
Sulfate-reducing bacteria (SRB), the strict anaerobes, constitute a particular group of prokaryotes that can metabolize sulfate. In dissimilatory sulfate reduction, the activation of sulfate is first catalyzed by ATP sulfurylase to produce adenosine 5′-phosphosulfate (APS), which is then reduced by adenylysulfate reductase (adenosine 5′-phosphosulfate reductase, APS reductase or APSR) to sulfite. Sulfite is subsequently reduced by dissimilatory sulfite reductase (Dsr) to three products: trithionate (S₃O₆²⁻), thiosulfate (S₂O₃²⁻) or sulfide (S²⁻). We have determined crystal structures of APSR and Dsr from Desulfovibrio gigas, a much studied representatives of SRB. APSR comprises six αβ-heterodimers that form a hexameric structure. The flavin adenine dinucleotide (FAD) is non-covalently attached to the C-terminal segment of the β-subunit [1, 3]. The structures of the αβ-heterodimer of Dsr-I contains eight [4Fe-4S] clusters, two saddle-shaped siroihemes and two flat sirohydrochlorins. In Dsr-II, the [4Fe-4S] cluster associated with the siroheme in Dsr-I is replaced by a [3Fe-4S] cluster. The γ-subunit C-terminus is inserted into a positively charged channel formed between the α- and β-subunits, with its conserved terminal Cys104 side chain covalently linked to the CHA atom of the siroheme in Dsr-I. In Dsr-II, the thioether bond is broken, and the Cys104 side chain moves closer to the bound sulfite at the siroheme pocket. These different forms of Dsr offer structural insights into a mechanism of sulfite reduction that can lead to S₂O₃²⁻, S₃O₆²⁻ and S²⁻ [2].


Keywords: sulfate reduction; enzyme catalysis; electron paramagnetic resonance

MS12-01 Structural basis of signal peptide recognition by the signal recognition particle. Elisabeth Sauer-Eriksson, Tobias Hainzl, Shenghua Huang, Gitte Meriläinen, Kristoffer Brännström, Elisabeth Sauer-Eriksson

The signal recognition particle (SRP) recognizes and binds to the signal peptide of nascent proteins as they emerge from the ribosome. The conserved core of SRP consists of SRP RNA and the SRP54 protein, and plays the key role in signal–peptide recognition and binding to the SRP receptor. Proper communication between the two SRP54 domains, the GTPase- and the M-domain, is vital for the function of the particle so that signal–peptide binding at the M domain directs receptor binding at the GTPase domain. By studying crystal structures of the SRP RNA in complex with its different protein partners, many of the structural states of the SRP have been revealed. The structures of the Methanococcus jannaschii SRP54-SRP19-S domain RNA complex in its free form [1] and in complex with an hydrophobic idealized signal peptide comprising 14 leucine and alanine residues [2] provide an explanation for how signal peptide binding at the M domain triggers a reorientation of the GTPase domain by local structuring and α-helix formation of the GM linker.


Keywords: signal recognition particle; protein-nucleic acid structures; X-ray structure