

MS06-P07 | STRUCTURAL STUDY TWO DIFFERENT FORMS OF SMAP FROM HALOBACTERIUM SALINARUM WHICH HAVE A DIFFERENT RNA-BINDING ABILITY

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Archaeal Sm-like proteins belong to the large LSM family, which is characterized by the ability to adopt Sm fold. It is comprised of a 5-stranded β -sheet capped by an N-terminal α -helix. Despite Lsm proteins are structurally conserved, the functions of the proteins in Archaea, Bacteria and Eukarya are different. Eukaryotic Sm/Lsm are part of several RNP particles and involved in the RNA processing. Bacterial Lsm protein Hfq exhibits RNA-chaperone activity, facilitate the interaction of regulatory sRNA with mRNA, thus regulating gene expression. Nowadays, there is little information about the functions of the archaeal Lsm proteins SmAP; some data shows that they appear to be involved in the processing of RNA.

Our work is concerned by structural and functional studies of SmAP from *Halobacterium salinarum* (HsaSmAP). We've found this protein is represented in databases in two forms: a length of 60 and 69 amino acids. Both variants of HsaSmAP have been isolated and their affinity to oligo(A) RNA, oligo(U) RNA, AMP and GMP have been measured. A difference in the affinity of the alternatives to the RNA has been found. The proteins were crystallized and X-ray diffractions data have been collected at ERSF in Grenoble. In contrast with majority of Lsm proteins, HsaSmAP has no unstructured N- and C-terminus or extended loops between secondary structure elements thus representing a minimal Lsm core. However, SmAP from *H. salinarum* has the characteristic for the Lsm proteins doughnut-shape form with seven monomers organized into a torus.

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