2P043 多剤排出トランスポーター AcrB の Motion-Tree による解析 Motion-Tree analysis of the multidrug transporter AcrB

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AcrB is one of the proton-driven multidrug transporters from the Gram-negative bacteria *E. coli*, and forms homo trimer with different conformations that are sequentially converted during drug export. These cyclic conformational changes are called functionally rotating mechanism. We have studied about the structural changes through functionally rotating mechanism using the Motion-Tree analysis, which is a new method to describe the structural change as rigid body motions, and some of the key motions were observed. In the present study, we added the analysis of rigid body motions by using other conventional methods, and obtained the supportive information for the results of Motion-Tree analysis. We will show the detail of the results in the poster presentation.

2P044 Conformational states of HAMP domains interacting with SRII-membrane systems: A molecular dynamics approach

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Signal transduction in sensory rhodopsin-transducer (SRII-HtrII) complex is still elusive due to structural inadequacy in *N. pharaonis*. We studied SRII-HtrII complex by molecular dynamics simulation in various force fields, lipid bilayers, and environments. Results showed, the HtrII having two four-helix bundles (HAMP1 and 2) was stable at 323K and 1.15M NaCl concentration. MM/PBSA computed ΔG of -355.4 (ground), -229.1 (intermediate) state, and -156.6, -92.6 and -83.7 kJ/mol for different HtrII dimer fragments. Mutation at T189 and N74 (SRII), and E43 and S62 (HtrII) minified the ΔG . The HAMP conformation and stability were highly influenced by the complex state (monomer/1:1/2:2). The helix rotations depicted a new insights into the signaling mechanism.

2P045 高速 X 線 1 分子追跡法によるニコチン性アセチルコリン受 容体の機能運動 3D X-ray Single Molecule Tracking of nAChRs in Open, Resting, and Desensitization States

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The nicotinic acetylcholine receptor (nAChR) is well-studied neurotransmitter receptors and there are several conformational states of nAChRs, such as open, resting, desensitized states. However the structural information of each state and mechanism of changing states remains incompletely understood. We addressed to elucidate dynamic information of nAChRs in different states by single molecule technique with diffracted X-ray tracking. We found that the combined tilting and twisting motions of α -subunit nAChR were enhanced with ACh, those motions were inhibited with toxins, and only tilting motion was inhibited with excess nicotine in the solution. The finding is consistent with recent electron crystallography study and the detailed dynamic information will be discussed.

2P046 ドメイン運動の階層的な解析により描かれる SERCA の反応 による構造変化

**Conformational changes of SERCA in response to reactions
described by hierarchical domain-motion analysis**

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Sarco(endo)plasmic reticulum Ca^{2+} -ATPase (SERCA) pumps Ca^{2+} across membranes against a large concentration gradient. The X-ray structures reveal rearrangement of transmembrane helices coupled with large-scale cytoplasmic domain motions. To characterize the conformational changes, we illustrate 'Motion Tree (MT)' based on crystal structures of SERCA. MT elucidates coupling between the motions of transmembrane helices and the cytoplasmic domain motions in individual reaction step. By gathering information from all MTs, rigid structural units of SERCA throughout the whole enzymatic cycle are identified. We discuss conformational changes of SERCA in response to individual reactions by characterizing its intrinsic conformational rigidity and flexibility.

2P047 大腸菌機械受容チャネル MscL の開口における脂質膜環境に 影響される脂質-タンパク質間相互作用の解析

**Analysis on Lipid-Protein Interactions Affected by Membrane
Environment in Mechano-Gating of the E.coli
Mechanosensitive Channel MscL**

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One of mechanosensitive channels MscL is homopentamer with two transmembrane inner and outer helices and opened by sensing membrane tension. It is known that MscL in thinner bilayer can open easily, however, its atomic detail remains unclear. So in this study, we prepared four types of membrane with different thickness and performed MD simulations for the opening process of MscL. As a result, MscL in thinner membrane model actually opened more widely. Furthermore, a helical structure of the periplasmic side of the outer helices, corresponding to be a major tension sensor region, was slightly broken. From these results, it is suggested that the breaking may be important for stable interaction with lipids and energetically favorable in the opening process of MscL.

2P048 天然変性タンパク質と変性状態蛋白質の構造特性の比較 A Comparison of structural properties between an intrinsically disordered protein and denatured state of proteins

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The unfolded protein in solution consists of an ensemble with a great number of conformations. As an experiment gives only a piece of structural information of the unfolded protein, it is necessary to integrate diverse experimental data for elucidating its structural properties. We developed a computational method for generating conformations of unfolded protein. It enables us to generate a large number of conformations very rapidly. Using our method, we have tried to find an ensemble which best reproduces experimental residual dipolar couplings data. As a result, the structural properties of α -synuclein was clarified. In the annual meeting, we will discuss differences in structural properties between α -synuclein and some other denatured state of proteins.