Abstract Submitted
for the OSS14 Meeting of
The American Physical Society

Conformational Dynamics of a Ligand-Free Adenylate Kinase[1]
HYUN DEOK SONG, FANGQIANG ZHU, Indian Univ-Purdue Univ — Adenylate kinase (AdK) is a phosphoryl-transfer enzyme with important physiological functions. Based on a ligand-free open structure and a ligand-bound closed structure solved by crystallography, here we use molecular dynamics simulations to examine the stability and dynamics of AdK conformations in the absence of ligands. We first perform multiple simulations starting from the open or the closed structure, and observe their free evolutions during a simulation time of 100 or 200 nanoseconds. In all seven simulations starting from the open structure, AdK remained stable near the initial conformation. The eight simulations initiated from the closed structure, in contrast, exhibited large variation in the subsequent evolutions, with most (seven) undergoing large-scale spontaneous conformational changes and approaching or reaching the open state. To characterize the thermodynamics of the transition, we propose and apply a new sampling method that employs a series of restrained simulations to calculate a one-dimensional free energy along a curved pathway in the high-dimensional conformational space. Our calculated free energy profile features a single minimum at the open conformation, and indicates that the closed state, with a high (∼13 kcal/mol) free energy, is not metastable, consi

[1]The simulations were performed on a high-performance Linux cluster at School of Science, IUPUI

Hyun Deok Song
Indian Univ-Purdue Univ

Date submitted: 14 Mar 2014 Electronic form version 1.4