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

Students' Annual Seminar

Simplifying chemical-shift assignment of large proteins using solid-state NMR

Pragyan Parimita Parida

In my annual talk I will be discussing a method that distinguishes residues depending on the secondary structures that they form in protein samples in the solid state. This method is an alternative to traditional approaches requiring assignment for secondary structure determination where Cα and Cβ chemical shifts are used to predict the torsion angle of the peptide segment in question. As such, our method will enable identification of secondary structure elements even in situations where the identity of the resonance in question is not established. When the structure of the protein is known, this method can directly inform chemical shift assignments. I will demonstrate the use of this method is obtaining partial assignments of a bacterial cytoskeletal protein ParM (~36 kDa protein) in its filamentous state.

Additionally, I will also present the expression and purification optimisation of another prokaryotic cytoskeletal protein MreB protein and the development of a novel construct for the large-scale production of highly soluble and stable TEV protease.

Friday, Apr 26th 2024

09:30 Hrs (Tea / Coffee 09:15 Hrs)

Seminar Hall, TIFR-H