In silico で観察するタンパク質の柔らかで機能的な運動
Observing soft functional motion of proteins in silico

Akio Kitao (IMCB, Univ. Tokyo)

Proteins exert large conformational fluctuations and changes, which are essential for their functions. This softness is a key to understand the mechanism of protein function and regulation. Molecular dynamics simulation has become a powerful tool to observe protein motion at atomic resolution normally up to microsecond order and it is still difficult to simulate slower motions by molecular dynamics without the use of special-purpose super computers. We have been developing molecular simulation methods to investigate soft protein motions efficiently. These methods utilize anisotropic nature of protein fluctuations. Relationship between soft protein motion and function elucidated by the simulation methods will be demonstrated.

Continuous tracking of protein folding at microsecond resolution by a line confocal detection of single molecule fluorescence

Satoshi Takahashi (IMRAM, Tohoku Univ.)

We developed a line-confocal microscope combined with fast sample flow (Oikawa et al., Sci. Rep. 3, 2151 (2013)), and achieved the time resolution of 20 microsecond in measuring single molecule FRET efficiency. We investigated the B domain of protein A (BdpA) and ubiquitin doubly labeled with donor and acceptor fluorophores. While the traces observed for BdpA can be interpreted in the framework of two-state mechanism, the native traces showed the gradual shift in the FRET efficiency, which is reminiscent of the downhill folding proteins. We also observed the folding process of ubiquitin after a rapid dilution of the denaturant. The data suggest the appearance of broad substrates of the unfolded ubiquitin in the native solution condition.

光応答性タンパク質の機能転換が明らかにする柔らかで機能的な構造機能相関
“Soft” structure-function relationship revealed by functional conversion of photoreceptive proteins

Hideki Kandori (Nagoya Institute of Technology)

Various protein functions often derive from a common protein architecture, as is seen for microbial rhodopsins (sensor, pump, channel). Researchers believe that such structure-function relationship has been optimized during evolution, but we sometimes achieved functional conversions. This suggests that structure and function are flexibly coupled with each other, and “softness” of such biomolecular systems is a key to understand functional conversion. I will present our experimental efforts on photoreceptive proteins such as rhodopsins and flavoproteins. We try to find new protein functions from nature, as we did for a light-driven sodium pump. We also like to attain functional conversions by mutation, as we did for light-driven proton and chloride pumps.

酵素活性におけるタンパク質の柔軟性の役割
Crucial Role of Protein Flexibility in Enzymatic Catalysis

Shigehiko Hayashi (Department of Chemistry, Graduate School of Science, Kyoto University)

Protein functional processes involve dynamic molecular conformational changes of complex protein systems which often correlate with enzymatic chemical reactions. Hence molecular mechanism of enzymatic activities and coupling of the chemical reactions with protein molecular dynamics underlying functional processes need to be revealed for understanding of molecular nature of protein functions. In the talk, our recent molecular simulation studies on enzymatic reactions in Ras-GAP GTPase and on conformational changes of the chromophore in retinal proteins will be presented, and role of protein conformational changes and flexibility in chemical processes will be discussed.

人工細胞回路を用いた DNA コンピューティングの実現
DNA computing through biological nanopore in droplet network system

Ryuji Kawano (TUAT)

The goal of this study is to establish the calculating system using DNA and biological nanoprobes in artificial cell network. We are envisioning for living cells as being a replacement for the kinds of computers that we have now. As an opening gambit, we propose a binary system of NAND logic gate by using single-stranded DNA (ssDNA) and alpha-hemolysin (aHL) nanopore. Here individual ssDNA is used as inputs and outputs are obtained by monitoring electrical signal. This method is significantly different from the conventional computation using DNA in the respect that electrical signals are directly obtained. Therefore, rapid calculation in the droplet network is expected in comparison with conventional computations.