roll fold	n/a;n/a;n/a	[illegible]	[illegible]
comp26385_c1_seq3.p1	Ec-28_000150.1	Domain of unknown function DUF1336	n/a;n/a;n/a	[illegible]	[illegible]
comp30749_c0_seq3.p1	Ec-28_000160.1	Endonuclease/exonuclease/phosphatase	n/a;n/a;n/a	[illegible]	[illegible]
comp30983_c0_seq3.p1	Ec-28_000170.1	hypothetical protein	GO:0000287;GO:0004427;GO:0006796;GO:0005737	Coil:	[illegible]
comp29378_c0_seq1.p1	Ec-28_000190.1	Leucine-rich repeat	GO:0005515	[illegible]	[illegible]
comp20457_c0_seq1.p1	Ec-28_000200.1	Tetratricopeptide-like helical domain	GO:0005515	[illegible]	[illegible]
comp24375_c0_seq1.p1	Ec-28_000220.1	GOLD	GO:0006810;GO:0016021	[illegible]	[illegible]
comp27943_c0_seq1.p1	Ec-28_000230.1	RNA cap guanine-N2 methyltransferase	GO:0008168;GO:0009452;GO:0001510	[illegible]	[illegible]
comp32177_c6_seq3.p1	Ec-28_000240.1	ABC transporter-like	NA	[illegible]	[illegible]
comp29515_c1_seq2.p1	Ec-28_000250.1	eukaryotic translation initiation factor 4E like2	GO:0003723;GO:0003743;GO:0005737;GO:0006413	[illegible]	[illegible]
comp21320_c0_seq1.p1	Ec-28_000270.1	NAD(P)-binding domain	GO:0003824;GO:0005488;GO:0008152	[illegible]	[illegible]
comp31307_c0_seq1.p1	Ec-28_000300.1	Quinonprotein alcohol dehydrogenase-like superfamily	n/a;n/a;n/a	[illegible]	[illegible]
comp20772_c0_seq1.p1	Ec-28_000310.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp27699_c0_seq7.p1	Ec-28_000320.1	Longin-like domain	GO:0006810	[illegible]	[illegible]
comp34800_c0_seq1.p1	Ec-28_000330.1	coated vesicle membrane protein	GO:0006810;n/a;GO:0016021	[illegible]	[illegible]
comp24886_c0_seq1.p1	Ec-28_000340.1	WD40/YVTN repeat-like-containing domain	GO:0005515	[illegible]	[illegible]
comp32531_c1_seq8.p1	Ec-28_000350.1	Ankyrin repeat-containing domain	n/a;GO:0005515	[illegible]	[illegible]
comp29983_c0_seq2.p1	Ec-28_000360.1	expressed unknown protein	NA	Coil:	[illegible]
comp20342_c0_seq2.p1	Ec-28_000390.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008152;GO:0008168	[illegible]	[illegible]
comp29221_c0_seq5.p1	Ec-28_000420.1	AAA+ (ATPases Associated with a wide variety of cellular Activities) superfamily	GO:0000166;GO:0017111	[illegible]	[illegible]
comp24808_c0_seq1.p1	Ec-28_000430.1	Sec1-like, domain 2	GO:0006904;GO:0016192	[illegible]	[illegible]
comp24157_c0_seq1.p1	Ec-28_000440.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp12512_c0_seq1.p1	Ec-28_000450.1	Trimeric LpxA-like	GO:0008415;GO:0016740	[illegible]	[illegible]
comp31663_c0_seq6.p1	Ec-28_000480.1	FAD/NAD-linked reductase, dimerisation domain	GO:0050660;GO:0055114;GO:0016491	[illegible]	[illegible]
comp24881_c0_seq1.p2	Ec-28_000490.1	Ubiquitin-conjugating enzyme E2	GO:0019787;GO:0043687;GO:0051246	[illegible]	[illegible]
comp29260_c2_seq2.p1	Ec-28_000520.1	Adenine phosphoribosyltransferase-like	GO:0009116;GO:0016740	[illegible]	[illegible]
comp27878_c0_seq3.p1	Ec-28_000530.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp13693_c0_seq1.p1	Ec-28_000540.1	MutL protein homolog 3	GO:0005524	[illegible]	[illegible]
comp25363_c0_seq1.p2	Ec-28_000560.1	photosystem II 12 kDa extrinsic protein	GO:0009523;GO:0009654;GO:0015979;GO:0019898;GO:0042549	[illegible]	[illegible]
comp25363_c0_seq1.p1	Ec-28_000570.1	Protein prenyltransferase, alpha subunit	GO:0018342;GO:0008318	[illegible]	[illegible]
comp29708_c0_seq2.p1	Ec-28_000580.1	possible vitamin K epoxide reductase, plastid protein	NA	[illegible]	[illegible]
comp25529_c0_seq1.p1	Ec-28_000660.1	hypothetical protein	GO:0046872;GO:0003824	[illegible]	[illegible]
comp11989_c0_seq1.p1	Ec-28_000670.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31050_c0_seq2.p1	Ec-28_000680.1	Two component sensor histidine kinase	GO:0016310;GO:0016772	[illegible]	[illegible]
comp31050_c0_seq3.p1	Ec-28_000680.2	Two component sensor histidine kinase	GO:0016310;GO:0016772	[illegible]	[illegible]
comp26892_c1_seq1.p1	Ec-28_000690.1	DEAD box helicase	GO:0000166;GO:0003676;GO:0003824;GO:0005524;GO:0005622;GO:0006260;GO:0006281;GO:0006310;GO:0008026;GO:0043140;GO:0044237	[illegible]	[illegible]
comp31618_c0_seq1.p1	Ec-28_000720.1	Putative SNARE-associated Golgi protein	GO:0016021	[illegible]	[illegible]
comp30915_c0_seq11.p1	Ec-28_000730.1	Protein kinase domain	GO:0004672;GO:0005524;GO:0006468	[illegible]	[illegible]
comp32043_c0_seq1.p1	Ec-28_000760.1	Protein DA1 like	n/a;n/a;n/a	[illegible]	[illegible]
comp31842_c1_seq1.p1	Ec-28_000770.1	P-loop containing nucleoside triphosphate hydrolase	GO:0005634;GO:0030163;GO:0005737;GO:0016787	[illegible]	[illegible]
comp31842_c2_seq9.p1	Ec-28_000790.1	conserved unknown protein	n/a;n/a;n/a	Coil: ; SignalP-TM:	[illegible]
comp23878_c0_seq1.p1	Ec-28_000800.2	WF40 domain protein	NA	[illegible]	[illegible]
comp31704_c1_seq6.p1	Ec-28_000810.1	Ring finger domain protein	NA	[illegible]	[illegible]
comp20220_c0_seq1.p1	Ec-28_000820.1	conserved unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp32887_c2_seq2.p3	Ec-28_000830.1	Ribosomal protein L28	GO:0005840;GO:0005622;GO:0006412;GO:0003735	[illegible]	[illegible]
