3P031 X 線 1 分子追跡法による蛋白質安定性の解析**Protein Stability Analysis of MHC/peptide Complex from X-ray Single Molecule Tracking**

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MHC (Major HistoCompatibility) is a dimer protein which is known as antigen peptide presentation in the immune system. However, perspectives on the antigen peptide presentation mechanism have not yet been unified. Therefore, we focused on the single molecule motion and chose six different peptides binding MHC/peptide complex for the comparison. We measured multi-molecule analysis to complement molecular dynamics data from single-molecule measurement.

We succeeded in confirming the relationship between single-molecule dynamics from Diffracted X-ray Tracking (DXT) and dimer stability from SDS-PAGE. DXT will be observed the in vivo single molecule stability without separation of dimer proteins.

3P032 表層ストレス応答を制御する膜内切断プロテアーゼ RseP のタンデム PDZ ドメインによる基質選別機構**Substrate discrimination mechanism by a PDZ tandem in the intramembrane protease RseP that regulates extracytoplasmic stress response**

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During the σ^E pathway of the extracytoplasmic stress response in *Escherichia coli*, intramembrane protease RseP cleaves the anti- σ^E protein RseA only after membrane-anchored protease DegS truncates the periplasmic part of RseA. Here we analyzed the 3D structure of the two tandemly-arranged PDZ domains (PDZ tandem) of an RseP orthologue and revealed that the two putative ligand-binding grooves constitute a single pocket-like structure. Complete removal of the PDZ tandem from *E. coli* RseP led to the deregulated cleavage of RseA without prior truncation by DegS. From these and other results we propose that the PDZ tandem serves as a size-exclusion filter to discriminate between the intact and truncated forms of RseA.

3P033 Design of Photo-controllable Cyclic Peptides

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β -sheet-like Cyclic Peptide Nanotubes (CPNs) offer a variety of applications in chemistry, biology and micro electronics. CPNs are produced by stacking of cyclic peptides (CPs) containing alternated D-L- α amino acids. CPs can adopt a flat, closed-ring shape and stack through intermolecular hydrogen bonding oriented perpendicular to the plane of the ring structure. However, it is difficult to control self-assemblies of CPs without drastically changing pH or temperature. Photoregulation using chromophores, such as azobenzene, is a powerful approach to control a function and conformation of biomolecules. Herein we report design, synthesis, and characterization of novel azobenzen-CPs complex in which the β -sheet content can be reversibly photo-controlled.

3P034 脂質-タンパク質相互作用の解明を目指した重原子標識脂肪酸の利用**Toward an understanding of lipid-protein interactions, the use of the heavy atom labeled fatty acid analogues**

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Fatty acid binding protein (FABP) is small cytosolic protein that is involved in fatty acid (FA) processing. FABP are also widely distributed in all tissues and exhibits high-affinity binding to a single long-chain FA. In order to understand the functions of lipids and the role of lipid-protein interactions, we performed the crystal structure analysis of FABP in complex with FA. However, the electron density of alkyl chain of the FA molecule was initially very poor. This result suggests that the FA may be highly flexible molecule or possess some different conformations. To verify this, we used the FA analogues with Se or Br atoms instead of C atoms of FA. We report the crystal structures of FABP in complex with FA analogues.

3P035 嗅覚受容体モデルとしてのオプシン立体構造**Opsin, Structural Model for Olfactory Receptors**

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Among the large family of G protein-coupled receptors, about half of them are olfactory receptors (ORs), for which high-resolution structures remain elusive. Rhodopsin is the photoreceptor in vision and its ligand, retinal, shares high hydrophobicity with OR ligands. Here we report a new crystal structure of the opsin apoprotein. A molecule of octylglucoside was identified in the ligand-binding pocket and stabilizing the active receptor conformation. As prototypic mimics of odorants, several detergents were tested for their capability to enter opsin's ligand-binding pocket. The study provides an explanation on how hydrophobic odorants can enter OR, supports odorant-receptor hydrogen bonding for OR activation and establishes opsin as a new basis for OR homology modeling.

3P036 13-cis 型が優勢となる ASR 変異体の研究**Study of *Anabaena* Sensory Rhodopsin mutant P206D that contains the 13-cis form dominantly**

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Anabaena Sensory Rhodopsin (ASR) is a microbial rhodopsin found in *Anabaena* (*Notstoc*) sp. PCC7120, a freshwater cyanobacterium. ASR regulates transcription by sensing light. We found that the photoreaction of ASR is completely photochromic; the stable photoproduct of the all-trans form is 100 % 13-cis, and that of the 13-cis form is 100 % all-trans [1].

In present study, we focus on an interesting mutant, ASR P206D. Pro206 is characteristic for ASR, because the corresponding amino acid is highly conserved Asp in microbial rhodopsins (Asp212 in BR). HPLC analysis shows that ASR P206D contains 13-cis retinal dominantly both in dark and light conditions. We will discuss its photoreaction and structural change.

[1] Kawanabe et al., *J. Am. Chem. Soc.* 129, 8644 (2007).