structures due to the difference in the crystal packing or in the ligand-binding state.

- 3P-019 Go モデルによるタンパク質のフォールディングシミュレーションと残基間平均距離統計に基づくフォールディング機構予測との比較
Protein folding simulation based on the Go model and comparison with the predictions of folding mechanism based on the interresidue average distance statistics

Masatake Sugita (1), Takeshi Kikuchi (2) ((1) Dept. Bioinformatics, Col. Life Sci., Ritsumeikan Univ.; (2) Dept. Bioinformatics, Col. Life Sci., Ritsumeikan Univ)

We have tried to predict the protein folding pathway using the analyses of a contact map based on the interresidue average distance statistics, Average Distance Map (ADM). On the other hand, it is known that the Go model can reproduce protein folding processes based on protein native structures. Recently, we have tried to simulate the folding mechanism of Protein G using a coarse grained Go-model and showed that our method predicts the folding pathway of the Protein G, i.e., our simulation give the folding process similar to that obtained by the experiment, and predicted by the ADM analysis. In our model, we take the properties of the native structure into consideration by incorporating the native hydrogen bonds and hydrophobic interactions in the interresidue potential in addition to the simple Go-type potential. In this work, we perform the Monte Carlo simulation using the present coarse grained Go model for the proteins which are topologically homologous to protein G but show different folding mechanisms. We will examine the differences among the folding processes of these proteins predicted by our model, and we compare the results to those by ADM analyses. We will also discuss the further application of our method in the relation to the prediction made by ADMs. 1) E. L. McCallister et al., Nature Str Biol., 7, 8, 669(2000) 2) T. Kikuchi., Amino Acids., 35, 541(2008)

- 3P-020 T4 ファージ尾部基盤を構成するウェッジの in vitro 分子集合
Baseplate Wedge Assembly of Bacteriophage T4 in vitro

Moh Lan Yap (1), Yasunori Monzaki (1), Kazuhiro Mio (2), Leiman Petr (3), Shuji Kanamaru (1), Fumio Arisaka (1) ((1) Grad. Sch. of Biosci. and Biotech., Tokyo Institute of Technology; (2) National Institute of Advanced Industrial Science and Technology, AIST; (3) École Polytechnique Fédérale de Lausanne, Institut de physique des systèmes biologiques, Cubotron, Switzerland)

The wedge assembly of phage T4 is a well-known example of the strictly ordered interactions of protein subunits in macromolecular assembly. A central hub and six wedges combine to form a hexagonal tail baseplate. Seven gene products gp11, gp10, gp7, gp8, gp6, gp53, and gp25 associate sequentially in this order to form a wedge in vivo. Gp11 is an exception of this ordered sequential assembly pathway, where it can be added at any stage of the assembly pathway. We report the first trial of the whole wedge assembly in vitro by utilizing expressed proteins. In this study, gp8, gp6, (gp10)₃(gp7)(gp8)₂, and (gp10)₃(gp7)(gp8)₂(gp6)₂, were isolated and sedimentation velocity analyses of the individual proteins and the complexes indicated that they are hydrodynamically homogeneous and that the complexes are stable. Addition of gp53 to the complex resulted in forming hexagonal particles and addition of gp25 increases the efficiency of the formation of these particles. These particles resemble the baseplate in expanded star-shaped conformation. It might be possible that these star-shaped structures are in equilibrium between hexagon and star conformations. Attachment of the gp11 and the short tail fiber, gp12 may fix the hexagon conformation. Addition of gp11 and gp12 to the baseplate-like hexameric wedges is underway.

- 3P-021 ヒトガレクチン1の糖結合活性の pH 依存性
pH dependence of the galactoside-binding activity of human galectin-1

Katsuyuki Takeuchi (1), Hirotsugu Hiramatsu (1), Hideo Takeuchi (1) ((1) Graduate School of Pharmaceutical Science, Tohoku University)

Human galectin-1 (hGal-1) is one of the animal lectins that specifically bind β -galactosides. hGal-1 exists as a dimer under physiological conditions and each subunit has one galactoside-binding site. The hGal-1-mediated bridging of two carbohydrate molecules on different cell surfaces is considered to be important in cell adhesion and cell signaling. The mechanism of the galactoside-binding is, however, not well understood. In this study, we have investigated the pH dependence of the galactoside-binding activity of hGal-1 and its mechanism.

The galactoside-binding activity obtained from the peak shift of Trp fluorescence showed a transition at pH 6.2 with higher activities on the neutral-to-alkaline side. Each subunit of hGal-1 contains two His residues and the pK_a values of the His side chains were obtained to be 6.1 and 7.4 by ultraviolet resonance Raman spectroscopy. The coincidence of the pH of activity transition and one of the pK_a values of the His residues strongly suggests an involvement of a His residue in the pH dependence of the galactoside-binding activity. Possibly, the His residue is involved in the binding of galactoside through direct hydrogen bonding with the galactoside molecule. Furthermore, the His residue seems to be involved in the structural stabilization of the galactoside-binding pocket because

the secondary structure and the environment of the Trp side chain change with the protonation of the His residues.