comp32887_c2_seq2.p1	Ec-28_000850.1	CLU domain	n/a;n/a;n/a	[illegible]	[illegible]
comp27904_c0_seq3.p1	Ec-28_000870.1	WW domain protein	GO:0005515	[illegible]	[illegible]
comp28515_c0_seq1.p6	Ec-28_000880.3	Hypothetical protein	n/a;n/a;n/a	[illegible]	[illegible]
comp28515_c0_seq1.p1	Ec-28_000910.1	Clathrin light chain	GO:0030130;GO:0016192;GO:0006886;GO:0030132;GO:0005198	[illegible]	[illegible]
comp29547_c0_seq1.p1	Ec-28_000930.2	Magnesium transporter NIPA	GO:0015095;GO:0015693;GO:0016021	[illegible]	[illegible]
comp31898_c0_seq14.p1	Ec-28_000940.1	SOUL heme-binding protein-like	n/a;n/a;n/a	[illegible]	[illegible]
comp12353_c0_seq1.p2	Ec-28_000950.1	Mitochondrial Processing Peptidase beta subunit	GO:0046872;GO:0003824	NA	[illegible]
comp12353_c0_seq1.p1	Ec-28_000960.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	[illegible]	[illegible]
comp31130_c0_seq1.p1	Ec-28_000970.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp23713_c0_seq2.p1	Ec-28_000990.1	Rossmann-like alpha/beta/alpha sandwich fold	GO:0004066;GO:0006529	[illegible]	[illegible]
comp31679_c0_seq9.p2	Ec-28_001000.1	C2H2 zinc finger, ankyrin repeat protein	n/a;n/a;n/a	[illegible]	[illegible]
comp31679_c0_seq9.p1	Ec-28_001010.1	cyclopropane-fatty-acyl-phospholipid synthase/ oxidoreductase	GO:0008610;GO:0008825;GO:0009055	[illegible]	[illegible]
comp29808_c0_seq1.p1	Ec-28_001030.2	E3 UFM1-protein ligase 1	n/a;n/a;n/a	[illegible]	[illegible]
comp27047_c0_seq1.p2	Ec-28_001030.5	E3 UFM1-protein ligase 1	n/a;n/a;n/a	[illegible]	[illegible]
comp27047_c0_seq1.p1	Ec-28_001040.1	Pyridine nucleotide-disulphide oxidoreductase, NAD-binding domain	GO:0050660;GO:0055114;GO:0016491	[illegible]	[illegible]
comp12405_c0_seq1.p1	Ec-28_001050.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	[illegible]	[illegible]
comp32566_c1_seq3.p1	Ec-28_001060.2	Alpha/Beta hydrolase fold	GO:0008152;GO:0016787	[illegible]	[illegible]
comp31663_c0_seq11.p1	Ec-28_001070.1	Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain	GO:0055114;GO:0045454	[illegible]	[illegible]
comp20262_c1_seq1.p1	Ec-28_001110.1	Zinc finger, RING-type	GO:0005515;GO:0008270	[illegible]	[illegible]
comp12385_c0_seq1.p1	Ec-28_001150.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp29700_c0_seq3.p1	Ec-28_001170.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;GO:0008168;GO:0032259	[illegible]	[illegible]
comp28483_c0_seq2.p1	Ec-28_001180.1	Polyribonucleotide nucleotidyltransferase, RNA-binding domain	GO:0006396;GO:0003723;GO:0004654;GO:0000175;GO:0006402	[illegible]	[illegible]
comp24599_c0_seq1.p1	Ec-28_001220.1	hypothetical protein	n/a;n/a;n/a	NA	[illegible]
comp32588_c0_seq12.p1	Ec-28_001240.1	Set domain protein	GO:0005634	NA	[illegible]
comp31161_c5_seq3.p1	Ec-28_001270.1	Homeodomain-like	GO:0003677	[illegible]	[illegible]
comp34360_c0_seq1.p3	Ec-28_001290.1	expressed unknown protein	n/a;n/a;n/a	[illegible]	[illegible]
comp30305_c0_seq3.p1	Ec-28_001310.1	Alpha-ketoglutarate-dependent dioxygenase AlkB-like	GO:0005576	[illegible]	[illegible]
comp32520_c2_seq1.p1	Ec-28_001390.2	glycosyl transferase family 2 protein	n/a;n/a;n/a	[illegible]	[illegible]
comp27136_c0_seq6.p1	Ec-28_001400.1	Histone deacetylase domain protein	GO:0004407;GO:0016575	[illegible]	[illegible]
comp31790_c0_seq4.p1	Ec-28_001420.3	Forkhead-associated (FHA) domain	GO:0005515	Coil:	[illegible]
comp29800_c0_seq6.p1	Ec-28_001430.2	conserved unknown protein	GO:0003824;GO:0008152	[illegible]	[illegible]
comp29800_c0_seq7.p1	Ec-28_001430.3	conserved unknown protein	GO:0003824;GO:0008152	NA	[illegible]
comp33657_c0_seq1.p1	Ec-28_001490.1	Mannosyl-oligosaccharide 1,2-alpha-mannosidase, family GH47	GO:0016020;GO:0005509;GO:0004571	[illegible]	[illegible]
comp29604_c0_seq3.p1	Ec-28_001510.1	conserved unknown protein	n/a;n/a;n/a	NA	[illegible]
comp27641_c0_seq3.p1	Ec-28_001560.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp16380_c0_seq1.p1	Ec-28_001570.1	C2H2 zinc finger protein	n/a;GO:0005622;GO:0046872;GO:0008270	[illegible]	[illegible]
comp30358_c0_seq3.p1	Ec-28_001580.1	Nucleolar, Nop52	GO:0006364;GO:0030688	[illegible]	[illegible]
comp21290_c0_seq1.p1	Ec-28_001680.1	Monooxygenase, FAD-binding	GO:0008152;GO:0016491	[illegible]	[illegible]
comp32699_c0_seq31.p1	Ec-28_001690.1	expressed unknown protein	n/a;n/a;n/a	NA	[illegible]
comp34413_c0_seq1.p1	Ec-28_001730.1	Urease accessory protein UreF	GO:0006807;GO:0016151	[illegible]	[illegible]
comp28351_c0_seq1.p1	Ec-28_001750.1	Nucleosome assembly protein (NAP)	GO:0005634;GO:0006334	[illegible]	[illegible]
comp35038_c0_seq1.p1	Ec-28_001760.1	40S ribosomal protein S15	GO:0005840;GO:0003723;GO:0005622;GO:0006412;GO:0003735	[illegible]	[illegible]
comp25800_c0_seq2.p1	Ec-28_001780.1	Zinc/iron permease	GO:0016020;GO:0055085;GO:0046873;GO:0030001	NA	[illegible]
comp32124_c2_seq13.p1	Ec-28_001790.1	haloacid dehalogenase-like hydrolase family protein	GO:0008152;GO:0008967	[illegible]	[illegible]

