

Internal Seminar

Design, Diversity and Destiny of a Protein Domain: Through the Lens of $\beta\gamma$ -Crystallins

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During the evolution of a protein, its physical characteristics are shaped by the functional requirements imposed by the biological niche it occupies. $\beta\gamma$ -Crystallin is a widespread superfamily of proteins with a diverse set of properties and functions associated with its members. The microbial $\beta\gamma$ -crystallins have gained their own identity as largely Ca^{2+} -binding domains serving various functions, distinct from their kin, the lens $\beta\gamma$ -crystallins, which are robust, structural proteins. This superfamily exhibits immense variation in the terms of stability, ligand binding, domain architecture and functional diversity, thus being an impressive model to study the interrelation among these aspects. Exploring this group leads us towards a glucanase enzyme being modulated by a $\beta\gamma$ -crystallin domain in Ca^{2+} -dependent fashion, a tradeoff between ligand-binding and intrinsic stability and a bridge between the folded and unfolded states.

Thursday, Oct 6th 2016

2:00 PM (Tea/Coffee at 1:45 PM)

Seminar Hall, TCIS