

Physics Colloquium

Michigan Technological University

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4:00 pm

Room 139, Fisher Hall

A Kinetic Model for the Nucleation Mechanism of Protein Folding Based on a First Passage Time Analysis

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Abstract:

Proteins play an overwhelmingly dominant role in life. For a protein to carry out a specific biological function, it has to adopt a well-defined 3D structure. The formation of this "native" structure of a biologically active protein constitutes the core of a "protein folding problem". One of the possible pathways of protein folding involves the formation of a number of tertiary contacts. Once a critical number thereof is established, the native structure is immediately formed without passing through any detectable intermediates. This mechanism is similar to nucleation because it involves the formation of a cluster containing native residues which grows by absorbing residues from the unfolded part of the protein. I will present a kinetic model for the nucleation mechanism of protein folding. A protein is considered as a random heteropolymer made of hydrophobic, hydrophilic, and neutral beads, with fixed and equal bond lengths and bond angles. As a crucial idea, an overall potential field around the cluster of native residues (whereto an external residue is subjected) is considered to be a combination of the average dihedral and average pairwise potentials assigned to the bead. The overall potential as a function of the distance from the cluster has a double well shape which allows one to determine its emission and absorption rates by using a first passage time analysis. Knowing these rates as functions of three independent variables of a ternary cluster, one can develop a kinetic theory for the nucleation mechanism of protein folding in terms of ternary nucleation and evaluate the protein folding time.