**Table 2.** The list of the identified proteins in the thylakoid membranes of the *ch1-1* plants by LC-MS/MS analysis.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus | TAIR Description | Mascot score | Number of matched peptides |
| AT1G01170 | Protein of unknown function (DUF1138) | 247 | 5 |
| AT1G01620 | plasma membrane intrinsic protein 1C | 92 | 2 |
| AT1G02280 | translocon at the outer envelope membrane of chloroplasts 33 | 64 | 1 |
| AT1G02910 | tetratricopeptide repeat (TPR)-containing protein | 107 | 3 |
| AT1G03130 | photosystem I subunit D-2 | 2603 | 76 |
| AT1G03160 | FZO-like | 147 | 3 |
| AT1G03600 | photosystem II family protein | 1296 | 33 |
| AT1G03630 | protochlorophyllide oxidoreductase C | 1324 | 28 |
| AT1G03860 | prohibitin 2 | 39 | 1 |
| AT1G04620 | coenzyme F420 hydrogenase family / dehydrogenase, beta subunit family | 312 | 6 |
| AT1G04630 | GRIM-19 protein | 239 | 3 |
| AT1G05140 | Peptidase M50 family protein | 187 | 4 |
| AT1G05190 | Ribosomal protein L6 family | 141 | 3 |
| AT1G05790 | lipase class 3 family protein | 705 | 18 |
| AT1G06430 | FTSH protease 8 | 1235 | 28 |
| AT1G06680 | photosystem II subunit P-1 | 2293 | 46 |
| AT1G06690 | NAD(P)-linked oxidoreductase superfamily protein | 88 | 2 |
| AT1G06950 | translocon at the inner envelope membrane of chloroplasts 110 | 937 | 17 |
| AT1G07070 | Ribosomal protein L35Ae family protein | 36 | 1 |
| AT1G07320 | ribosomal protein L4 | 72 | 2 |
| AT1G07660 | Histone superfamily protein | 36 | 1 |
| AT1G07920 | GTP binding Elongation factor Tu family protein | 669 | 14 |
| AT1G08640 | Chloroplast J-like domain 1 | 80 | 2 |
| AT1G08880 | Histone superfamily protein | 124 | 3 |
| AT1G09170 | P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain | 38 | 1 |
| AT1G10610 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 36 | 1 |
| AT1G11180 | Secretory carrier membrane protein (SCAMP) family protein | 74 | 2 |
| AT1G11270 | F-box and associated interaction domains-containing protein | 43 | 1 |
| AT1G11660 | heat shock protein 70 (Hsp 70) family protein | 35 | 1 |
| AT1G12250 | Pentapeptide repeat-containing protein | 468 | 7 |
| AT1G12900 | glyceraldehyde 3-phosphate dehydrogenase A subunit 2 | 395 | 8 |
| AT1G13440 | glyceraldehyde-3-phosphate dehydrogenase C2 | 52 | 1 |
| AT1G14150 | PsbQ-like 2 | 458 | 8 |
| AT1G14345 | NAD(P)-linked oxidoreductase superfamily protein | 470 | 8 |
| AT1G15210 | pleiotropic drug resistance 7 | 53 | 1 |
| AT1G15480 | Tetratricopeptide repeat (TPR)-like superfamily protein | 36 | 1 |
| AT1G15690 | Inorganic H pyrophosphatase family protein | 259 | 5 |
| AT1G15820 | light harvesting complex photosystem II subunit 6 | 2806 | 49 |
| AT1G15980 | NDH-dependent cyclic electron flow 1 | 892 | 17 |
| AT1G16350 | Aldolase-type TIM barrel family protein | 36 | 1 |
| AT1G18060 | unknown protein | 88 | 2 |
| AT1G18170 | FKBP-like peptidyl-prolyl cis-trans isomerase family protein | 623 | 11 |
| AT1G18730 | NDH dependent flow 6 | 52 | 1 |
| AT1G19150 | photosystem I light harvesting complex gene 6 | 39 | 1 |
| AT1G20020 | ferredoxin-NADP()-oxidoreductase 2 | 3235 | 72 |
| AT1G20180 | Protein of unknown function (DUF677) | 37 | 1 |
| AT1G20260 | ATPase, V1 complex, subunit B protein | 95 | 2 |
| AT1G20620 | catalase 3 | 642 | 12 |
| AT1G21500 | unknown protein | 822 | 19 |
| AT1G22410 | Class-II DAHP synthetase family protein | 39 | 1 |
| AT1G22700 | Tetratricopeptide repeat (TPR)-like superfamily protein | 171 | 4 |
| AT1G24360 | NAD(P)-binding Rossmann-fold superfamily protein | 114 | 3 |
| AT1G26380 | FAD-binding Berberine family protein | 37 | 1 |
| AT1G28380 | MAC/Perforin domain-containing protein | 38 | 1 |