comp25366_c0_seq2.p1	Ec-28_001820.1	Protein farnesyltransferase subunit beta	GO:0005965;GO:0042127;GO:0003824;GO:0018343	SIGNAL_PEPTIDE: Signal peptide region; PTHR11774: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR026872: Protein farnesyltransferase subunit beta; IPR008930: Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR001330: Prenyltransferase/squalene oxidase; PF13249: Prenyltransferase-like	NA
comp32929_c0_seq1.p1	Ec-28_001830.1	GAF domain-like	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029016: GAF domain-like; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31099_c0_seq3.p1	Ec-28_001850.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp29974_c0_seq1.p1	Ec-28_001870.1	expressed unknown protein	n/a;n/a;n/a	NA	NA
comp20282_c0_seq1.p1	Ec-28_001890.2	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp32579_c0_seq9.p1	Ec-28_001900.1	PC-Esterase	n/a;n/a;n/a	IPR026057: PC-Esterase	NA
comp14559_c0_seq1.p1	Ec-28_001940.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19994_c0_seq1.p1	Ec-28_001970.1	Pinin/SDK/MemA protein	n/a;n/a;n/a	IPR006786: Pinin/SDK/MemA protein; Coil:	NA
comp33620_c0_seq1.p1	Ec-28_001980.1	Plastid lipid-associated protein/fibrillin conserved domain	GO:0005198;n/a	IPR006843: Plastid lipid-associated protein/fibrillin conserved domain	NA
comp21444_c0_seq1.p1	Ec-28_001990.1	Zinc finger, DHHC-type, palmitoyltransferase	GO:0008270	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR001594: Zinc finger, DHHC-type, palmitoyltransferase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR22883: ; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20620_c0_seq2.p1	Ec-28_002000.1	Protein of unknown function DUF583	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR007607: Protein of unknown function DUF583; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32076_c0_seq2.p1	Ec-28_002010.1	Protein of unknown function DUF583	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR007607: Protein of unknown function DUF583; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM:	NA
comp32279_c2_seq12.p1	Ec-28_002020.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp32279_c2_seq2.p1	Ec-28_002030.1	DEAD box helicase	n/a;n/a;n/a	PTHR13710: ; IPR011991: Winged helix-turn-helix DNA-binding domain; IPR004589: DNA helicase, ATP-dependent, RecQ type; IPR011545: DEAD/DEAH box helicase domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR014001: Helicase superfamily 1/2, ATP-binding domain; IPR001650: Helicase, C-terminal	KOG0351
comp32196_c0_seq8.p2	Ec-28_002040.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32618_c1_seq1.p1	Ec-28_002090.1	conserved hypothetical protein	NA	IPR025638: Protein of unknown function DUF4336; IPR001279: Beta-lactamase-like	NA
comp31234_c0_seq1.p2	Ec-28_002100.1	Protein of unknown function DUF583	GO:0031177	IPR007607: Protein of unknown function DUF583	NA
comp32808_c1_seq3.p1	Ec-28_002110.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp32248_c6_seq2.p1	Ec-28_002120.1	Protein of unknown function DUF583	n/a;n/a;n/a	IPR007607: Protein of unknown function DUF583	NA
comp25371_c0_seq1.p1	Ec-28_002130.1	sexually induced protein 3	n/a;n/a;n/a	PTHR24035: ; G3DSA:2.10.25.10: ; SIGNAL_PEPTIDE: Signal peptide region; IPR000742: Epidermal growth factor-like domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR013032: EGF-like, conserved site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; PR00011: Type III EGF-like signature; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR013111: EGF-like domain, extracellular; SignalP-noTM: ; G3DSA:2.170.300.10: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27159_c1_seq1.p1	Ec-28_002140.1	NUDIX hydrolase domain	GO:0016787	IPR015797: NUDIX hydrolase domain-like; IPR000086: NUDIX hydrolase domain	NA
comp26697_c0_seq3.p1	Ec-28_002150.1	Mitochondrial intermediate peptidase (N-terminal)	GO:0004222;GO:0006508	PTHR11804: ; IPR024077: Neurolysin/Thimet oligopeptidase, domain 2; IPR001567: Peptidase M3A/M3B; IPR024080: Neurolysin/Thimet oligopeptidase, N-terminal; IPR024079: Metallopeptidase, catalytic domain; Coil: ; SSF55486:	NA
comp25208_c0_seq2.p1	Ec-28_002160.1	hypothetical protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30477_c0_seq6.p1	Ec-28_002170.1	Flagellin assembly, membrane protein MviN	GO:0006855;GO:0015238;GO:0015297;GO:0016020;GO:0055085	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR11206: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR004268: Peptidoglycan biosynthesis protein MurJ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp26777_c0_seq1.p1	Ec-28_002230.2	hypothetical protein	n/a;n/a;n/a	IPR004087: K Homology domain; IPR004088: K Homology domain, type 1; Coil:	NA
comp24624_c0_seq1.p1	Ec-28_002250.1	Histone H3, probable CenH3	GO:0003677	NA	NA
comp31590_c0_seq3.p1	Ec-28_002260.1	Alpha/Beta hydrolase fold	n/a;n/a;n/a	IPR029059: Alpha/beta hydrolase fold-5; IPR029058: Alpha/Beta hydrolase fold	NA
comp31590_c0_seq5.p1	Ec-28_002260.2	Alpha/Beta hydrolase fold	n/a;n/a;n/a	IPR029059: Alpha/beta hydrolase fold-5	NA
comp31530_c2_seq3.p1	Ec-28_002280.1	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	PTHR23109: ; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; IPR019410: Nicotinamide N-methyltransferase-like	NA
