Tata Institute of Fundamental Research
Survey No. 36/P, Gopanpally Village, Serilingampally, Ranga Reddy Dist., Hyderabad – 500 046

Seminar

Studying dynamics of proteins using solution NMR spectroscopy

Subhendu Pandit

TIFR, Hyderabad

Proteins play a variety of roles in various biological processes (Karplus and McCammon 1983; Holland and Blight 1993). As the structure of a protein intricately connected to its function, several biophysical tools like X-ray crystallography, Cryo-EM, and NMR spectroscopy have been developed to study protein structure. However, proteins are not rigid molecules with a single conformation but are constantly are in motion adopting different conformations (Boehr et al., 2009; Karplus and Kuriyan 2005; Moore 2012; Dill and Chan 1997; Onuchic et al., 1997). In this talk, I will describe the conformational dynamics of a ribosome binding protein known as the hibernation-promoting factor (HPF). HPF binds to bacterial ribosomes (E. coli) during nutrient-deprived conditions and prevents its translational activity (Ueta et al., 2008). Doing so helps bacteria conserve energy and survive in a stressful environment. Using the ^{15}N CEST experiment, we showed that the major state of HPF is in slow exchange with two minor states at 52°C.

Using $^{1}H^{N}$ CPMG NMR (Carr and Purcell 1954; Meiboom and Gill 1958) relaxation dispersion experiment, we also characterised the dynamics of the N-terminal domain of two isoforms of ApoE (namely, ApoE3 NTD and ApoE4 NTD). Both of these two isoforms exchange in millisecond time scale with very similar exchange rate (k_{ex}~4000 s^{-1}). But they differ in terms of the population of the minor conformers.

Thursday, Aug 3rd 2023

2:30 PM (Tea / Coffee 2.15 PM)

Seminar Hall, TIFR-H