Low resolution model of the histidine kinase protein ΔRv0902c from *Mycobacterium Tuberculosis*

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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 ΔRv0902c 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.

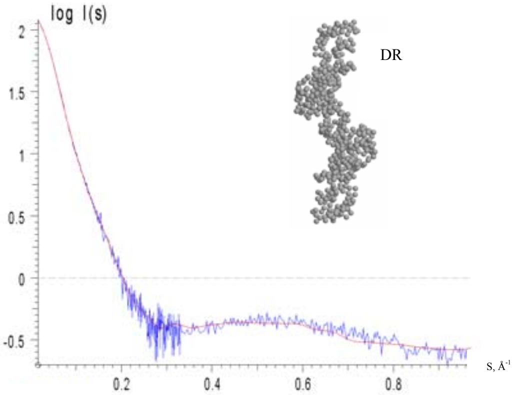

Figure 1: Fit of the dummy residues model DR to the scattering data .

[1] J.S. Parkinson, et all, *Annu. Rev. Genet*. 26, 71 (1992).
[2] J.L. Appleby, et all*, Cell* 86, 845 (1996).
[3] F. Ewann et all, *Infec. And Immun*. 70, 2256 (2002).
[4] D.I. Svergun at all, *Biophys. J.* 80, 2946 (2001).