| AT1G29910 | chlorophyll A/B binding protein 3 | 3814 | 90 |
| AT1G30380 | photosystem I subunit K | 373 | 10 |
| AT1G31330 | photosystem I subunit F | 2525 | 60 |
| AT1G32220 | NAD(P)-binding Rossmann-fold superfamily protein | 410 | 7 |
| AT1G32770 | NAC domain containing protein 12 | 38 | 1 |
| AT1G34000 | one-helix protein 2 | 538 | 17 |
| AT1G35680 | Ribosomal protein L21 | 50 | 1 |
| AT1G42960 | expressed protein localized to the inner membrane of the chloroplast. | 43 | 1 |
| AT1G44575 | Chlorophyll A-B binding family protein | 4965 | 121 |
| AT1G45474 | photosystem I light harvesting complex gene 5 | 648 | 13 |
| AT1G48030 | mitochondrial lipoamide dehydrogenase 1 | 210 | 4 |
| AT1G49240 | actin 8 | 55 | 1 |
| AT1G50250 | FTSH protease 1 | 2321 | 46 |
| AT1G50450 | Saccharopine dehydrogenase | 352 | 6 |
| AT1G51110 | Plastid-lipid associated protein PAP / fibrillin family protein | 613 | 14 |
| AT1G51400 | Photosystem II 5 kD protein | 323 | 6 |
| AT1G51980 | Insulinase (Peptidase family M16) protein | 362 | 8 |
| AT1G52220 | FUNCTIONS IN: molecular\_function unknown | 145 | 3 |
| AT1G52230 | photosystem I subunit H2 | 796 | 25 |
| AT1G53240 | Lactate/malate dehydrogenase family protein | 42 | 1 |
| AT1G53310 | phosphoenolpyruvate carboxylase 1 | 36 | 1 |
| AT1G54350 | ABC transporter family protein | 67 | 1 |
| AT1G54500 | Rubredoxin-like superfamily protein | 556 | 9 |
| AT1G54520 | unknown protein | 268 | 5 |
| AT1G54780 | thylakoid lumen 18.3 kDa protein | 3973 | 88 |
| AT1G55480 | protein containing PDZ domain, a K-box domain, and a TPR region | 246 | 9 |
| AT1G55670 | photosystem I subunit G | 909 | 23 |
| AT1G56070 | Ribosomal protein S5/Elongation factor G/III/V family protein | 54 | 1 |
| AT1G56500 | haloacid dehalogenase-like hydrolase family protein | 1760 | 35 |
| AT1G59840 | cofactor assembly of complex C | 39 | 1 |
| AT1G61520 | photosystem I light harvesting complex gene 3 | 3179 | 76 |
| AT1G64680 | unknown protein | 45 | 1 |
| AT1G64770 | NDH-dependent cyclic electron flow 1 | 399 | 9 |
| AT1G65230 | Uncharacterized conserved protein (DUF2358) | 187 | 4 |
| AT1G65260 | plastid transcriptionally active 4 | 590 | 10 |
| AT1G66200 | glutamine synthase clone F11 | 44 | 1 |
| AT1G66300 | F-box/RNI-like/FBD-like domains-containing protein | 35 | 1 |
| AT1G67090 | ribulose bisphosphate carboxylase small chain 1A | 76 | 2 |
| AT1G67580 | Protein kinase superfamily protein | 39 | 1 |
| AT1G67700 | unknown protein | 58 | 1 |
| AT1G68830 | STT7 homolog STN7 | 45 | 1 |
| AT1G69440 | Argonaute family protein | 36 | 1 |
| AT1G71500 | Rieske (2Fe-2S) domain-containing protein | 2583 | 36 |
| AT1G71810 | Protein kinase superfamily protein | 251 | 5 |
| AT1G72150 | PATELLIN 1 | 36 | 1 |
| AT1G72640 | NAD(P)-binding Rossmann-fold superfamily protein | 63 | 1 |
| AT1G73060 | Low PSII Accumulation 3 | 40 | 1 |
| AT1G73690 | cyclin-dependent kinase D1 | 35 | 1 |
| AT1G73990 | signal peptide peptidase | 247 | 4 |
| AT1G74070 | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | 620 | 15 |
| AT1G74470 | Pyridine nucleotide-disulphide oxidoreductase family protein | 2326 | 45 |
| AT1G74640 | alpha/beta-Hydrolases superfamily protein | 50 | 1 |
| AT1G74730 | Protein of unknown function (DUF1118) | 566 | 16 |
| AT1G74850 | plastid transcriptionally active 2 | 45 | 1 |
| AT1G74880 | NAD(P)H:plastoquinone dehydrogenase complex subunit O | 244 | 6 |
| AT1G77140 | vacuolar protein sorting 45 | 71 | 2 |
| AT1G77290 | Glutathione S-transferase family protein | 36 | 1 |
| AT1G77490 | thylakoidal ascorbate peroxidase | 830 | 15 |
