SAXS analysis of the response regulator FixJ

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Bacterial adaptation to the environment most commonly involves the two-component signaling system through the coordinated activation of specific sensory kinases and signal processing response regulators. The regulator generally consists of two domains: the receiver domain which contains the aspartate residue phosphorylatable by the cognate kinase and a DNA-binding output domain, which is involved in the regulation of gene transcription.

FixL/FixJ is a prototypical system responsible for the regulation of nitrogen fixation in the symbiotic bacterium *Sinorhizobium meliloti* [1]. The FixJ receiver domain inhibits the latent activity of the C-terminal domain within the native protein and this inhibition is relieved by phosphorylation of the receiver domain [2]. The crystal structures of the unphosphorylated (monomer) and phosphorylated (dimer) forms of the N-terminal receiver domain of the response regulator FixJ (FixJN) have been solved [3, 4]. As no structure is currently available for the full length FixJ, SAXS experiments were done to obtain the molecular envelope of the full-length FixJ using the SAXS data and the available crystallographic informations. This envelope should allow to position the C-terminal domain with respect to the N-terminal domain. This description and the available crystallographic data will provide a further step towards the understanding of the functional role of the interface between the N- and C- terminal domains in FixJ.

Monodisperse conditions could be found for the FixJ protein solution which allowed to perform SAXS measurements at high protein concentrations (figure 1). Scattering data collected on the X33 camera of the EMBL were processed using the program SAPOKO [5]. The distance distribution functions $p(\mathrm{r})$ and the radii of gyration R_g were evaluated by the indirect Fourier transform program GNOM [6]. The low resolution particle shape of FixJ was restored from the experimental data using an *ab initio* procedure implemented in the program DAMMIN [7].

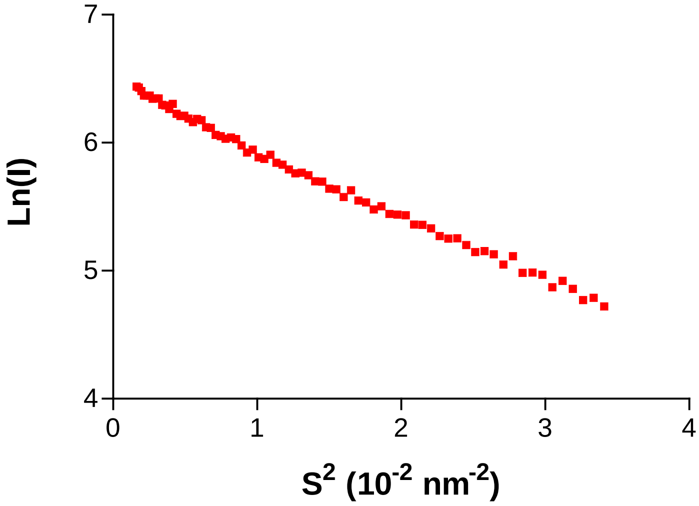

Figure 1: Guinier plot of small-angle X-ray scattering data of FixJ

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