TIFR Centre for Interdisciplinary Sciences
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Seminar

Allostery in chaperonins: how and why?

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Chaperonins consist of two back-to-back stacked heptameric rings with a cavity at each end where protein folding can take place. They assist protein folding by undergoing large conformational changes that are controlled by ATP binding and hydrolysis. The concerted Monod–Wyman–Changeux and sequential Koshland–Némethy–Filmer models of cooperativity are often used to describe such allosteric switching. In general, however, it has been impossible to distinguish between these different allosteric models using ensemble measurements of ligand binding in bulk protein solutions. In this talk, two approaches that break this impasse will be described: one that is kinetic and a second that is based on native mass spectrometry. Using these approaches, it was possible to show that the chaperonin GroEL from E. coli undergoes concerted intra-ring conformational changes whereas its eukaryotic homologue CCT/TRiC undergoes sequential intra-ring conformational changes. The impact of these different allosteric mechanisms on the folding functions of GroEL and CCT/TRiC will be discussed.

Friday, Jan 20th 2017

4:00 PM (Tea/Coffee at 3:45 PM)

Seminar Hall, TCIS