comp31530_c2_seq2.p2	Ec-28_002280.2	S-adenosyl-L-methionine-dependent methyltransferase	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; PTHR14614:SF29: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR14614:	NA
comp30930_c0_seq1.p1	Ec-28_002290.1	Serine-threonine/tyrosine-protein kinase catalytic domain	GO:0004672;GO:0006468	PTHR23257: ; IPR000719: Protein kinase domain; G3DSA:1.10.510.10: ; PTHR23257:SF513: ; IPR001245: Serine-threonine/tyrosine-protein kinase catalytic domain; IPR011009: Protein kinase-like domain	NA
comp22021_c0_seq1.p1	Ec-28_002300.1	SET domain protein	GO:0005515	NA	NA
comp26189_c0_seq1.p1	Ec-28_002310.1	Rab3 GTPase-activating protein catalytic subunit	GO:0005097	IPR026147: Rab3 GTPase-activating protein catalytic subunit; Coil:	NA
comp33904_c0_seq1.p1	Ec-28_002330.1	Vesicle coat complex COPI, epsilon subunit	GO:0006890;GO:0005515;GO:0005198	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; IPR006822: Coatomer, epsilon subunit; IPR013026: Tetratricopeptide repeat-containing domain	KOG3081
comp12222_c0_seq1.p1	Ec-28_002370.1	Copine	n/a;n/a;n/a	IPR000008: C2 domain; IPR010734: Copine; PTHR10857: ; IPR002035: von Willebrand factor, type A	KOG1327
comp29552_c1_seq2.p1	Ec-28_002390.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp14947_c0_seq1.p1	Ec-28_002410.1	Sar1A, Ras superfamily GTPase	GO:0005622;GO:0006886;GO:0005525	IPR024156: Small GTPase superfamily, ARF type; PTHR11711: ; IPR005225: Small GTP-binding protein domain; IPR006687: Small GTPase superfamily, SAR1-type; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR006689: Small GTPase superfamily, ARF/SAR type	NA
comp32886_c0_seq7.p1	Ec-28_002420.1	RNA recognition motif domain	GO:0003676;GO:0000166	SSF54928: ; IPR000504: RNA recognition motif domain; IPR012677: Nucleotide-binding alpha-beta plait domain	NA
comp24572_c0_seq1.p1	Ec-28_002430.2	ATPase, V1 complex, subunit H, C-terminal	GO:0000221;GO:0015991;GO:0016820	PTHR10698:SF0: ; PF03224: V-ATPase subunit H; IPR011987: ATPase, V1 complex, subunit H, C-terminal; IPR004908: ATPase, V1 complex, subunit H; IPR011989: Armadillo-like helical; IPR016024: Armadillo-type fold	NA
comp31901_c0_seq21.p1	Ec-28_002440.1	1,3-beta-glucan synthase, family GT48	GO:0000148;GO:0003843;GO:0006075;GO:0016020	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR12741: ; IPR003440: Glycosyl transferase, family 48; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR026899: 1,3-beta-glucan synthase subunit FKS1-like, domain-1; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20228_c0_seq1.p1	Ec-28_002460.1	Glycosyltransferase, family GT47	GO:0016020;GO:0016021;GO:0015012	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004263: Exostosin-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR027674: Exostosin 3/Exostosin-like 3; PTHR11062: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24335_c0_seq1.p1	Ec-28_002510.1	Galactose mutarotase-like domain	GO:0003824;GO:0005975;GO:0030246	IPR008183: Aldose 1-/Glucose-6-phosphate 1-epimerase; IPR011013: Galactose mutarotase-like domain; IPR014718: Glycoside hydrolase-type carbohydrate-binding, subgroup; PTHR10091: ; IPR018052: Aldose 1-epimerase, conserved site	NA
comp33038_c0_seq18.p1	Ec-28_002560.1	Alkaline phosphatase D-related	n/a;n/a;n/a	IPR029052: Metallo-dependent phosphatase-like; IPR018946: Alkaline phosphatase D-related	NA
comp30581_c0_seq3.p1	Ec-28_002570.2	Peptidase A22A, presenilin	GO:0004190;GO:0016021	IPR006639: Presenilin/signal peptide peptidase; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR10202:SF13: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR001108: Peptidase A22A, presenilin	NA
comp30531_c0_seq6.p1	Ec-28_002580.1	Protein phosphatase 2C (PP2C)-like domain	GO:0003824;GO:0004722;GO:0006470	IPR001932: PPM-type phosphatase domain; IPR015655: Protein phosphatase 2C	NA
comp32611_c1_seq1.p1	Ec-28_002600.1	Major intrinsic protein	GO:0016020;GO:0006810;GO:0005215	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR023271: Aquaporin-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR022357: Major intrinsic protein, conserved site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000425: Major intrinsic protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32410_c0_seq2.p1	Ec-28_002620.1	hypothetical protein	n/a;n/a;n/a	NA	NA
comp33055_c0_seq3.p1	Ec-28_002630.1	2-Isopropylmalate synthase	GO:0003852;GO:0046912;GO:0009098;GO:0019752	IPR013785: Aldolase-type TIM barrel; SIGNAL_PEPTIDE: Signal peptide region; IPR000891: Pyruvate carboxyltransferase; IPR005675: Citramalate synthase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; PTHR10277: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002034: Alpha-isopropylmalate/homocitrate synthase, conserved site; IPR013709: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain; SSF51569: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG2367
