NIMBioS
National Institute for Mathematical and Biological Synthesis

"Dynamic modeling of proteins: physical basis for molecular evolution"

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Tuesday, April 6, 2010
3:30 pm, Room 403, Blount Hall, 1534 White Ave.

Dynamic modeling of a coarse-grained elastic protein model provides an effective way of exploring the relationship between protein structure and function. In particular, functionally important residues are identified by a variety of computational methods based on the fluctuation analysis. The results from the modeling provide great insights into how random mutagenesis of proteins can give rise to desired property (protein engineering of bioluminescence system) and how molecular physics constrains evolutionary pathways of proteins (emergence of drug resistance behaviors in HIV-1 protease).

Join us for refreshments in the NIMBioS Lobby at 3 pm