| AT1G78140 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | 151 | 3 |
| AT1G78620 | Protein of unknown function DUF92, transmembrane | 39 | 1 |
| AT1G78630 | Ribosomal protein L13 family protein | 211 | 3 |
| AT1G78820 | D-mannose binding lectin protein with Apple-like carbohydrate-binding domain | 51 | 1 |
| AT1G78830 | Curculin-like (mannose-binding) lectin family protein | 91 | 2 |
| AT1G78900 | vacuolar ATP synthase subunit A | 209 | 4 |
| AT1G78915 | Tetratricopeptide repeat (TPR)-like superfamily protein | 197 | 4 |
| AT1G79040 | photosystem II subunit R | 859 | 31 |
| AT1G79600 | Protein kinase superfamily protein | 474 | 11 |
| AT1G80030 | Molecular chaperone Hsp40/DnaJ family protein | 156 | 3 |
| AT2G01140 | Aldolase superfamily protein | 208 | 6 |
| AT2G01870 | unknown protein | 96 | 4 |
| AT2G02170 | Remorin family protein | 37 | 1 |
| AT2G02740 | ssDNA-binding transcriptional regulator | 83 | 1 |
| AT2G03750 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | 38 | 1 |
| AT2G05070 | photosystem II light harvesting complex gene 2.2 | 4130 | 99 |
| AT2G05310 | unknown protein | 38 | 1 |
| AT2G05620 | proton gradient regulation 5 | 355 | 8 |
| AT2G05710 | aconitase 3 | 44 | 1 |
| AT2G07698 | ATPase, F1 complex, alpha subunit protein | 1177 | 25 |
| AT2G18710 | SECY homolog 1 | 137 | 3 |
| AT2G20260 | photosystem I subunit E-2 | 1796 | 37 |
| AT2G20450 | Ribosomal protein L14 | 35 | 1 |
| AT2G20890 | photosystem II reaction center PSB29 protein | 2309 | 51 |
| AT2G21330 | fructose-bisphosphate aldolase 1 | 4547 | 111 |
| AT2G21870 | copper ion binding | 52 | 1 |
| AT2G21960 | unknown protein | 303 | 7 |
| AT2G22170 | Lipase/lipooxygenase, PLAT/LH2 family protein | 75 | 1 |
| AT2G22230 | Thioesterase superfamily protein | 48 | 1 |
| AT2G22750 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 40 | 1 |
| AT2G23670 | homolog of Synechocystis YCF37 | 879 | 15 |
| AT2G24420 | DNA repair ATPase-related | 41 | 1 |
| AT2G26340 | unknown protein. | 64 | 1 |
| AT2G27710 | 60S acidic ribosomal protein family | 109 | 2 |
| AT2G27730 | copper ion binding | 543 | 7 |
| AT2G28630 | 3-ketoacyl-CoA synthase 12 | 45 | 1 |
| AT2G28800 | 63 kDa inner membrane family protein | 392 | 11 |
| AT2G28900 | outer plastid envelope protein 16-1 | 325 | 5 |
| AT2G29140 | pumilio 3 | 73 | 2 |
| AT2G29540 | RNApolymerase 14 kDa subunit | 35 | 1 |
| AT2G30390 | ferrochelatase 2 | 117 | 3 |
| AT2G30950 | FtsH extracellular protease family | 2065 | 49 |
| AT2G32340 | TraB family protein | 45 | 1 |
| AT2G32630 | Pentatricopeptide repeat (PPR-like) superfamily protein | 42 | 1 |
| AT2G32850 | Protein kinase superfamily protein | 35 | 1 |
| AT2G33150 | peroxisomal 3-ketoacyl-CoA thiolase 3 | 84 | 2 |
| AT2G33800 | Ribosomal protein S5 family protein | 113 | 2 |
| AT2G34460 | NAD(P)-binding Rossmann-fold superfamily protein | 1144 | 22 |
| AT2G34730 | myosin heavy chain-related | 37 | 1 |
| AT2G35490 | Plastid-lipid associated protein PAP / fibrillin family protein | 1078 | 17 |
| AT2G35760 | Uncharacterised protein family (UPF0497) | 121 | 4 |
| AT2G36145 | unknown protein | 36 | 1 |
| AT2G36160 | Ribosomal protein S11 family protein | 119 | 2 |
| AT2G36885 | unknown protein | 36 | 1 |
| AT2G37170 | plasma membrane intrinsic protein 2 | 40 | 1 |
| AT2G37230 | Tetratricopeptide repeat (TPR)-like superfamily protein | 235 | 9 |
| AT2G38040 | acetyl Co-enzyme a carboxylase carboxyltransferase alpha subunit | 50 | 1 |
| AT2G39470 | PsbP-like protein 2 | 469 | 11 |
| AT2G39730 | rubisco activase | 666 | 13 |
| AT2G40000 | ortholog of sugar beet HS1 PRO-1 2 | 184 | 5 |
| AT2G40010 | Ribosomal protein L10 family protein | 38 | 1 |