comp24734_c0_seq1.p1	Ec-28_002660.1	Enoyl-CoA hydratase	GO:0008152;GO:0003824	IPR029045: ClpP/crotonase-like domain; IPR001753: Crotonase superfamily; PTHR11941:	KOG0016
comp24960_c0_seq4.p1	Ec-28_002670.1	Hypothetical protein	n/a;n/a;n/a	NA	NA
comp19450_c0_seq1.p1	Ec-28_002710.1	Nonaspanin (TM9SF)	GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR004240: Nonaspanin (TM9SF); TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21286_c0_seq1.p1	Ec-28_002720.1	conserved unknown protein	n/a;n/a;n/a	PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp114816_c0_seq1.p1	Ec-28_002730.3	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp30110_c0_seq1.p1	Ec-28_002770.1	FAD dependent oxidoreductase	GO:0055114;GO:0016491	PTHR13847: ; IPR006076: FAD dependent oxidoreductase; G3DSA:3.50.50.60: ; SSF51905: ; SignalP-TM:	NA
comp11955_c0_seq1.p1	Ec-28_002810.1	Ribosomal protein S16 domain	GO:0003735;GO:0005622;GO:0005840;GO:0006412	IPR000307: Ribosomal protein S16; IPR023803: Ribosomal protein S16 domain	NA
comp32463_c2_seq5.p1	Ec-28_002820.1	Pectin lyase fold/virulence factor	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR011050: Pectin lyase fold/virulence factor; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31261_c0_seq7.p3	Ec-28_002840.1	putative initiation factor eIF3 g subunit	GO:0005737;GO:0003743;GO:0000166;GO:0005852	SSF54928: ; IPR000504: RNA recognition motif domain; IPR024675: Eukaryotic translation initiation factor 3 subunit G, N-terminal; IPR012677: Nucleotide-binding alpha-beta plait domain; IPR017334: Eukaryotic translation initiation factor 3 subunit G	NA
comp21494_c0_seq1.p1	Ec-28_002880.1	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008168	IPR004033: UbiE/COQ5 methyltransferase; IPR023576: UbiE/COQ5 methyltransferase, conserved site; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; PS51257: Prokaryotic membrane lipoprotein lipid attachment site profile.; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR10108: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp21494_c0_seq1.p2	Ec-28_002900.1	eukaryotic translation initiation factor 4E- like 1	GO:0003723;GO:0005737;GO:0006413;GO:0003743	IPR001040: Translation Initiation factor eIF- 4e; IPR023398: Translation Initiation factor eIF- 4e-like domain	NA
comp21550_c0_seq2.p1	Ec-28_002910.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp31261_c0_seq7.p1	Ec-28_002920.1	Ankyrin repeat-containing domain	n/a;GO:0005515	IPR020683: Ankyrin repeat-containing domain; PTHR24198: ; Coil: ; IPR002110: Ankyrin repeat	NA
comp27326_c0_seq1.p1	Ec-28_002930.1	tRNA-specific 2-thiouridylase	GO:0008033;GO:0016783;GO:0016740	IPR014729: Rossmann-like alpha/beta/alpha sandwich fold; IPR004506: tRNA-specific 2-thiouridylase; SSF52402: ; G3DSA:2.40.30.10: ; IPR023382: Adenine nucleotide alpha hydrolase-like domains	NA
comp30484_c0_seq5.p1	Ec-28_002940.1	Zinc finger, RING/FYVE/PHD-type	n/a;n/a;n/a	IPR001841: Zinc finger, RING-type; SIGNAL_PEPTIDE: Signal peptide region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR12477: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR013083: Zinc finger, RING/FYVE/PHD-type; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp33718_c0_seq1.p1	Ec-28_002960.1	Integrase, N-terminal zinc-binding domain-like	n/a;n/a;n/a	IPR002876: Transcriptional regulator TACO1-like; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR017856: Integrase, N-terminal zinc-binding domain-like; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR026564: Transcriptional regulator TACO1-like, domain 3; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR026563: Transcriptional regulator TACO1-like, domain 2; IPR029072: YebC-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp27954_c0_seq1.p1	Ec-28_002970.1	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B, C-terminal	GO:0006412;GO:0016884	IPR003789: Aspartyl/glutamyl-tRNA amidotransferase subunit B-related; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR019004: Uncharacterised domain YOR215C, mitochondrial; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR023168: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B, C-terminal; G3DSA:1.10.1510.10: ; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp28755_c0_seq2.p1	Ec-28_002990.1	Heavy metal-associated domain, HMA	GO:0030001;GO:0046872	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR008250: P-type ATPase, A domain; SSF81653: ; IPR023214: HAD-like domain; G3DSA:3.30.70.100: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF81665: ; IPR001757: P-type ATPase; PR00942: Copper-transporting ATPase 1 signature; PF00702: haloacid dehalogenase-like hydrolase; IPR018303: P-type ATPase, phosphorylation site; IPR006121: Heavy metal-associated domain, HMA; IPR023299: P-type ATPase, cytoplasmic domain N; PTHR24093: ; IPR017969: Heavy-metal-associated, conserved site; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31821_c0_seq3.p1	Ec-28_003040.1	Myosin head, motor domain	GO:0005524;GO:0003774;GO:0005515;GO:0016459	IPR001609: Myosin head, motor domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; Coil: ; G3DSA:1.20.5.190: ; PTHR13140: ; IPR000048: IQ motif, EF-hand binding site	NA
