3P068 タンパク質と麻酔薬の相互作用に関する研究
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Study of the interaction between protein and anesthetic
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Anesthetics have in common the capacity to partition indiscriminately into all biological membranes and act as general perturbants of membrane structure and function, but anesthetic mechanisms have not yet been clarified. Some measurement techniques are used to investigate the interaction between the anesthetic and the biological materials. In this study, the binding of local anesthetics to proteins (bovine serum albumin (BSA) and lysozyme) was examined by using the electrode selectively sensitive to local anesthetic cations. The electromotive forces (EMF) of the local anesthetic dibucaine and tetracaine cation-selective electrodes were measured relative to an Ag-AgCl reference electrode in the absence and the presence of protein at pH5.5. In the absence of protein, both the dibucaine and tetracaine electrodes showed a linear response with a Nernstian slope over the concentration of 10⁻⁶ M. In the presence of BSA or lysozyme, the response curve was shifted toward the higher concentration of anesthetics, which means the decrease of the concentration of free anesthetic cation due to the binding to BSA or lysozyme. The binding isotherms of anesthetics to BSA were calculated from a pair of response curves. The slope of binding isotherm increased steeply above a certain concentration of local anesthetics, which means that the binding form of local anesthetic into BSA or lysozyme is the multiple-step.

3P070 中性子散乱によるアクチンの運動特性の直接測定
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Direct measurements of internal dynamics of actin by neutron scattering
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Actin plays crucial roles in various aspects of cell motility. Flexibility of F-actin, a filamentous polymer formed by polymerization of the monomers (G-actin), is important for such a variety of functions. This flexibility allows F-actin to interact with various kinds of actin-binding proteins, thereby expressing multiple functions. Understanding the variety of functions of actin thus requires understanding the flexibility of F-actin. As a first step towards this ultimate purpose, we have started a series of experiments to characterize dynamics of G-actin and F-actin. Here, we carried out elastic incoherent neutron scattering (EINS) and quasi-elastic neutron scattering (QENS) experiments on G-actin and F-actin under hydrated states. The experiments were done on the instruments IN16 and IN5 in the Institut Laue-Langevin, Grenoble, France. The mean square displacement (MSD) was estimated from the EINS measurements. Temperature dependence of MSD showed different behaviors in G-actin and F-actin. The QENS spectra, by which the dynamics of actin could be characterized as diffusion motions within a restricted region, also showed clear differences in G-actin and F-actin. Analysis of the EINS and QENS spectra obtained suggested that actin has dynamical heterogeneity, a region showing similar softness, or flexibility, both in G-actin and F-actin and that becoming more flexible in G-actin than in F-actin. The results of the detailed analysis will be presented.

3P069 Characterization and molecular assembly of the neck proteins, gp13 and p14, of bacteriophage T4
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Characterization and molecular assembly of the neck proteins, gp13 and p14, of bacteriophage T4
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After packaging of DNA into the head of bacteriophage T4 is completed, a neck is formed at the portal vertex of the head to be ready for the tail attachment. The main components of the neck are gp13 and gp14 (gp: gene product), which consist of 309 and 256 amino acid residues, respectively. In order to elucidate the structure and subunit arrangement in the neck, overexpression systems of gene 13 and gene 14 were constructed separately and together. Both proteins were purified by several chromatographies. Far-UV circular dichroism (CD) spectra of gp13 and gp14 indicated that gp13 is rich in α -helices, whereas gp14 is rich in β -sheets. Sedimentation velocity analysis of gp13 and gp14 revealed that both proteins are present as monomers in solution. Under physiological conditions purified gp13 and purified gp14 did not form complex, but ammonium sulfate treatment induced a complex which had the sedimentation coefficient of 16.3S for the major component of the oligomers and the molecular weight of 472,000. Based on the molar ratio 2:1 for gp13 and gp14 and taking the molecular weights of 34,745 and 29,575 calculated from the amino acid sequence for gp13 and gp14, respectively, a stoichiometry of 10:5 is most likely, with a resulting molecular weight of 495,300. It was concluded that the gp13-gp14 complex is a hetero-15-mer or (gp13)₁₀(gp14)₅. Electron microscopy of this complex revealed some distinct shape and size with a ring-like structure of 15 nm in diameter.

3P071 パーコレーション転移における蛋白質水和水の構造とダイナミクス
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3aF08 Structure and dynamics of the protein hydration water at the percolation transition
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Structure and dynamics of hydration water on protein were examined at various hydration levels to study hydration effect on protein dynamics. It was found that hydration dependent protein dynamical transition was observed at round 240K, which is more significant above the threshold hydration level h=0.30 (g water/g protein). At the low hydration level, hydration water is localized. On the other hand, at the higher hydration level the connectivity of the hydration water forms on the protein surface via hydrogen bond. The hydrogen bond network among the hydration water encircle the whole protein and the hydration water is percolated on the protein surface above the threshold hydration level. The protein dynamical transition is highly correlated with the percolation transition of the hydration water. At the percolation transition the translational dynamics of the hydration water markedly increase. The anomalous dynamical behavior of hydration water is coupled with the protein dynamics via hydrogen-bond network at protein-water interface. Such a dynamical coupling drives the hydration dependent protein dynamical transition.