1SD03  
**The Biophysical Society of Japan General Incorporated Association**

Proteins recognize their own substrates. In many cases, intrinsic flexibility of protein plays a key role in molecular recognition, where ligand binding causes a conformational change. Although the low-frequency modes are well known as a set of degrees of freedom for large conformational changes, the dynamical mechanism has remained unclear. In order to reveal the dynamical mechanism, we need to perform molecular dynamics (MD) simulation on the timescale of conformational change. In the present study, we choose adenylate kinase (AK) as the target protein system undergoing conformational changes upon ligand binding. We investigated dynamics of AK both with and without the ligands in all-atom MD simulations with explicit water. The simulations were performed by the MD program system, MARBLE, with the force field parameter of CHARMM22. After energy minimization and equilibration in the NVE ensemble, product runs were carried out for 10 ns in the NVE ensemble. In the absence of the ligands, AK was unstable in the closed form, and changed its conformation into the open form. We successfully simulated the complete relaxation process. PCA analysis revealed the existence of a transition state and dynamical barrier in the process. On the other hand, binding of the ligands drove the closure of AK. Simulation results indicated that a drastic change of AK fluctuations occurred along with the domain closure, though AK did not reach the closed form. A full picture of AK dynamics will be presented in the lecture.

S.Fuchigami, M.Ikeguchi and A.Kidera: Protein function is driven by the intrinsic dynamics

1SD04  
**Time scales to attain local ergodicity through vibrational relaxation in proteins**

Fujisaki Hiroshi, Zhang Yong, O STRAUB JOHN E. (Chemistry Department, Boston University)

When a protein is excited by ligand binding, ATP attachment, or laser pulses, there occurs vibrational energy relaxation (VER). Energy initially "injected" into a localized region "flows" to the rest of the protein and surrounding solvent. VER is essential for attaining local ergodicity, and is known to vary in time scale over many orders of magnitude. An important challenge is to relate VER to fundamental reaction processes associated with protein function. The development of an accurate understanding of VER in proteins is an essential step toward the goal of controlling protein dynamics and understanding the time scales for attaining local ergodicity in proteins. VER will be explored in the context of selected modes in cytochrome c, myoglobin and model peptides, using a number of theoretical approaches. One is the equilibrium simulation approach, with quantum correction factors. Another is the reduced model approach, which describes the protein as an ensemble of normal modes interacting through nonlinear coupling elements. A more recently developed approach, inspired by the path integral theory of Mikami, Shiga and Okazaki, accounts for anharmonicity in the system oscillator, and third and fourth order coupling between the system and bath. We explore the similarities and differences between theoretical predictions, and provide a detailed comparison with experimental results. Extensions of that work to selected vibrational modes in other proteins will also be presented.

Hiroshi Fujisaki, Yong Zhang and JOHN E. STRAUB: Time scales to attain local ergodicity through vibrational relaxation in proteins

1SD05  
**Vibrational dynamics and energy transport in proteins**

Leitner David M. (Department of Chemistry, University of Nevada, Reno)

Computational studies of vibrational dynamics and energy transport in proteins will be discussed. Vibrational energy transport in proteins exhibits anomalous subdiffusion, a property that is closely connected to protein geometry. We use information about vibrational energy transport in proteins and clusters to compute thermal transport coefficients for these objects. I shall also discuss recent computational work on vibrational energy transfer in proteins due to anharmonic coupling of vibrational modes, focusing on energy flow pathways and the influence of water, and comparing with experimentally measured energy transfer rates.

David M. Leitner: Vibrational dynamics and energy transport in proteins

1SD06  
**Dynamical Foundation for Molecular Function of Proteins in the Multidimensional State Space Structure**

M.Toda and T.Komatsuzaki: Dynamical Foundation for Molecular Function of Proteins in the Multidimensional State Space Structure

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