Abstract Submitted
for the OSS16 Meeting of
The American Physical Society

Application of statistical procedures based on mutual information in the protein Calbindin D-9k for detecting the allosteric pathways MAHENDRA THAPA, MARK RANCE, University of Cincinnati — Calbindin D_{9k} (CAB) is a small (molecular weight of 8700 D with only 75 amino acids) calcium-binding protein that binds two calcium ions in a cooperative fashion at its two binding sites. It is an attractive model system for computational studies of various dynamical and structural properties such as the molecular basis of cooperativity of calcium binding, chemical shifts and fluctuations of atoms under a variety of conditions. Because of the tremendous advancement in hardware and software computer technologies in recent years, longer and more realistic molecular dynamics (MD) simulations of a protein are possible now in reasonable periods of time. These advances were exploited to generate multiple, all-atom MD simulations of CAB via the AMBER software package, and the results from the resulting trajectories were employed not only to compare with the corresponding experimental NMR results but also for the theoretical. Application of statistical procedures based on mutual information, via the GSATools and MutInf software, provided valuable insights regarding correlated motions between the two calcium binding loops of calbindin D_{9k} and identified residues that may play a direct role in the allosteric pathway. However, from our initial work in this area, it is not yet clear what the optimum protocol is for the application of the methodology. But even from the preliminary results we obtained, it is possible to design computational studies of mutant versions of calbindin D_{9k} in an effort to identify the physical mechanisms underlying the observed positive cooperativity of calcium ion binding.

Mahendra Thapa
University of Cincinnati

Date submitted: 18 Mar 2016 Electronic form version 1.4