
Students' Annual Webinar

Studying dynamics of proteins using solution NMR spectroscopy

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Proteins play a variety of roles in various biological processes (Karplus and McCammon 1983; Holland and Blight 1993). As the structure of a protein is 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 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.

References:

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Onuchic J. N., Schulten Z. L., Wolynes P. G., *Annual Reviews in Physical Chemistry* 1997, 48, 545-600.
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4:00 PM