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NOTE

# Functional curation of the *Sulfolobus solfataricus* P2 and *S. acidocaldarius* 98-3 complete genome sequences

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**Abstract** The thermoacidophiles *Sulfolobus solfataricus* P2 and *S. acidocaldarius* 98-3 are considered key model organisms representing a major phylum of the Crenarchaeota. Because maintaining current, accurate genome information is indispensable for modern biology, we have updated gene function annotation using the arCOGs database, plus other available functional, structural and phylogenetic information. The goal of this initiative is continuous improvement of genome annotation with the support of the *Sulfolobus* research community.

**Keywords** Archaea · Thermoacidophiles · Genome analysis · Genomics

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Both *Sulfolobus* species are obligate aerobes that thrive in thermoacidophilic habitats. *S. solfataricus* (strain P2, DSM1617; Zillig et al. 1980) optimally grows at 80°C and pH 3.2/3.5; *S. acidocaldarius* (98-3, DSM 639; Brock et al. 1972) has similar optimal growth between 75 and 80°C and pH 2–3. Whereas *S. solfataricus* grows hetertrophically on peptidolytic constituents and a wide variety of simple and complex sugars, *S. acidocaldarius* relies on tryptone for heterotrophic growth, but has enhanced growth with the addition of selected carbohydrates, such as sucrose, xylose, and glucose (Grogan 1989; Zaparty and Siebers 2010).

The genome of the *S. solfataricus* strain P2 is nearly 3 million base pairs (Mbp) with 3,033 predicted open reading frames (ORFs) (She et al. 2001b). In particular, this genome exhibits a high level of plasticity due in part to 200 diverse insertion sequence elements (Martusewitsch et al. 2000; Redder et al. 2001; She et al. 2001a; Brügger et al. 2002, 2004). In contrast, the genome of *S. acidocaldarius* is significantly more compact at 2.2 Mbp with 2,329 predicted ORFs, notably lacking insertion sequence elements (Chen et al. 2005).

*S. solfataricus* and *S. acidocaldarius* have become model organisms because they are easily maintained in the laboratory under defined growth conditions, and have recently developed gene expression and deletion systems (Worthington et al. 2003; Albers et al. 2006; Deng et al. 2009; Wagner et al. 2009). With complete genome

sequences, both organisms offer exciting opportunities for metabolic engineering, synthetic biology, and white biotechnology (Frazzetto 2003).

In the *Sulfolobus* Systems Biology (SulfoSYS) project, the effect of temperature change on a biological network, i.e. central carbohydrate metabolism, has been studied using biochemistry as well as genome-based high-throughput approaches (Albers et al. 2009; Pham et al. 2009; Zaparty et al. 2009). To provide a solid basis for future post-genome analyses, both Sulfolobus genomes have been updated using the recently developed clusters of orthologous groups database that is specific to archaeal genomes (arCOGs) (Makarova et al. 2007). This has enabled assignment of general or specific function to more than 770 protein-coding genes formerly annotated as hypothetical proteins.

Additional experimental, structural, and phylogenetic information were integrated from BRENDA (http://www.brenda-enzymes.org/), scientific literature searches (http://www.ncbi.nlm.nih.gov/pubmed/), and information from SulfoSYS partners. This information has allowed improvement and/or verification of annotation for 175 ORFs from *S. solfataricus* P2 (14 from orthologs reported in other *S. solfataricus* strains) and 33 ORFs from *S. acidocaldarius*. Recently published deep sequencing data for *S. solfataricus* transcription start sites (Wurtzel et al. 2010) has also enabled improved start codon positioning for 162 ORFs, as well as inclusion of 80 new ORFs.

The goal of this initiative is to continuously improve genome annotation with involvement of the scientific community. A submission form for newly characterized enzymes is available at the SulfoSYS homepage (http://www.sulfosys.com/). The curated *S. solfataricus* P2 and *S. acidocaldarius* 98-3 genomes are available at the SulfoSYS homepage (http://www.sulfosys.com, see "Hot Stuff", Genome annotation) as well as the UCSC Archaeal Genome Browser (http://archaea.ucsc.edu/sulfoSYS/).

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