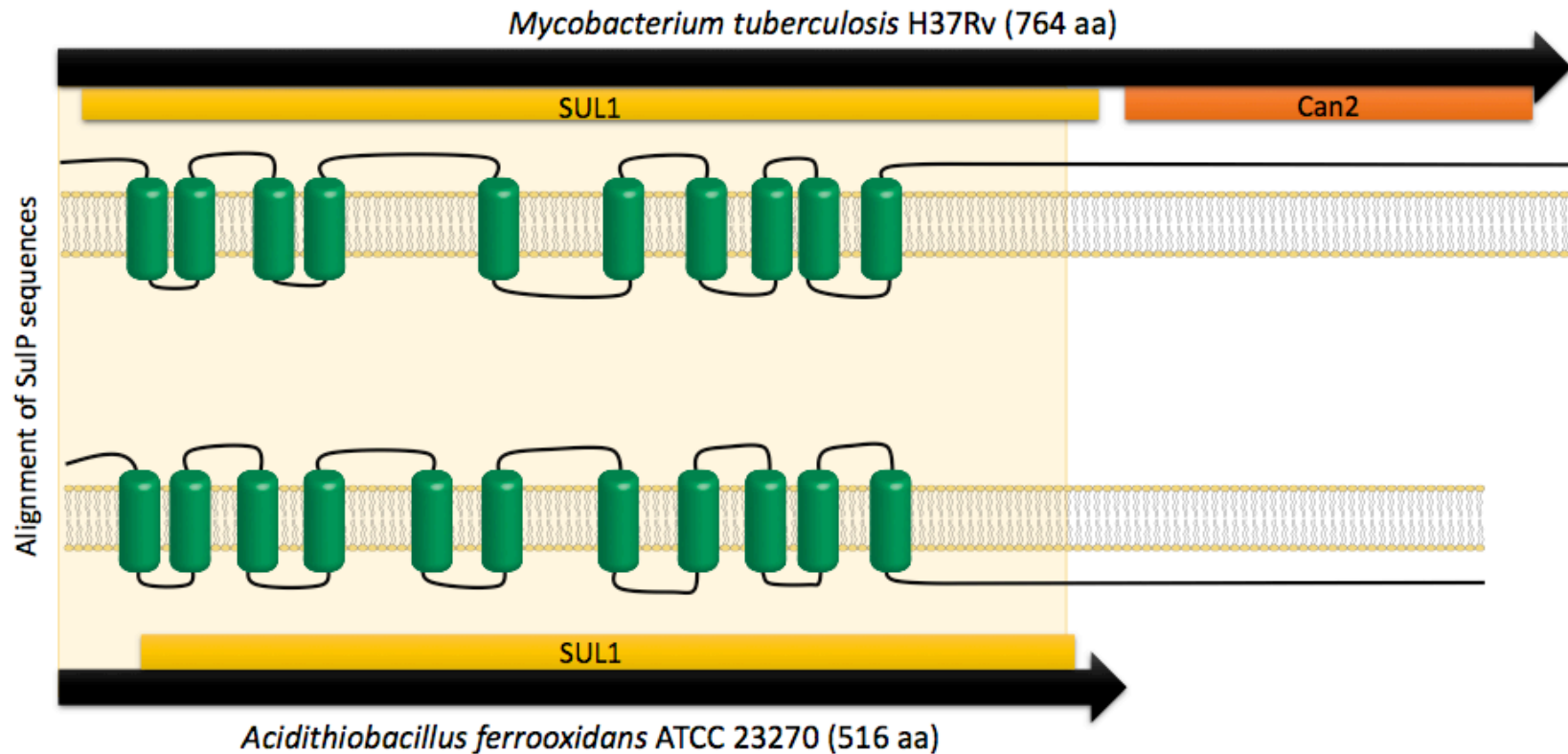


**Effect of CO<sub>2</sub> Concentration on Uptake and Assimilation of Inorganic Carbon in the Extreme  
Acidophile *Acidithiobacillus ferrooxidans***

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**SUPPLEMENTAL FIGURE S<sub>1</sub>**



Alignments of the SulP-Can gene fusion of *Mycobacterium tuberculosis* H37Rv (NP\_217790.1) with SulP of *Acidithiobacillus ferrooxidans* (ACK80903.1, locus tag AFE\_0286). Black arrows represent the coding sequence of each gene. Above the black arrows are shown the domain structures, where Sul1 = COG0659: Sulfate permease or related transporter, MFS superfamily [Inorganic ion transport and metabolism] and CynT = COG0288: a member of the superfamily cl00391, Carbonic anhydrase [Inorganic ion transport and metabolism]. Above the domain structures, the predicted respective transmembrane domains are shown using the Phobius prediction server (Lukas Käll, Anders Krogh and Erik L. L. Sonnhammer. Advantages of combined transmembrane topology and signal peptide prediction – the Phobius web server. *Nucleic Acids Res.*, 35:W429-32, July 2007).