

Crystal Structure of Atypical Cytoplasmic ABC-ATPase SufC
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Biosynthesis of Fe-S clusters requires several specific proteins. The *suf* operon has been recently identified as a third system for the assembly of Fe-S clusters. The *suf* operon of *Escherichia coli* comprises *sufA*, *sufB*, *sufC*, *sufD*, *sufS*, and *sufE*. Most of *suf* genes are conserved in various organisms, but the *suf* operon is seldom found in complete form. The most conserved *suf* genes are SufC and SufB. SufC is a cytoplasmic ABC-ATPase, probably the most essential Suf protein. SufC interacts with SufB and SufD in a stable complex, and the SufBCD complex interacts with other Suf proteins in the Fe-S cluster assembly.

We have determined the crystal structure of SufC from *Thermus thermophilus* HB8 in a nucleotide-free state and an ADP-Mg bound state at 1.7Å and 1.9Å resolution, respectively. The structure of SufC consists of two domains: the ABC $\alpha\beta$ domain, which is structurally similar to the typical core fold of ABC-ATPase, and the α helical domain. In the ABC $\alpha\beta$ domain, three residues following the end of the Walker B motif form a novel 3_{10} helix, which is not observed in other ABC ATPases. This results in an unorthodox conformation of a conserved glutamate residue involved in ATP hydrolysis. Compared to other ABC-ATPase structures, significant displacement occurs at a linker region between the ABC $\alpha\beta$ and α helical domains, leading to an atypical surface structure around the Q loop. This surface feature suggests that SufC interacts with SufB and SufD in a different manner from that observed in the structure of ABC transporters.

Keywords: ABC-ATPase, structural biology, Suf protein