1010-82-111 **Zhong Chen*** (zc@csbl.bmb.uga.edu), Computational Systems Biology Lab, Dept. of Biochemistry and Molecular Biology, University of Georgia, Athens, GA 30602, and **Ying Xu**.
Multi-Scale Hierarchical Structure Prediction of Helical Transmembrane Proteins.

Membrane proteins play important roles in many cellular processes, but our understanding of their 3-dimensional structures and functions is still limited due to the non-trivial task of structural determination by experimental means. As the first step toward a multi-scale, hierarchical computational approach for membrane protein structure prediction, the packing of transmembrane helices was modeled at the residual and atomistic levels, respectively. For predictions at the residual level, the helix-helix and helix-lipid interactions were described by a set of knowledge-based energy functions. For predictions at the atomistic level, CHARMM19 force field was employed. To facilitate the system to overcome energy barriers in a complex free-energy landscape, Wang-Landau sampling was carried out by performing a random walk in the energy and conformational spaces, where each state was visited with equal probability. Native-like structures were predicted at both levels for 2- and 7-helix systems as local or global free energy minima. Interestingly, consistent results were obtained from simulations at residual and atomistic levels for the same system, strongly suggesting the feasibility of a hierarchical approach for membrane protein structure prediction. (Received August 22, 2005)