Visulaization of proteins in solution - in situ

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Abstract

Time dependent visualization of proteins in situ, e.g. their degradation during manufacturing and storage, the impact of salts upon their conformations are of broad interest in industrial biotechnology. The interest gets broader and arouses interest wihin the field of material sciences if it comes to self assemblies.

The outmost of cells of a broad spectrum of bacteria and archae are covered by layer proteins (S-layers). Consequently these are strongly involved in metabolic processes in response to the environment, serving numerous functions including structural stabilization, cell adhesion, pathogenicity, drug resistance and mineralization [1]. These two-dimensional crystals of S-layers have been recognized as a distinct class among numerous protein architectures found in nature [2, 4] that present various lattice periodicities commensurate with the dimensions of synthetic nano-materials, such as quantum dot and carbon nano-tubes. These long-range order self assemblies attractive bio-molecules for nano-scale templates for prospective nano-material engineering [3]. The assembly process in particular its detailed mechanism is understood if at all, poorly.

We combine Differential Scanning Calorimetry, in situ atomic force microscopy [5], Small Angle X-ray Scattering [6], Transmission electron microscopy as well as tomography with reversed Molecular dynamic simulations and reverse Monte Carlo simulations, to model possible crystallization pathways and conformational changes in situ.

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Figures

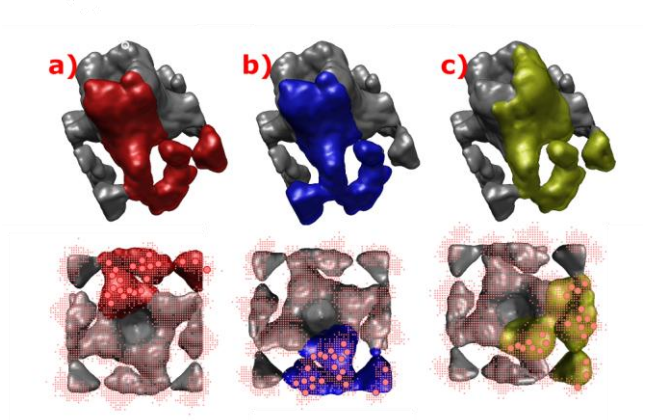

Figure 1. Gray data refer to 3D experimental data of SbpA unit cell. a-c) Three complementary conformations of an SbpA monomer are superimposed. Pink circles refer to possible positions of secondary structure elements.