2P031 Mechanism of glycan receptor recognition for influenza virus Hemagglutinins: Comparative molecular dynamis studies

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The heamagglutinin (HA) of influenza viruses mediate receptor binding, the initial event in virus infection. The differences in receptor-binding specificity of human and avian viruses are determined by the amino acid residues in the HA receptor-binding pocket. Asp at position 190 and 225 of H1 HAs confer binding to human-type receptors, whereas E190 and G225 confer binding to avian-type receptors. However some isolated viruses have E190 or G225, and D190E/D225G substituted virus does not prefer avian-receptor always. To clarify the detail effects of changes on binding for different HAs, molecular dynamics simulations were performed for the H1HA-glycan receptor complexes which comprise wild type and one point amino acid substituted HAs at positions 190 or 225.

2P032 比較粗視化シミュレーションを用いたタンパク質-リガンド結合過程の解析

The factors determining protein-ligand binding processes revealed by comparative coarse-grained simulations

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Clarifying the mechanism of protein-ligand interactions is one of the most important research subjects in the field of biophysics. However, most of the research efforts have been devoted to predicting docked structures. The process of the ligand binding remains to be clarified. Previously, we analyzed ligand binding processes of several protein ligand pairs that differ in physicochemical and geometric properties of the ligands and the ligand-binding pockets using the coarse-grained simulation. The results suggested that the ligand binding process depends on these properties. In this study, we applied this method to various additional protein-ligand systems. We will discuss the generality of the tendencies of the ligand binding processes.

2P033 DM 分子はペプチド交換時の MHC 複合体の動きを制御する DM defines motions of peptide/MHC complex for peptide exchange

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DM catalyze peptide exchange reaction of MHC II. Crystal structures suggest that DM bound form of MHC II generate novel threshold for peptide binding by creating a hydrogen bond inside the binding groove, that form half bound intermediate peptides complexs. To examine the hypothesis, we used fluorescein labeled peptides to check the degree of quenching that results in a remarkable difference; fluorescein peptides give twice a signal with DM, which suggests peptides floating half way from MHC II. DXT analyses with gold nano-crystal at the same position of the peptide revealed that peptide/MHC complex has two ground states without DM, and the two states converged to a single state by addition of DM. We will discuss the mechanism of DM action based on these observations.

2P034 高速 AFM による MukB の構造と機能の観察 High-speed AFM observation of structure and function of MukB

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MukB is a structural maintenance of chromosomes (SMC) protein that performs chromosome segregation and condensation in E. coli. Structurally, MukB forms homodimer at a central globular dimerization domain each of which is followed by a long coiled-coil and an ATPase head domain. Although it is important to understand how MukB interacts with DNA and maintains chromosomal structure, these reaction mechanisms at the single molecular level remain poorly understood. Here, we apply high-speed AFM to directly observe structure and function of MukB. At the moment, structural details of single MukB and binding manners between MukB and plasmid DNA were visualized at nanometer spatial resolution. In the presentation, we will report the obtained results.

2P035 アミロイドベータペプチドのオリゴマー形成機構の解析 Analyses of the oligomerization mechanism of amyloid β peptides

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The deposition of senile plaques is observed in the brains of Alzheimer's disease (AD) patients. Amyloid β peptide (A β) oligomers, formed in the process of senile plaque production, appear to be neurotoxic in AD. The A β (1-40), A β (1-42) and A β (1-43) species, which have different C-terminal lengths, were previously identified. A β (1-42) and A β (1-43) aggregate more easily than A β (1-40). Additionally, N-terminally modified A β species, pyroglutamate A β s, are also more prone to aggregation than unmodified A β s. To elucidate the roles of A β species on the A β oligomer formation, we utilized solution NMR, PICUP (Photo-Induced Cross-linking of Unmodified Proteins) and ESI-TOF MS. Our results indicated that multiple regions of A β contribute to the oligomer formation.

2P036 カメレオンモデルを用いた酸素結合に伴うヘモグロビンのアロステリック転移の研究

A study of the allosteric transition of hemoglobin associated with oxygen binding using chameleon model

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We investigate the mechanism of the allosteric transition of hemoglobin by Langevin dynamics simulation using a new coarse-grained potential model, "the chameleon model". In this model, the energy minimum of local potential is switched between two positions depending on the local structure around the interaction site. We characterized the allosteric transition by the average structure of the transition state ensemble as well as the correlation of the movement of each residue. We found the positive correlation between the structural change around Fe atom and the global structural changes, which has been considered as sequential events in the Perutz model. Based on these results, we discuss the molecular mechanism underlying the cooperativity of allosteric transition.