



**L.H. BAKER CENTER FOR BIOINFORMATICS AND
BIOLOGICAL STATISTICS AND IGERT
SEMINAR SERIES**

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“Unfoldome and Unfoldomics: Introducing Intrinsically Disordered Proteins”

Intrinsically disordered proteins (IDPs) lack stable tertiary and/or secondary structure under physiological conditions in vitro. Computational studies revealed that they are highly abundant in nature, as ~25-30% of eukaryotic proteins are mostly disordered, and >50% of eukaryotic proteins and > 70% of signaling proteins have long disordered regions. Often, these IDPs are involved in regulation, signaling and control pathways, where binding to multiple partners and high-specificity/low-affinity interactions play a crucial role. It is suggested that functions of IDPs may arise from the specific disorder form, from inter-conversion of disordered forms, or from transitions between disordered and ordered conformations. The choice between these conformations is determined by the peculiarities of the protein environment, and many IDPs possess an exceptional ability to fold in a template-dependent manner. IDPs are highly abundant among hub proteins. They are associated with alternative splicing. This association helps proteins to avoid folding difficulties and provides a novel mechanism for developing tissue-specific protein interaction networks. Numerous IDPs are commonly associated with such devastating maladies as cancer, cardiovascular disease, amyloidoses, neurodegenerative diseases, and diabetes. Novel strategies for drug discovery are based on these proteins.

Date: Thursday, April 8th, 2010

Time: 12:40—1:40PM

Room: Snedecor Hall Room 3105