| AT2G40100 | light harvesting complex photosystem II | 417 | 9 |
| AT2G41040 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | 42 | 1 |
| AT2G42130 | Plastid-lipid associated protein PAP / fibrillin family protein | 157 | 3 |
| AT2G42220 | Rhodanese/Cell cycle control phosphatase superfamily protein | 1066 | 20 |
| AT2G43030 | Ribosomal protein L3 family protein | 210 | 3 |
| AT2G43560 | FKBP-like peptidyl-prolyl cis-trans isomerase family protein | 217 | 4 |
| AT2G44640 | FUNCTIONS IN: molecular\_function unknown | 42 | 1 |
| AT2G44870 | unknown protein | 351 | 6 |
| AT2G44970 | alpha/beta-Hydrolases superfamily protein | 36 | 1 |
| AT2G45740 | peroxin 11D | 73 | 1 |
| AT2G45960 | plasma membrane intrinsic protein 1B | 96 | 2 |
| AT2G46820 | photosystem I P subunit | 1536 | 33 |
| AT2G47510 | fumarase 1 | 41 | 1 |
| AT3G01060 | unknown protein | 319 | 5 |
| AT3G01390 | vacuolar membrane ATPase 10 | 51 | 1 |
| AT3G01440 | PsbQ-like 1 | 723 | 17 |
| AT3G01480 | cyclophilin 38 | 120 | 3 |
| AT3G02090 | Insulinase (Peptidase family M16) protein | 129 | 3 |
| AT3G03100 | NADH:ubiquinone oxidoreductase, 17.2kDa subunit | 87 | 2 |
| AT3G04260 | plastid transcriptionally active 3 | 90 | 2 |
| AT3G07180 | GPI transamidase component PIG-S-related | 37 | 1 |
| AT3G07700 | Protein kinase superfamily protein | 150 | 3 |
| AT3G08030 | Protein of unknown function, DUF642 | 37 | 1 |
| AT3G08580 | ADP/ATP carrier 1 | 1060 | 31 |
| AT3G08920 | Rhodanese/Cell cycle control phosphatase superfamily protein | 426 | 11 |
| AT3G08940 | light harvesting complex photosystem II | 3202 | 69 |
| AT3G09630 | Ribosomal protein L4/L1 family | 38 | 1 |
| AT3G10060 | FKBP-like peptidyl-prolyl cis-trans isomerase family protein | 826 | 22 |
| AT3G10130 | SOUL heme-binding family protein | 120 | 3 |
| AT3G10690 | DNA GYRASE A | 297 | 7 |
| AT3G10920 | manganese superoxide dismutase 1 | 37 | 1 |
| AT3G12470 | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | 38 | 1 |
| AT3G14110 | Tetratricopeptide repeat (TPR)-like superfamily protein | 495 | 7 |
| AT3G14415 | Aldolase-type TIM barrel family protein | 149 | 4 |
| AT3G14590 | Calcium-dependent lipid-binding (CaLB domain) family protein | 124 | 3 |
| AT3G15110 | unknown protein | 253 | 6 |
| AT3G15120 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | 40 | 1 |
| AT3G15360 | thioredoxin M-type 4 | 156 | 3 |
| AT3G15520 | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | 222 | 4 |
| AT3G15840 | post-illumination chlorophyll fluorescence increase | 40 | 1 |
| AT3G16000 | MAR binding filament-like protein 1 | 1298 | 27 |
| AT3G16250 | NDH-dependent cyclic electron flow 1 | 74 | 2 |
| AT3G16950 | lipoamide dehydrogenase 1 | 45 | 1 |
| AT3G17930 | unknown protein | 186 | 6 |
| AT3G18720 | F-box family protein | 39 | 1 |
| AT3G18890 | NAD(P)-binding Rossmann-fold superfamily protein | 1302 | 27 |
| AT3G21055 | photosystem II subunit T | 375 | 5 |
| AT3G21430 | DNA binding | 76 | 2 |
| AT3G23400 | Plastid-lipid associated protein PAP / fibrillin family protein | 2308 | 46 |
| AT3G25520 | ribosomal protein L5 | 116 | 2 |
| AT3G25760 | allene oxide cyclase 1 | 87 | 2 |
| AT3G25805 | unknown protein | 160 | 6 |
| AT3G25920 | ribosomal protein L15 | 198 | 5 |
| AT3G26060 | Thioredoxin superfamily protein | 173 | 4 |
| AT3G26070 | Plastid-lipid associated protein PAP / fibrillin family protein | 1027 | 22 |
| AT3G26570 | phosphate transporter 2 | 47 | 1 |
| AT3G26740 | CCR-like | 41 | 1 |
| AT3G27160 | Ribosomal protein S21 family protein | 120 | 2 |
| AT3G27830 | ribosomal protein L12-A | 592 | 10 |
| AT3G27925 | DegP protease 1 | 489 | 8 |
| AT3G30842 | pleiotropic drug resistance 10 | 43 | 1 |