comp31228_c0_seq1.p1	Ec-28_003050.2	Pentatricopeptide repeat	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002885: Pentatricopeptide repeat; Coil: ; PTHR24015: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp12814_c0_seq1.p1	Ec-28_003060.1	Peptidase S26A, signal peptidase I	GO:0006508;GO:0008236;GO:0016020	IPR019759: Peptidase S24/S26A/S26B; IPR019533: Peptidase S26; IPR015927: Peptidase S24/S26A/S26B/S26C; IPR000223: Peptidase S26A, signal peptidase I; IPR019757: Peptidase S26A, signal peptidase I, lysine active site; IPR028360: Peptidase S24/S26, beta-ribbon domain	NA
comp28963_c0_seq4.p1	Ec-28_003080.1	3-ketoacyl-CoA synthase	GO:0008152;GO:0003824;GO:0008415	IPR016038: Thiolase-like, subgroup; IPR016039: Thiolase-like; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR012392: Very-long-chain 3-ketoacyl-CoA synthase; IPR013747: 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III C-terminal; IPR013601: FAE1/Type III polyketide synthase-like protein; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30854_c0_seq4.p1	Ec-28_003110.1	Arf GTPase activating protein	GO:0032312;GO:0008060;GO:0005515;GO:0008270	IPR001164: Arf GTPase activating protein; IPR000008: C2 domain; SSF57863: ; PTHR23180:	NA
comp29825_c0_seq2.p2	Ec-28_003120.1	Light harvesting complex protein	GO:0009765;GO:0016020	SIGNAL_PEPTIDE: Signal peptide region; IPR022796: Chlorophyll A-B binding protein; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR023329: Chlorophyll a/b binding protein domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR001344: Chlorophyll A-B binding protein, plant; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp12723_c0_seq1.p1	Ec-28_003140.1	Vesicle transport protein, SFT2-like	GO:0006810;GO:0016021	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR007305: Vesicle transport protein, Got1/SFT2-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011691: Vesicle transport protein, SFT2-like; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28964_c0_seq1.p1	Ec-28_003150.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; PF13424: Tetratricopeptide repeat; IPR011990: Tetratricopeptide-like helical domain; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; IPR002151: Kinesin light chain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; PTHR19959: ; SignalP-noTM: ; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32008_c0_seq2.p1	Ec-28_003160.1	basal body protein	NA	Coil: ; SSF57997:	NA
comp28474_c0_seq1.p1	Ec-28_003180.1	hypothetical protein	n/a;n/a;n/a	Coil:	NA
comp21370_c0_seq1.p1	Ec-28_003190.1	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	GO:0008270;GO:0009086;GO:0003871	G3DSA:3.20.20.210: ; PTHR30519: ; IPR013215: Cobalamin-independent methionine synthase MetE, N-terminal; SSF51726: ; IPR002629: Cobalamin-independent methionine synthase MetE, C-terminal/archaeal; IPR006276: Cobalamin-independent methionine synthase	KOG2263
comp27661_c0_seq1.p1	Ec-28_003200.1	Ubiquitin fusion degradation protein UFD1	GO:0006511	IPR004854: Ubiquitin fusion degradation protein UFD1	NA
comp34279_c0_seq1.p1	Ec-28_003210.1	Dolichol-phosphate mannosyltransferase subunit 3	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR013174: Dolichol-phosphate mannosyltransferase subunit 3; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR16433: ; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp29731_c0_seq1.p1	Ec-28_003240.1	Putative phospholipase	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR029058: Alpha/Beta hydrolase fold; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR022742: Putative lysophospholipase; PTHR11614: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	no relat
comp32520_c3_seq6.p1	Ec-28_003250.2	GINS complex, subunit Sld5	n/a;n/a;n/a	SSF160059: ; PTHR21206:SF0: ; IPR008591: GINS complex subunit Sld5; Coil: ; SSF158573: ; IPR031633: DNA replication complex GINS protein SLD5, C-terminal	NA
comp32245_c0_seq19.p1	Ec-28_003280.1	expressed unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24530_c0_seq1.p1	Ec-28_003310.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp33063_c0_seq5.p1	Ec-28_003320.1	vanadium-dependent bromoperoxidase	GO:0016020;GO:0003824	IPR016119: Bromoperoxidase/chloroperoxidase, C-terminal; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR000326: Phosphatidic acid phosphatase type 2/haloperoxidase; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp31458_c2_seq2.p1	Ec-28_003325.1	hypothetical protein	GO:0003677;GO:0003824	SIGNAL_PEPTIDE: Signal peptide region; IPR020045: 5'-3' exonuclease, C-terminal domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR10133: ; IPR020046: 5'-3' exonuclease, alpha-helical arch, N-terminal; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; G3DSA:1.10.150.20: ; IPR002421: 5'-3' exonuclease, N-terminal; IPR008918: Helix-hairpin-helix motif, class 2; IPR029060: PIN domain-like; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp30046_c1_seq1.p1	