



presents Guest Speaker :

Ken Dill

*Department of Pharmaceutical Chemistry, University of
California, San Francisco*

*Using Protein Folding Physics in Physics-Based
Protein Structure Prediction* □

Predicting protein structures from their amino acid sequences has been challenging within physics-based modeling because of the size and difficulty of this global optimization problem. However, many real proteins fold very quickly (microseconds). We show here how insights from physical protein folding can be used to speed up computational protein structure prediction.

Student Presentation (15 mins)

**Kelvin Zhang, Bioinformatics Training Program for
Health Research**

January 12, 2006, 3:30 pm

Chan Auditorium, Child & Family Research Institute, Oak St. at 28th

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