| AT3G43540 | Protein of unknown function (DUF1350) | 107 | 2 |
| AT3G44880 | Pheophorbide a oxygenase family protein with Rieske [2Fe-2S] domain | 235 | 5 |
| AT3G45050 | unknown protein | 41 | 1 |
| AT3G45140 | lipoxygenase 2 | 2148 | 47 |
| AT3G46060 | RAB GTPase homolog 8A | 126 | 2 |
| AT3G46730 | NB-ARC domain-containing disease resistance protein | 116 | 3 |
| AT3G46780 | plastid transcriptionally active 16 | 6283 | 104 |
| AT3G47070 | LOCATED IN: thylakoid, chloroplast thylakoid membrane, chloroplast, chloroplast envelope | 1252 | 24 |
| AT3G47390 | cytidine/deoxycytidylate deaminase family protein | 39 | 1 |
| AT3G47470 | light-harvesting chlorophyll-protein complex I subunit A4 | 2061 | 38 |
| AT3G47520 | malate dehydrogenase | 126 | 2 |
| AT3G47860 | chloroplastic lipocalin | 41 | 1 |
| AT3G48000 | aldehyde dehydrogenase 2B4 | 38 | 1 |
| AT3G48850 | phosphate transporter 3 | 38 | 1 |
| AT3G50820 | photosystem II subunit O-2 | 6939 | 158 |
| AT3G51140 | Protein of unknown function (DUF3353) | 61 | 1 |
| AT3G51820 | UbiA prenyltransferase family protein | 93 | 2 |
| AT3G52070 | unknown protein | 38 | 1 |
| AT3G52300 | ATP synthase D chain, mitochondrial | 283 | 4 |
| AT3G54890 | photosystem I light harvesting complex gene 1 | 422 | 8 |
| AT3G55330 | PsbP-like protein 1 | 206 | 6 |
| AT3G55410 | 2-oxoglutarate dehydrogenase, E1 component | 190 | 4 |
| AT3G56010 | unknown protein | 45 | 1 |
| AT3G56650 | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | 296 | 6 |
| AT3G56940 | dicarboxylate diiron protein, putative (Crd1) | 288 | 6 |
| AT3G58010 | plastoglobulin 34kD | 146 | 5 |
| AT3G58540 | unknown protein | 36 | 1 |
| AT3G58600 | Adaptin ear-binding coat-associated protein 1 NECAP-1 | 127 | 4 |
| AT3G59200 | F-box/RNI-like superfamily protein | 36 | 1 |
| AT3G59780 | Rhodanese/Cell cycle control phosphatase superfamily protein | 773 | 13 |
| AT3G60750 | Transketolase | 38 | 1 |
| AT3G60810 | unknown protein | 95 | 2 |
| AT3G61470 | photosystem I light harvesting complex gene 2 | 510 | 9 |
| AT3G61620 | 3'-5'-exoribonuclease family protein | 44 | 1 |
| AT3G61870 | unknown protein | 1506 | 24 |
| AT3G63140 | chloroplast stem-loop binding protein of 41 kDa | 38 | 1 |
| AT3G63160 | FUNCTIONS IN: molecular\_function unknown | 378 | 9 |
| AT3G63410 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | 241 | 3 |
| AT4G00860 | Protein of unknown function (DUF1138) | 151 | 2 |
| AT4G01037 | Ubiquitin carboxyl-terminal hydrolase family protein | 95 | 3 |
| AT4G01050 | thylakoid rhodanese-like | 2572 | 52 |
| AT4G01150 | unknown protein | 2039 | 38 |
| AT4G01690 | Flavin containing amine oxidoreductase family | 492 | 10 |
| AT4G01800 | Albino or Glassy Yellow 1 | 609 | 13 |
| AT4G02530 | chloroplast thylakoid lumen protein | 579 | 13 |
| AT4G02725 | unknown protein | 120 | 3 |
| AT4G02770 | photosystem I subunit D-1 | 2466 | 79 |
| AT4G03280 | photosynthetic electron transfer C | 2557 | 44 |
| AT4G03520 | Thioredoxin superfamily protein | 47 | 1 |
| AT4G04020 | fibrillin | 1163 | 18 |
| AT4G04640 | ATPase, F1 complex, gamma subunit protein | 5958 | 202 |
| AT4G04940 | transducin family protein / WD-40 repeat family protein | 37 | 1 |
| AT4G05180 | photosystem II subunit Q-2 | 2059 | 65 |
| AT4G06744 | Leucine-rich repeat (LRR) family protein | 45 | 1 |
| AT4G09010 | ascorbate peroxidase 4 | 1678 | 43 |
| AT4G09320 | Nucleoside diphosphate kinase family protein | 36 | 1 |
| AT4G09650 | ATP synthase delta-subunit gene | 1992 | 42 |
| AT4G10340 | light harvesting complex of photosystem II 5 | 14400 | 365 |
| AT4G11010 | nucleoside diphosphate kinase 3 | 40 | 1 |