Ec-28_003330.1	Leucine rich repeat receptor kinase	GO:0003677;GO:0005634;GO:0003824	IPR017441: Protein kinase, ATP binding site; IPR002290: Serine/threonine/dual specificity protein kinase, catalytic domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR011009: Protein kinase-like domain; SignalP-TM: ; PTHR23257: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR000719: Protein kinase domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; G3DSA:3.80.10.10: ; SSF52058: ; G3DSA:3.30.200.20: ; SIGNAL_PEPTIDE: Signal peptide region; IPR001245: Serine-threonine/tyrosine-protein kinase catalytic domain; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SignalP-noTM: ; G3DSA:1.10.510.10: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24846_c1_seq1.p1	Ec-28_003360.1	expressed unknown protein	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32705_c2_seq5.p1	Ec-28_003370.1	Winged helix-turn-helix DNA-binding domain	n/a;n/a;n/a	IPR011991: Winged helix-turn-helix DNA-binding domain; SSF46785: ; SSF50729: ; IPR001849: Pleckstrin homology domain; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR011993: Pleckstrin homology-like domain; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR000591: DEP domain	NA
comp26816_c0_seq1.p1	Ec-28_003380.1	conserved unknown protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp34282_c0_seq1.p1	Ec-28_003390.1	Ubiquitin	GO:0006464;GO:0005515	G3DSA:3.10.20.90: ; PTHR10666: ; IPR019956: Ubiquitin; IPR029071: Ubiquitin-related domain; IPR000626: Ubiquitin-like	NA
comp30559_c0_seq4.p1	Ec-28_003410.1	expressed unknown protein	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp25943_c0_seq4.p1	Ec-28_003430.1	Hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp32861_c0_seq17.p1	Ec-28_003440.1	ExV-1-7 domain protein	NA	NA	NA
comp11676_c0_seq1.p1	Ec-28_003470.1	phosphoenolpyruvate carboxylase	GO:0008964;GO:0006099;GO:0015977	PTHR30523: ; IPR018129: Phosphoenolpyruvate carboxylase, active site; IPR015813: Pyruvate/Phosphoenolpyruvate kinase-like domain; G3DSA:1.20.1440.90: ; IPR022805: Phosphoenolpyruvate carboxylase, bacterial/plant-type; Coil: ; IPR021135: Phosphoenolpyruvate carboxylase	NA
comp27507_c1_seq2.p1	Ec-28_003500.1	TIC 20 related, plastid import	GO:0005509	IPR018247: EF-Hand 1, calcium-binding site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR011992: EF-hand domain pair; IPR002048: EF-hand domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SSF47473: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp24744_c0_seq1.p2	Ec-28_003510.1	Magnesium transporter	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; IPR018937: Magnesium transporter; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31084_c0_seq3.p1	Ec-28_003520.1	HD/PDEase domain	GO:0003824	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF109604: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002073: 3'5'-cyclic nucleotide phosphodiesterase, catalytic domain; IPR023174: 3'5'-cyclic nucleotide phosphodiesterase, conserved site; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11347: ; IPR023088: 3'5'-cyclic nucleotide phosphodiesterase; IPR003607: HD/PDEase domain; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31084_c0_seq6.p2	Ec-28_003530.1	conserved unknown protein	n/a;n/a;n/a	NA	NA
comp32922_c2_seq2.p1	Ec-28_003540.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp19484_c0_seq1.p1	Ec-28_003550.1	Zinc finger, RING-type	GO:0005515;GO:0008270	IPR017907: Zinc finger, RING-type, conserved site; IPR001841: Zinc finger, RING-type; PTHR15898: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SSF57850: ; IPR018957: Zinc finger, C3HC4 RING-type; IPR013083: Zinc finger, RING/FYVE/PHD-type; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp30837_c0_seq2.p1	Ec-28_003570.1	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	IPR027417: P-loop containing nucleoside triphosphate hydrolase; PTHR13748: ; IPR003495: CobW/HypB/UreG domain; IPR011629: Cobalamin (vitamin B12) biosynthesis CobW-like, C-terminal	NA
comp30837_c0_seq4.p1	Ec-28_003570.3	P-loop containing nucleoside triphosphate hydrolase	n/a;n/a;n/a	NA	NA
comp13718_c0_seq1.p1	Ec-28_003580.2	expressed unknown protein	GO:0031177	PTHR16830: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR011004: Trimeric LpxA-like; G3DSA:2.160.10.10: ; Coil: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp31898_c0_seq13.p2	Ec-28_003620.1	Pseudouridine synthase, TruD	GO:0003723;GO:0001522;GO:0009451;GO:0009982	IPR020103: Pseudouridine synthase, catalytic domain; IPR001656: Pseudouridine synthase, TruD; IPR011760: Pseudouridine synthase, TruD, insertion domain	NA
