s1.m5.p11 **Low resolution model of the histidine kinase protein ΔRv0902c from *Mycobacterium Tuberculosis*.** E. Nowak, D.I. Svergun and P.A.Tucker, *EMBL, Notkestrasse 85, 22603 Hamburg, Germany*. *E-mail: elan@embl-hamburg.de*

Keywords: Histidine kinase protein; SAXS

Bacterial adaptation to the environment most commonly requires signal transduction through the coordinated activation of specific sensory kinases and signal processing response regulators (so-called two-component systems). The open reading frame Rv0902c from Mycobacterium Tuberculosis has been identified by sequence comparison, as a sensor histidine kinase. Histidine kinase proteins regulate a large variety of cellular responses, including bacterial chemotaxis, osmoregulation, photosensitivity, sporulation, plant response to ethylene and microbial pathogenesis [1,2]. Rv0902c with its response regulator Rv0903c is required for early intercellular multiplication of *Mycobacterium Tuberculosis* [3]. Rv 0902c is a multidomain protein containing the HAMP, Histidine Kinase (HK) and ATPase domains with two predicted transmembrane regions. Several constructs without the membrane anchor containg one ATPase, three (HAMP, HK & ATPase), two (HK&ATPase) domains were cloned. We obtain soluble dimeric and monomeric protein for multidomain constructs and ATPase respectively. SAXS experiments were carried out on Rv0902c constructs to obtain information about domain organization. The measured radius of gyration R_g=3.34nm for three domain construct DRv0902c with estimated mass of about 53 kDa confirms the dimeric nature. The low resolution particle shape of ΔRv0902c [Fig.1] determined from experimental data using an *ab initio* procedure implemented in the program GASBOR [4] and will be presented.

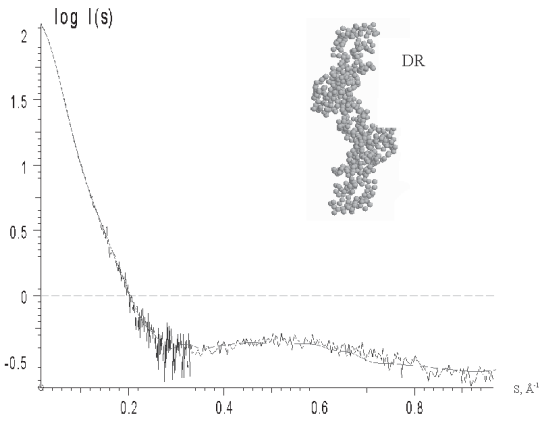

Figure 1: Fit of the dummy residues model DR to the scattering data.

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s1.m5.p12 **Co-axial association of eye lens aquaporin AQP0.** Dinesh Palanivelu [a], Peter Agre [b], David Kozono [b], Ariel Lustig [c], Kitaru Suda [a], Tilman Schirmer [a], [a] *Division of Structural Biology, Biozentrum, University of Basel, Switzerland,* [b] *Departments of Biological Chemistry and Medicine, Johns Hopkins School of Medicine, USA,* [c] *Division of Biophysical chemistry, Biozentrum, University of Basel, Switzerland*. *E-mail: dinesh.palanivelu@unibas.ch*

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The major intrinsic protein (MIP26, AQP0) of vertebrate eye lenses is known to function as a water and solute channel and is the founding member of the aquaporin (AQP) superfamily. Insight into the structural basis of this function can be deduced from the recently determined X-ray structure of the homologous AQP1 [1]. In addition, however, it has been reported that AQP0 mediates contact between the membranes of adjacent lens fiber cells [2], which is consistent with the extraordinarily narrow extracellular spaces. 2-D structural analysis by atomic-force and cryo-electron microscopy demonstrates that AQP0 can interact in a highly specific manner via their extracellular surfaces to form tongue-and-groove fit between apposing membranes demonstrating the adhesive role of AQP0 [3]. Mutants of AQP0 that prevent proper folding or targeting cause cataract in vertebrates [4]. Thus, this protein is of great medical relevance and makes it an interesting object for structure determination.

His-tagged bovine AQP0 has been expressed in yeast and purified. Conditions for solubilization have been optimized. Monodispersity and oligomerization state of the protein were checked by analytical ultracentrifugation, blue native gel electrophoresis and microscopy. Crystals have been obtained in the presence of n-Decyl-β-D-Maltoside and other detergents. Although the crystals are not very well ordered, it was possible to obtain a complete data set to 7.0 Å resolution at the SLS synchrotron. The structure was solved by molecular replacement with AQP1. The result shows head-to-head aggregation of tetramers (point symmetry 42) in the cubic crystal lattice (space group *I*432, *a*=*b*=*c*=188 Å). This interaction possibly represents the in vivo aggregation mode between AQP0 tetramers from juxtaposed membranes in the eye lens.

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