| AT4G11960 | PGR5-like B | 36 | 1 |
| AT4G12360 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | 37 | 1 |
| AT4G12800 | photosystem I subunit l | 693 | 14 |
| AT4G13200 | unknown protein | 414 | 7 |
| AT4G13500 | unknown protein | 91 | 2 |
| AT4G14070 | acyl-activating enzyme 15 | 50 | 1 |
| AT4G14210 | phytoene desaturase 3 | 356 | 6 |
| AT4G15233 | ABC-2 and Plant PDR ABC-type transporter family protein | 115 | 3 |
| AT4G15510 | Photosystem II reaction center PsbP family protein | 38 | 1 |
| AT4G16920 | Disease resistance protein (TIR-NBS-LRR class) family | 37 | 1 |
| AT4G17530 | RAB GTPase homolog 1C | 48 | 1 |
| AT4G17600 | Chlorophyll A-B binding family protein | 58 | 1 |
| AT4G19100 | Protein of unknown function (DUF3464) | 40 | 1 |
| AT4G19170 | nine-cis-epoxycarotenoid dioxygenase 4 | 304 | 7 |
| AT4G20130 | plastid transcriptionally active 14 | 38 | 1 |
| AT4G20260 | plasma-membrane associated cation-binding protein 1 | 124 | 1 |
| AT4G20300 | Protein of unknown function (DUF1639) | 36 | 1 |
| AT4G20360 | RAB GTPase homolog E1B | 127 | 2 |
| AT4G21280 | photosystem II subunit QA | 3650 | 101 |
| AT4G22240 | Plastid-lipid associated protein PAP / fibrillin family protein | 1148 | 18 |
| AT4G22890 | PGR5-LIKE A | 1608 | 25 |
| AT4G23890 | unknown protein | 900 | 20 |
| AT4G24190 | Chaperone protein htpG family protein | 52 | 1 |
| AT4G24750 | Rhodanese/Cell cycle control phosphatase superfamily protein | 341 | 6 |
| AT4G25080 | magnesium-protoporphyrin IX methyltransferase | 873 | 15 |
| AT4G27440 | protochlorophyllide oxidoreductase B | 736 | 14 |
| AT4G27700 | Rhodanese/Cell cycle control phosphatase superfamily protein | 928 | 21 |
| AT4G28300 | Protein of unknown function (DUF1421) | 36 | 1 |
| AT4G28660 | photosystem II reaction center PSB28 protein | 52 | 1 |
| AT4G28740 | FUNCTIONS IN: molecular\_function unknown | 217 | 4 |
| AT4G28750 | Photosystem I reaction centre subunit IV / PsaE protein | 1555 | 49 |
| AT4G29780 | unknown protein | 36 | 1 |
| AT4G30010 | unknown protein | 79 | 2 |
| AT4G31390 | Protein kinase superfamily protein | 217 | 5 |
| AT4G32260 | ATPase, F0 complex, subunit B/B', bacterial/chloroplast | 3793 | 96 |
| AT4G32470 | Cytochrome bd ubiquinol oxidase, 14kDa subunit | 162 | 3 |
| AT4G32770 | tocopherol cyclase, chloroplast / vitamin E deficient 1 (VTE1) / sucrose export defective 1 (SXD1) | 349 | 6 |
| AT4G33010 | glycine decarboxylase P-protein 1 | 94 | 2 |
| AT4G34240 | aldehyde dehydrogenase 3I1 | 67 | 1 |
| AT4G35250 | NAD(P)-binding Rossmann-fold superfamily protein | 868 | 19 |
| AT4G36390 | Methylthiotransferase | 39 | 1 |
| AT4G37200 | Thioredoxin superfamily protein | 545 | 9 |
| AT4G37925 | subunit NDH-M of NAD(P)H:plastoquinone dehydrogenase complex | 205 | 4 |
| AT4G37930 | serine transhydroxymethyltransferase 1 | 1141 | 20 |
| AT4G38100 | unknown protein | 84 | 2 |
| AT4G38970 | fructose-bisphosphate aldolase 2 | 3549 | 85 |
| AT4G39080 | vacuolar proton ATPase A3 | 64 | 1 |
| AT4G39200 | Ribosomal protein S25 family protein | 40 | 1 |
| AT4G39710 | FK506-binding protein 16-2 | 644 | 11 |
| AT4G39730 | Lipase/lipooxygenase, PLAT/LH2 family protein | 87 | 2 |
| AT5G01220 | sulfoquinovosyldiacylglycerol 2 | 44 | 1 |
| AT5G01530 | light harvesting complex photosystem II | 7395 | 147 |
| AT5G01920 | Protein kinase superfamily protein | 45 | 1 |
| AT5G02160 | unknown protein | 951 | 21 |
| AT5G03880 | Thioredoxin family protein | 431 | 8 |
| AT5G03900 | Iron-sulphur cluster biosynthesis family protein | 42 | 1 |
| AT5G04360 | limit dextrinase | 75 | 2 |
| AT5G04900 | NYC1-like | 47 | 1 |
| AT5G05200 | Protein kinase superfamily protein | 151 | 3 |
