



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

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**“Protein folding mechanisms and their  
application to structure prediction.”**

Despite decades of investigation, a major unresolved question is how the amino acid sequence of a protein codes for its structure. The talk will cover the two major aspects of *The Protein Folding Problem: Folding mechanisms and structure prediction*. The experimental studies will identify the major pathway events including properties of the rate-limiting transition state. Principles derived from these studies are employed in a folding algorithm designed to mimic the true folding pathway. In our iterative fixing algorithm, structure emerges as an integral component of the folding process. We find that a  $C_{\beta}$ -level model without homology information can outperform current homology-based prediction methods for both secondary and tertiary structure. Hence simplified yet realistic protein models can be used to accurately predict structure given appropriate search strategies.

**Date: Thursday, October 29th**  
**Time: 12:40—1:40PM**  
**Room: Snedecor Hall Room 3105**