- 3P-022 細菌べん毛ペリプラズムタンパク質 FlgA の X線結晶構造と機能解析
X-ray Crystal Structure and Functional Analysis of a Periplasmic Flagellar Protein FlgA

Hideyuki Matsunami (1), Samatey Fadel A. (1), Shigehiro Nagashima (2), Katsumi Imada (2), Keiichi Namba (2) ((1) Trans-Membrane Trafficking Unit, OIST; Dynamic NanoMachine Project, ICORP, JST; (2) Dynamic NanoMachine Project, ICORP, JST; Grad. Sch. Frontier. Biosci., Osaka Univ.)

Bacterial motility is achieved by rotation of flagella. The bacterial flagellum is a macromolecular complex that allows bacterial cells to swim in liquid environment. The complex is composed of the helical filament, the flexible hook and the basal body embedded in bacterial inner and outer membranes penetrating peptidoglycan layer. The basal body is divided into three sub-structures, the LP-ring, the MS-ring and the rod. The LP-ring, as molecular bushing, spans between bacterial outer membrane and peptidoglycan layer. FlgH and FlgI are the subunit proteins of the LP-ring and a periplasmic flagellar protein FlgA is involved in the P-ring assembly. Previous biochemical studies indicated that FlgA might associate with FlgI after secretion into the periplasm and act as a key protein for the flagellar P-ring assembly. Structural information is required to understand how FlgA works. The atomic structure of FlgA from *Salmonella enterica* serovar Typhimurium was determined by MAD method using a Pt-derivative crystal. The over-all structure revealed that FlgA comprised of two distinct domains as shown by limited-proteolysis experiment. The N-terminal domain whose function in the P-ring assembly is still unknown had a disulfide bond. The C-terminal domain forms a unique fold with β -structures. The C-terminal truncation of FlgA caused complete loss of motility and interaction with FlgI. We characterize functions of FlgA and propose the molecular mechanism of the flagellar P-ring assembly.

- 3P-023 Febuxostat とキサンチン脱水素酵素の鍵と鍵穴機構におけるタンパク質の揺らぎの重要性
Significance of enzyme fluctuation in the lock-key mechanism between xanthine oxidoreductase and Febuxostat

Hiroto Kikuchi (1), Hiroshi Fujisaki (2), Tadaomi Furuta (4), Ken Okamoto (3), Takeshi Nishino (3), Silke Leimkuhler (4) ((1) Dept. of Phys., Nippon Medical School; (2) Molecular Scale Team, Computational Science Research Program, RIKEN; (3) Dept. of Biochem. and Mol. Biol., Nippon Medical School; (4) Inst. of Biochem. and Biol., Univ. of Potsdam, Germany)

Ligand binding is an essential step to initiate chemical reactions and/or conformational changes in enzymes and the lock-key mechanism (shape complementarity) is still of central importance to understand the binding process. The structure-based drug design stems from this conceptualization to find better ligands (inhibitors) and many sophisticated docking algorithms and softwares have been devised and utilized. However, in the case of an enzyme, xanthine oxidoreductase (XOR), which is found in a wide range of organisms from bacteria to man, the experimental results showing the breakdown of the lock-key mechanism were reported. Although the 3D-structure of the ligand cavity for the mammalian XOR is almost the same as that for the bacterial XOR, a structure-based inhibitor of the mammalian XOR, Febuxostat, does not work for the bacterial XOR. This fact indicates the importance of choosing the species in the drug design, and also might show the limitation of the static picture of the lock-key mechanism of ligand binding. In this poster, we illustrate that the description of the binding process should be built upon a more dynamic picture. First, the 3D-structures of the ligand cavities for the mammalian and bacterial XOR are compared. Second, the binding affinity is calculated by a docking algorithm, and the limitation of the static picture of ligand binding is examined. Finally, molecular dynamics simulations are performed and a dynamic principle of ligand binding in the case of the mammalian and bacterial XORs is suggested.

- 3P-024 インターロイキン 13 受容体 $\alpha 2$ (IL-13R $\alpha 2$) の調製とその性質
Expression and Characterization of Interleukin-13 receptor $\alpha 2$ chain (IL-13R $\alpha 2$)

Fumiko Matsumoto (1), Taro Tamada (1), Eijiro Honjo (1), Shoichiro Ohta (2), Kenji Izuha (2), Ryota Kuroki (1) ((1) Molecular Structural Biology Group, Quantum Beam Science Directorate, Japan Atomic Energy Agency; (2) Division of Medical Biochemistry, Department of Biomolecular Sciences, Saga Medical School)

The allergic disease has dramatically increased in recent years. Interleukin-13 (IL-13) is a key cytokine critical to the development of T-cell-mediated humoral immune responses which are associated with allergy and asthma. IL-13 possesses two types of receptor: the heterodimer, composed of IL-13R $\alpha 1$ and IL-4R α , transducing the IL-13 signals; and the IL-13 $\alpha 2$, acting as a non-signaling "decoy" receptor. Although the extracellular region of IL-13R $\alpha 1$ and IL-13R $\alpha 2$ are composed of a common structure of the class I cytokine receptor superfamily and