| AT5G05740 | ethylene-dependent gravitropism-deficient and yellow-green-like 2 | 44 | 1 |
| AT5G06130 | chaperone protein dnaJ-related | 44 | 1 |
| AT5G07020 | proline-rich family protein | 294 | 4 |
| AT5G08050 | Protein of unknown function (DUF1118) | 421 | 9 |
| AT5G08670 | ATP synthase alpha/beta family protein | 232 | 5 |
| AT5G08680 | ATP synthase alpha/beta family protein | 908 | 20 |
| AT5G08740 | NAD(P)H dehydrogenase C1 | 460 | 8 |
| AT5G09590 | mitochondrial HSO70 2 | 123 | 2 |
| AT5G09660 | peroxisomal NAD-malate dehydrogenase 2 | 557 | 10 |
| AT5G11450 | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | 63 | 1 |
| AT5G12860 | dicarboxylate transporter 1 | 75 | 2 |
| AT5G12950 | Putative glycosyl hydrolase of unknown function (DUF1680) | 36 | 1 |
| AT5G13120 | cyclophilin 20-2 | 155 | 4 |
| AT5G13450 | delta subunit of Mt ATP synthase | 135 | 3 |
| AT5G14040 | phosphate transporter 3 | 46 | 1 |
| AT5G15090 | voltage dependent anion channel 3 | 103 | 2 |
| AT5G16660 | unknown protein | 209 | 2 |
| AT5G17170 | rubredoxin family protein | 1548 | 27 |
| AT5G17670 | alpha/beta-Hydrolases superfamily protein | 45 | 1 |
| AT5G17720 | alpha/beta-Hydrolases superfamily protein | 36 | 1 |
| AT5G18660 | NAD(P)-binding Rossmann-fold superfamily protein | 41 | 1 |
| AT5G19310 | Homeotic gene regulator | 37 | 1 |
| AT5G19760 | Mitochondrial substrate carrier family protein | 141 | 3 |
| AT5G19940 | Plastid-lipid associated protein PAP / fibrillin family protein | 788 | 16 |
| AT5G20140 | SOUL heme-binding family protein | 312 | 7 |
| AT5G20900 | jasmonate-zim-domain protein 12 | 36 | 1 |
| AT5G21430 | Chaperone DnaJ-domain superfamily protein | 420 | 8 |
| AT5G23060 | calcium sensing receptor | 3560 | 63 |
| AT5G23120 | photosystem II stability/assembly factor, chloroplast (HCF136) | 1276 | 24 |
| AT5G23300 | pyrimidine d | 62 | 1 |
| AT5G25980 | glucoside glucohydrolase 2 | 448 | 9 |
| AT5G27390 | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | 122 | 2 |
| AT5G27550 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | 42 | 1 |
| AT5G28540 | heat shock protein 70 (Hsp 70) family protein | 84 | 2 |
| AT5G28750 | Bacterial sec-independent translocation protein mttA/Hcf106 | 140 | 3 |
| AT5G35170 | adenylate kinase family protein | 139 | 3 |
| AT5G35370 | S-locus lectin protein kinase family protein | 35 | 1 |
| AT5G37360 | unknown protein | 900 | 16 |
| AT5G37510 | NADH-ubiquinone dehydrogenase, mitochondrial, putative | 107 | 2 |
| AT5G37710 | alpha/beta-Hydrolases superfamily protein | 36 | 1 |
| AT5G38660 | acclimation of photosynthesis to environment | 2430 | 38 |
| AT5G38880 | unknown protein | 77 | 2 |
| AT5G40640 | unknown protein | 190 | 5 |
| AT5G40750 | FBD / Leucine Rich Repeat domains containing protein | 204 | 5 |
| AT5G40810 | Cytochrome C1 family | 61 | 1 |
| AT5G40950 | ribosomal protein large subunit 27 | 84 | 2 |
| AT5G42270 | FtsH extracellular protease family | 2069 | 45 |
| AT5G42330 | unknown protein | 40 | 1 |
| AT5G42650 | allene oxide synthase | 2651 | 52 |
| AT5G44650 | Encodes a nucleus-encoded thylakoid protein, cooperates with the plastid-encoded Ycf3 protein in photosystem i assembly. Also induces tolerance to multiple environmental stresses and reduces photooxidative damage. | 48 | 1 |
| AT5G46110 | Glucose-6-phosphate/phosphate translocator-related | 134 | 4 |
| AT5G46390 | Peptidase S41 family protein | 35 | 1 |
| AT5G46800 | Mitochondrial substrate carrier family protein | 315 | 5 |
| AT5G48790 | Domain of unknown function (DUF1995) | 207 | 5 |
| AT5G49360 | beta-xylosidase 1 | 244 | 4 |
| AT5G50850 | Transketolase family protein | 137 | 2 |
