

Chez Pierre

Presents ...

Tuesday, March 1, 2011

2:00pm

MIT Room 4-331



SPECIAL CHEZ PIERRE SEMINAR

**Jeremy England
Princeton University**

"Life on the Edge: The Physics of Allosteric Conformational Change in Globular Protein Domains"

The protein folding problem – that is, the problem of understanding why a polypeptide chain composed of a particular sequence of amino acids should tend to adopt a particular three-dimensional shape while in aqueous solution – is thought to be difficult because of the large number of different inter- and intra-molecular forces that may simultaneously influence the conformational preferences of a protein chain. It is possible, however, that this difficulty is somewhat illusory, and that the interplay of only a few, basic features of a protein strongly constrains the relationship between its primary sequence and its tertiary structure. Here, I show for a variety of proteins that the native ensemble of conformations preferred by a given protein is principally a consequence of that protein's pattern of amino acid side-chain hydrophobicity, and information about this native ensemble may be extracted using linear programming for energy minimization. Despite the seeming complexity of the folding process, an analysis of these patterns solely in terms of the combined impact of intra-chain steric repulsion and the hydrophobic effect provides the key to explaining biologically important allosteric motions in real proteins.