s1.m5.p15 **Characterization of archaeal Sm proteins from *Sulfolobus solfataricus*: structural and functional analysis.** Dietrich Suck and Turgay Kilic, *European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany. E-mail: suck@embl.de*

Keywords: Sm proteins; Archaea; X-ray structure

Eukaryotic Sm and Sm-like (Lsm) proteins are a family of small proteins characterized by a bipartite sequence motif, known as the Sm domain, which contains an N-terminal alpha helix followed by five anti-parallel beta strands. Seven distinct Sm and Lsm proteins associate with RNA to form the core domain of small nuclear ribonucleoprotein particles (snRNPs), which are involved in various RNA-processing events such as mRNA decapping and degradation, pre-mRNA splicing, telomere replication, and histone 3' end processing. In spliceosomal snRNPs they bind to the so called Sm site, a U-rich, single-stranded region containing the consensus sequence $PAU_{4-6}GP$ (P; purine). Recently, Sm-related proteins were also detected in Archaea and bacteria. Archaeal Sm proteins show oligomerization and RNA binding properties similar to their eukaryotic counterparts, their function is however currently unknown. Archaeal genomes encode at most three Sm related proteins forming homo-heptameric or -hexameric complexes. As part of a structural and functional analysis of Sm-related proteins we have determined the structures of several archaeal Sm complexes from *Archaeoglobus fulgidus* [1,2] and *Pyrococcus abyssi* [3] and have recently solved the structure of the *E.coli* Hfq protein [4]. These structures show that the Sm monomer fold as well as the architecture of the Sm core domain has been conserved during evolution. In addition, they have allowed us to propose a model for the interaction of RNA with the eukaryotic Sm core proteins [3], suggesting that the Sm core represents a platform for interactions between pre-mRNA and snRNA. Continuing our studies on Sm-related proteins we have very recently obtained crystals of the Sm1- and Sm2-type proteins from the crenarchaeon *Sulfolobus solfataricus*. The structure of the SS-Sm1 protein has been determined at 1.9Å and is presently being refined. These structures will be discussed in relation to previously determined archaeal, bacterial and eukaryotic Sm protein structures. In parallel, biochemical assays *in vivo* and *in vitro* will be performed to identify the potential RNA or protein targets of archaeal Sm proteins.

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[3] Thore, S., Mayer, C., Sauter, C., Weeks, S. & Suck, D. (2003) *J. Biol.Chem.* **278**, 1239-1247.
[4] Sauter, C., Basquin, J. & Suck, D. (2003) *Nucl. Acids Res*. **31**, 4091-4098.

s1.m5.p16 **Crystal structure of the Zn/Co containing Adenylate Kinase from *D. gigas*.** José Trincao, Sergey Bursakov, José J.G. Moura, Isabel Moura and Maria Joao Romao, *REQUIMTE/CQFB, Departamento de Química, FCT, Universidade Nova de Lisboa, 2829-516 Caparica, Portugal, Portugal. E-mail: trincao@dq.fct.unl.pt*

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Adenylate kinase (AK) mediates the reversible transfer of phosphate groups from ATP to AMP. It contributes to the maintenance of a constant cellular level of ADP, necessary for energetic metabolism and nucleic acid synthesis. In contrast to the AK from Gram-negative bacteria, which requires only the presence of Mg^{2+} ion for this reaction, the enzyme from Gram-positive organisms also harbours a Zn^{2+} (or Co^{2+}) ion, believed to have a structural role. AK from D. gigas is a monomer in solution and has a molecular mass of 24.7 kDa[1]. Due to difficulties in obtaining a MR solution using models of AK from other organisms, the structure of AK from *D.gigas* was solved by MAD using the bound Zn as the anomalous scatterer. A single crystal was used to collect data to 2.1 A at the Zn peak, at the edge and at a remote wavelength. The crystal belongs to space group I222, with unit cell **a** = 39.6 Å, **b** = 119.8 Å and **c** = 150 Å. The structure was refined to a final R factor of 19.9 % (Rfree = 23.4 %). It shows a single molecule in the asymmetric unit. The crystal structure was used to confirm, correct and complete the available partial sequence of the AK from *D. gigas*.

Structural data will also be obtained for the Co-containing AK, as well as for complexes of the enzyme with substrate-analogues, which will help to gather a better understanding of the structural and catalytic properties of this class of adenylate kinases.

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