

Biophysical Characterization of Archaeal Cyclophilin Like Chaperone Protein

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Abstract : Chaperones are proteins that help other proteins fold correctly, and are found in all domains of life i.e., prokaryotes, eukaryotes and archaea. Various comparative genomic studies have suggested that the archaeal protein folding machinery appears to be highly similar to that found in eukaryotes. In case of protein folding; slow rotation of peptide prolyl-imide bond is often the rate limiting step. Formation of the prolyl-imide bond during the folding of a protein requires the assistance of other proteins, termed as peptide prolyl cis-trans isomerases (PPIases). Cyclophilins constitute the class of peptide prolyl isomerases with a wide range of biological function like protein folding, signaling and chaperoning. Most of the cyclophilins exhibit PPIase enzymatic activity and play active role in substrate protein folding which classifies them as a category of molecular chaperones. Till date, there is not very much data available in the literature on archaeal cyclophilins. We aim to compare the structural and biochemical features of the cyclophilin protein from within the three domains to elucidate the features affecting their stability and enzyme activity. In the present study, we carry out in-silico analysis of the cyclophilin proteins to predict their conserved residues, sites under positive selection and compare these proteins to their bacterial and eukaryotic counterparts to predict functional divergence. We also aim to clone and express these proteins in heterologous system and study their biophysical characteristics in detail using techniques like CD and fluorescence spectroscopy. Overall we aim to understand the features contributing to the folding, stability and dynamics of the archaeal cyclophilin proteins.

Keywords : biophysical characterization, x-ray crystallography, chaperone-like activity, cyclophilin, PPIase activity

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