| AT5G50920 | CLPC homologue 1 | 81 | 2 |
| AT5G51010 | Rubredoxin-like superfamily protein | 122 | 4 |
| AT5G51690 | 1-amino-cyclopropane-1-carboxylate synthase 12 | 38 | 1 |
| AT5G53490 | Tetratricopeptide repeat (TPR)-like superfamily protein | 339 | 9 |
| AT5G53580 | NAD(P)-linked oxidoreductase superfamily protein | 324 | 7 |
| AT5G54160 | O-methyltransferase 1 | 35 | 1 |
| AT5G54270 | light-harvesting chlorophyll B-binding protein 3 | 558 | 11 |
| AT5G55710 | FUNCTIONS IN: molecular\_function unknown | 335 | 7 |
| AT5G58260 | oxidoreductases, acting on NADH or NADPH, quinone or similar compound as acceptor | 213 | 5 |
| AT5G59250 | Major facilitator superfamily protein | 280 | 5 |
| AT5G60250 | zinc finger (C3HC4-type RING finger) family protein | 44 | 1 |
| AT5G60990 | DEA(D/H)-box RNA helicase family protein | 39 | 1 |
| AT5G61910 | DCD (Development and Cell Death) domain protein | 41 | 1 |
| AT5G62140 | unknown protein | 48 | 1 |
| AT5G64040 | photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN) | 3411 | 76 |
| AT5G64290 | dicarboxylate transport 2.1 | 98 | 3 |
| AT5G64940 | ABC2 homolog 13 | 106 | 2 |
| AT5G65220 | Ribosomal L29 family protein | 265 | 3 |
| AT5G65570 | Tetratricopeptide repeat (TPR)-like superfamily protein | 427 | 11 |
| AT5G66190 | ferredoxin-NADP()-oxidoreductase 1 | 3034 | 60 |
| AT5G66470 | RNA binding | 35 | 1 |
| AT5G66570 | PS II oxygen-evolving complex 1 | 7130 | 172 |
| AT5G66760 | succinate dehydrogenase 1-1 | 65 | 1 |
| AT5G67030 | zeaxanthin epoxidase (ZEP) (ABA1) | 264 | 4 |
| AT5G67500 | voltage dependent anion channel 2 | 243 | 4 |
| AT5G67590 | NADH-ubiquinone oxidoreductase-related | 36 | 1 |
| ATCG00020 | photosystem II reaction center protein A | 11300 | 361 |
| ATCG00120 | ATP synthase subunit alpha | 10375 | 286 |
| ATCG00130 | ATPase, F0 complex, subunit B/B', bacterial/chloroplast | 6366 | 147 |
| ATCG00150 | ATPase, F0 complex, subunit A protein | 307 | 7 |
| ATCG00190 | RNA polymerase subunit beta | 39 | 1 |
| ATCG00270 | photosystem II reaction center protein D | 6357 | 137 |
| ATCG00280 | photosystem II reaction center protein C | 9411 | 275 |
| ATCG00340 | Photosystem I, PsaA/PsaB protein | 3771 | 76 |
| ATCG00350 | Photosystem I, PsaA/PsaB protein | 1921 | 54 |
| ATCG00430 | photosystem II reaction center protein G | 354 | 9 |
| ATCG00470 | ATP synthase epsilon chain | 1343 | 28 |
| ATCG00480 | ATP synthase subunit beta | 19446 | 569 |
| ATCG00490 | ribulose-bisphosphate carboxylases | 946 | 20 |
| ATCG00500 | acetyl-CoA carboxylase carboxyl transferase subunit beta | 38 | 1 |
| ATCG00520 | unfolded protein binding | 300 | 7 |
| ATCG00540 | photosynthetic electron transfer A | 4587 | 112 |
| ATCG00560 | photosystem II reaction center protein L | 703 | 12 |
| ATCG00580 | photosystem II reaction center protein E | 692 | 14 |
| ATCG00680 | photosystem II reaction center protein B | 13205 | 276 |
| ATCG00700 | photosystem II reaction center protein N | 46 | 1 |
| ATCG00710 | photosystem II reaction center protein H | 1948 | 117 |
| ATCG00720 | photosynthetic electron transfer B | 2482 | 35 |
| ATCG00730 | photosynthetic electron transfer D | 804 | 32 |
| ATCG00770 | ribosomal protein S8 | 152 | 3 |
| ATCG00780 | ribosomal protein L14 | 86 | 2 |
| ATCG00800 | structural constituent of ribosome | 42 | 1 |
| ATCG00810 | ribosomal protein L22 | 56 | 1 |
| ATCG01060 | iron-sulfur cluster binding | 2667 | 51 |
| ATCG01070 | NADH-ubiquinone/plastoquinone oxidoreductase chain 4L | 413 | 10 |
| ATCG01090 | NADPH dehydrogenases | 233 | 5 |
| ATCG01110 | NAD(P)H dehydrogenase subunit H | 211 | 5 |
| ATMG00070 | NADH dehydrogenase subunit 9 | 162 | 4 |