



Title	Draft Genome Sequence of a Psychrotolerant Sulfur-Oxidizing Bacterium, <i>Sulfuricella denitrificans</i> skB26, and Proteomic Insights into Cold Adaptation
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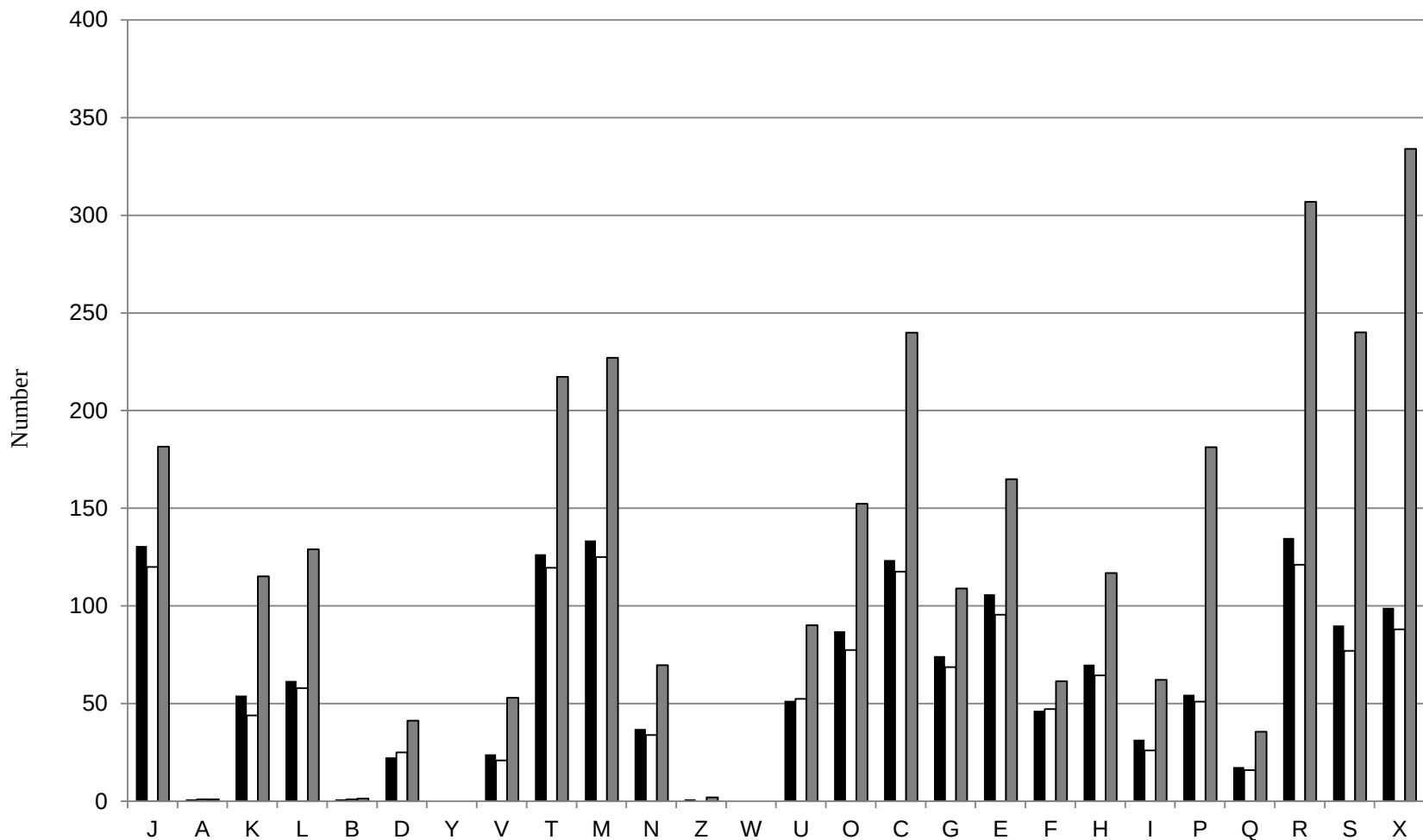


Figure S1. COG distribution of proteins identified from LT (black bar), MT (white bar), and that of all CDSs found in *S. denitrificans* draft genome (gray bar). One-letter abbreviations indicate the functional categories: J, translation, ribosomal structure and biogenesis; A, RNA processing and modification; K, transcription; L, replication, recombination and repair; B, chromatin structure and dynamics; D, cell cycle control, cell division, chromosome partitioning; Y, nuclear structure; V, defense mechanisms; T, signal transduction mechanisms; M, cell wall/membrane/envelope biogenesis; N, cell motility; Z, cytoskeleton; W, extracellular structure; U, intracellular trafficking, secretion, and vesicular transport; O, posttranslational modification, protein turnover, chaperones; C, energy production and conversion; G, carbohydrate transport and metabolism; E, amino acid transport and metabolism; F, nucleotide transport and metabolism; H, coenzyme transport and metabolism; I, lipid transport and metabolism; P, inorganic ion transport and metabolism; Q, secondary metabolites biosynthesis, transport and catabolism; R, general function prediction only; S, function unknown. In addition, X indicates CDSs that were not assigned in any category.