

## **Student's Annual Seminar**

### **Understanding Dynamic of Proteins Using Solution NMR Spectroscopy**

#### **Subhendu Pandit**

Proteins exist in multiple conformations in solution. Structures obtained from spectroscopic techniques like X-ray and Cryo-EM give information about the mostly populated conformation (ground state). Thus sparsely populated conformations (minor states, population around ~1%) remain invisible to these techniques. Previous studies suggest that, minor states are also important for protein function. Solution NMR spectroscopy is used to study dynamics of proteins and it can also give atomistic details of the low populated excited states (population > 0.5%).

When bacteria are under cold stress, they enter into a stationary phase where 70S ribosomes dimerize. In *E.coli*, Ribosome modulation factor (RMF) causes this dimer formation and Hibernation promoting factor (HPF), stabilize the dimers. On the other hand, protein YFIA inhibits this dimerization by inactivating 70S ribosome. Our systems of interest are these two ribosome binding proteins YFIA and HPF. YFIA is known to show dynamics in millisecond timescales. Using CPMG and CEST NMR experiments we have studied the dynamic processes present in these two proteins. Both of these two proteins exchange between one major state and two minor states. YFIA shows dynamics in millisecond time scales while HPF has dynamics in slower timescales (Second).

***Friday, Mar 29<sup>th</sup> 2019***

***4:00 PM (Tea/Coffee at 3:30 PM)***

***Seminar Hall, TIFR-H***