comp31898_c0_seq13.p1	Ec-28_003630.1	P-type ATPase	GO:0016021	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; IPR008250: P-type ATPase, A domain; SSF81653: ; IPR023214: HAD-like domain; G3DSA:3.30.70.100: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR027256: P-type ATPase, subfamily IB; IPR001757: P-type ATPase; SSF81665: ; IPR006122: Heavy metal-associated domain, copper ion-binding; PR00942: Copper-transporting ATPase 1 signature; IPR018303: P-type ATPase, phosphorylation site; IPR006121: Heavy metal-associated domain, HMA; IPR023299: P-type ATPase, cytoplasmic domain N; PTHR24093: ; IPR017969: Heavy-metal-associated, conserved site; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp21347_c0_seq1.p1	Ec-28_003670.1	Triose-phosphate transporter domain	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; SSF103481: ; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004853: Triose-phosphate transporter domain; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR11132: ; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28202_c1_seq2.p1	Ec-28_003680.1	Pre-rRNA-processing protein TSR2	n/a;n/a;n/a	IPR019398: Pre-rRNA-processing protein TSR2; PTHR21250:	NA
comp71210_c0_seq1.p1	Ec-28_003690.3	Quinoprotein alcohol dehydrogenase-like superfamily	n/a;n/a;n/a	NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SIGNAL_PEPTIDE: Signal peptide region; IPR017986: WD40-repeat-containing domain; IPR015943: WD40/YVTN repeat-like-containing domain; IPR001680: WD40 repeat; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.	NA
comp48002_c0_seq1.p1	Ec-28_003700.1	Ankyrin repeat-containing domain	GO:0005515	NA	NA
comp28976_c0_seq4.p1	Ec-28_003710.1	hypothetical protein	n/a;n/a;n/a	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp28651_c0_seq1.p1	Ec-28_003720.1	expressed unknown protein	n/a;n/a;n/a	Coil:	NA
comp16314_c0_seq1.p1	Ec-28_003730.1	Selenoprotein S	GO:0006886;GO:0030176;GO:0008430	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; Coil: ; IPR009703: Selenoprotein S; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp20745_c0_seq1.p1	Ec-28_003740.1	peroxidase	GO:0020037;GO:0055114;GO:0006979;GO:0004601	G3DSA:1.10.520.10: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR019794: Peroxidase, active site; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; IPR010255: Haem peroxidase; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR002207: Plant ascorbate peroxidase; SignalP-noTM: ; G3DSA:1.10.420.10: ; IPR019793: Peroxidases heam-ligand binding site; PTHR31356: ; IPR002016: Haem peroxidase, plant/fungal/bacterial; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp24138_c0_seq1.p1	Ec-28_003750.2	S-adenosyl-L-methionine-dependent methyltransferase	GO:0008171	SIGNAL_PEPTIDE: Signal peptide region; IPR029063: S-adenosyl-L-methionine-dependent methyltransferase; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; PTHR10509: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR002935: O-methyltransferase, family 3; PTHR10509:SF14: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	KOG1663
comp22310_c0_seq2.p1	Ec-28_003760.1	Metallo-dependent phosphatase-like	GO:0016787	CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR029052: Metallo-dependent phosphatase-like; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; IPR004843: Calcineurin-like phosphoesterase domain, apaH type; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.; PTHR31302:	NA
comp30198_c0_seq3.p1	Ec-28_003830.1	Tetratricopeptide-like helical domain	GO:0005515	SSF48452: ; IPR011990: Tetratricopeptide-like helical domain; PF13414: TPR repeat; PTHR15704: ; IPR013026: Tetratricopeptide repeat-containing domain; IPR019734: Tetratricopeptide repeat	NA
comp32873_c1_seq7.p1	Ec-28_003850.1	Mitochondrial carrier domain	GO:0005215;GO:0005488;GO:0005743;GO:0006810;GO:0016020;GO:0055085	PTHR24089: ; SIGNAL_PEPTIDE: Signal peptide region; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; IPR023395: Mitochondrial carrier domain; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; IPR018108: Mitochondrial substrate/solute carrier	NA
comp21119_c0_seq1.p1	Ec-28_003860.1	Major facilitator superfamily domain	n/a;n/a;n/a	TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.; SIGNAL_PEPTIDE: Signal peptide region; PTHR11360: ; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SignalP-TM: ; CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.; IPR020846: Major facilitator superfamily domain; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; SignalP-noTM: ; G3DSA:1.20.1250.20: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; TRANSMEMBRANE: Region of a membrane-bound protein predicted to be embedded in the membrane.	NA
comp23438_c0_seq1.p1	Ec-28_003870.3	conserved unknown protein	n/a;n/a;n/a	SIGNAL_PEPTIDE: Signal peptide region; PF14741: N-terminal glycosyl-hydrolase-114-associated domain; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; SignalP-TM: ; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region; Coil: ; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.	NA
comp32167_c0_seq26.p1	Ec-sdr_f_000040.1	Casein kinase	NA	NA	NA
comp34001_c0_seq1.p1	Ec-sdr_f_000080.1	Chloroplast clp protease P	NA	NA	NA
comp31508_c0_seq1.p1	Ec-sdr_f_000090.1	GTPase activating protein	NA	NA	NA
comp24675_c0_seq4.p1	Ec-sdr_f_000110.1	LRR protein	GO:0005515	NA	NA
comp30088_c0_seq2.p1	Ec-sdr_f_000170.1	Conserved hypothetical protein	NA	NA	NA