eukaryotic protein. High pressure typically induces depolymerization of the actin filament or loss of the actin ATPase activity in the species living in land or shallow water, whereas deep-sea fish α -actin is high pressure-adaptive. Although it has few amino acid substitutions, they contribute to tolerance to high pressure. ATP binding to monomeric α -actin promotes the polymerization at the end of the filament and ATP is hydrolyzed to ADP during the elongation of the filament. This catalysis needs divalent cation Ca^{2+} or Mg^{2+} that has high-affinity to ATP. The active site is located at the nucleotide cleft in the center of the protein. The divalent cation at active site is coordinated by 6 to 8 oxygens in crystal structures. The oxygen of Q137 side chain is directly coordinated to the cation. However, deep-sea α -actin fish has the substitution Q137K that is expected to contribute to the pressure tolerance. Molecular dynamics simulations of the actin molecules from distinct species at atmospheric pressure and high pressure have been performed in order to analyze the effects of the amino acid substitutions and the mechanism of the tolerance.

2P018 アミノ酸配列の連続性, 順序性を無視した蛋白質立体構造アライメントの新規手法
A novel method for non-sequential protein structure alignment.

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Protein structure comparison is fundamental approach for protein classification, studies of evolutionary relationships, and so on. Today, there are many structure alignment tools, most of which follow a simple sequential rule: two proteins are aligned in sequential order. That is because it is generally assumed that similar protein structures will align to each other in a sequential manner, conserving the direction of the chain. However, recent structural comparison studies have suggested that there are many examples of structural similarity that are non-sequential. The most popular example of these relationships may be circular permutations. Analyzing such non-sequential similarities would give us some new insights into physico-chemical properties and evolution of protein structures.

We have developed a novel method of non-sequential protein structure alignment utilizing geometric hashing technique and vectorial representation of secondary structure elements (SSE). The algorithm can identify the best structural alignment between protein pairs without constraints of sequential connectivity and that of SSE direction. Vectorial representation of SSE used in the method is different from the one which has been often used in the past. One SSE is represented by a number of vectors and the number of vector representing one SSE is depend on the length of SSE. Thus, the method can appropriately treat bent strands or bent helices. We will present the results of benchmark test and comparing to other structural alignment methods.

2P019 分子動力学シミュレーションによるグルタチオンとグルタチオン転移酵素 T2-2 の構造とダイナミクス
Structure and dynamics of glutathione and glutathione-transferase T2-2: a molecular dynamics study

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Glutathione is an antioxidant concerned with the detoxification metabolism in vivo and has a function to defecate toxic compounds from cells. Glutathione-transferase has been known to reduce the reactivity of toxic compounds by catalyzing their conjugation with glutathione. Glutathione-transferase is an enzyme that plays a critical role in the cellular detoxification process and resides in body tissues like kidney, bowel, lung and liver. The function of glutathione and glutathione-transferase has been through to implicate in detoxification. Thus, the understanding of the binding character between the glutathione and glutathione-transferase should be important in the realization of catalytic reaction mechanism and contribute the development of antibiotic drug. In this study, we analyze the structure and dynamics of the glutathione and the glutathione-transferase T2-2 in water solvent by the molecular dynamics simulations to understand the changes of structures due to the binding the glutathione and glutathione-transferase. We carried out the molecular dynamics simulations of the glutathione-transferase T2-2 contains glutathione and the one without glutathione. The dynamics of these model proteins are estimated by principal component analysis.

2P020 残基間平均距離統計に基づくフェレドキシン様フォールドのフォールディング機構の解析
The analyses of the folding mechanism of the Ferredoxin-like folds based on renewed inter-residue average distance statistics

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A protein in the Ferredoxin-like fold forms the same 3D structure even if the two proteins share low sequence identity, i.e., this 3D scaffold constitutes a "superfold". In the present work, we try to identify the important regions in the sequences for the formation of the 3D-scaffold by means of the methods based on inter-residue average distance statistics, i.e., an average distance map and the contact frequency of a pair of residues. In a previous study, we demonstrated that it is possible to identify the folding mechanism of the Ferredoxin-like fold with no 3D information but only sequence information. In this study, on the basis of previous work, we try to identify very important sequence regions or some characteristic structural motifs in the construction of Ferredoxin-like fold by analyzing with high accuracy predicted contact maps that are calculated with renewed inter-residue average distant statistics. The details will be presented at the conference.

2P021 側鎖の効果を取り入れた粗視化 Go モデルと ADM を併用した IgG 結合ドメイン関連タンパクのフォールディング機構の解析
Analyses of the folding mechanisms for the IgG binding domain related proteins based on a coarse grained Go model and ADM

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The Go-model can reproduce protein folding pathway using protein structure information. It accounts interactions which stabilize the native structure of a given protein. In the previous work, we reproduced the differences in the folding pathway of Protein G from that of Protein L using our Ca -Go-model. This Ca -Go-model makes it possible to simulate protein folding pathway with same accuracy to all-atom-Go-model by incorporating the differences in side-chain direction using virtual bond angle around Ca atoms. On the other hand, ADM(Average Distance Map) which is a sequence analysis method based on the statistical average distances between residues can predict the area which folds early. This method was successfully applied to predict folding pathways of globins. In this study, at first, we apply these methodologies to predict folding pathway of G311 and GB95. G311 and GB95 are designed protein based on Protein G. Secondly, we compare the results of predicted folding pathway of G311 and GB95 with the folding pathway of Protein G and Protein L. Protein G, Protein L, G311 and GB95 share same topology but have diverse sequence identity (24% to 64%). These proteins should implicitly contain information to fold same topology. We try to extract the information in the present study.

2P022 Pseudomonas sp. B-0831 由来 3 α -hydroxysteroid dehydrogenase の補因子および基質との複合体構造に関する理論的研究
Theoretical Study of Complex Structure of 3 α -Hydroxysteroid Dehydrogenase from Pseudomonas sp. B-0831, NAD(H), and Substrate

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3 α -Hydroxysteroid dehydrogenase from *Pseudomonas* sp. B-0831 (Ps3 α HSD) catalyzes the reversible oxidoreduction of the steroids between 3 α -hydroxysteroid and 3-ketosteroid. The crystal structure of the binary complex of Ps3 α HSD with NADH exhibited a heterodimer which is formed by *apo*- and *holo*-subunits, and the binding experiments showed the negative cooperativity in the NADH binding to Ps3 α HSD. In this study, we investigate the role of the structural heterodimer on the formation of ternary complex of Ps3 α HSD with NAD(H) and substrate using the computational method. Because the ternary complex structure of Ps3 α HSD with cofactor and substrate has not been determined, we performed docking calculation and molecular dynamics simulation to determine it using NADH and androstane as cofactor and substrate, respectively, as an oxidized model. When the complex of *holo*-subunit including NADH obtained from the crystal structure was used as a model to reduce computational efforts, no proper conformations were obtained. We next used the heterodimer structure, and the binding conformations were obtained. Since the distance between substrate and NADH is about 3.5 Å, we think that the conformation obtained from the calculation with the heterodimer was proper for the reduction of 3-ketosteroids. We will discuss the structural uniqueness of Ps3 α HSD based on further theoretical analyses and experimental results.

2P023 銅含有アミン酸化酵素触媒反応における時間分割 X 線結晶構造解析
Time-resolved X-ray crystal structure analysis of enzymatic reaction of copper amine oxidase from *Arthrobacter globiformis*