1P002 ATP アナログ結合ミオシン結晶データのバッチ解析による構造比較
○永井 喜則¹、輪柳 博²、香川 浩³、Hyde Stephen⁴

1pE05 ¹国士舘大・情科セ、²早稲田大・社会科学、³日本医大・物理、⁴AppliedMaths, RSPhySE, ANU

Comparative study of myosin structures using patch analysis for X-ray crystallography data of different ATP analog bound myosin

Y. Nagai(1), H. Wako(2), H. Kagawa(3), S. T. Hyde(4),(1:Center for Information Science, Kokushikan University, 2:School of Social Sciences, Waseda University, 3:Physics Laboratory, Nippon Medical School, 4:Department of Applied Mathematics, RSPhysSE, Australian National University)

We developed patch analysis to calculate Gaussian and mean curvatures for the virtual surface consisting of nine alpha carbons that located three local strands of a protein. The method is applied for the analysis of myosin motor domain to know how the structure changes are occurred with hydrolysis of ATP.. There exist studies of X-ray diffraction analysis for crystallized myosin motor domains with ATP analogs not going actual ATP hydrolysis. The used X-ray diffraction data were 1MMA (with MgADP), 1MMD (with MgADP-BeFx), 1MMG (with MgATP*S), 1MMN (with MgAMP-PNP), 1MND (MgADP-AlF4), 1VOM (MgADP-VO4) in the PDB code. They have a big beta sheet consists of 8 strands, a middle size of beta sheet by five strands, and one or two small beta sheets. The small beta sheet formed in varying C-terminal changes to the helix in 1MMA and 1MND. There were also found the varying a helix structure near another small beta sheet. There exist many local distortions or shifting of strands with binding the ATP analogs. Thus the small disorders of structures cause small value varying of curvatures of patches, but the shifting of strands causes the large value changing in the curvatures. Some case a short strand between two helices faced with one side endsare formed helix. Then this part becomes a long helix woth inner a little bit disordered.

1P004 方向性を考慮したタンパク質評価関数の改良
○牧野 祥嗣¹、伊藤 伸哉¹

¹富山県大・工・生物工学

The improvement of the orientation-dependent scoring function for proteins

Yoshihide Makino and Nobuya Itoh

The data deposited in the protein data bank (PDB) provides increasingly valuable information for the structural study of the protein. We previously developed a novel type of knowledge based scoring function for protein structure evaluation (Makino, et al., EABS and BSJ 2006). The derivation of the function consisted of the following procedures: The distances were measured between two amino acid residues in a protein molecule. For each amino acid pair, three parameters that define the orientation of pseudo C-beta atoms were also calculated. These four parameters were determined for all the amino acid pairs of non-redundant protein structure sets. The bin corresponding to the parameters was counted, and the tables of counts were made for each amino acid pair. When the subject protein structure was evaluated, the parameters for all the amino acid pairs were evaluated by referring to the database. This function was effective for discriminating between the native and near-native structures of barnase. We present here the modification of our previous function and the ability of the modified function for discriminating between native proteins and decoys. The additional factors of intramolecular interaction were integrated to the function, and the function was tested on the decoys' sets in the DecoysR'us database. The inclusion of hydrogen-bonding factor was improved the discrimination ability. The detailed results of inclusion of other interaction factors and tuning of the parameters are also presented.

1P003 IP₃ レセプター・リガンド結合コアの IP₃ 非結合時分子動力学シミュレーション
○井田 洋一¹、瀧上 壮太郎¹、池口 満徳¹、木寺 韶紀¹

¹横浜市大・国際総合・生体超分子

1pE06 Molecular dynamics simulations of the ligand-binding core of the inositol 1,4,5-trisphosphate receptor in the ligand-free state

Yoichi Ida(1), Sotaro Fuchigami(2), Mitsunori Ikeguchi(1) and Akinori Kidera(1),(1:Supramolecular Biology, International Graduate School of Arts and Sciences, Yokohama City University)

Inositol 1,4,5-trisphosphate receptor (IP₃R) is an intracellular Ca²⁺ release channel activated by inositol 1,4,5-trisphosphate (IP₃). IP₃R consists of five functionally distinct regions, one of which is the IP₃-binding core composed of α- and β-domains. IP₃ binds into the cleft between the two domains. The crystal structure of the IP₃-binding core was determined in the complex with IP₃ (PDB ID: 1N4K), but the structure of the ligand-free form has not been solved yet. In the absence of the ligand, it is suggested that the two domains are free to move with respect to each other with the linker region acting as a hinge. In this study, we tried to determine the structure of the IP₃-binding core in the ligand-free state by the molecular dynamics simulation. First, we constructed a simulation system by modeling four missing loops in the crystal structure using MODELLER. MD simulations was then performed by removing IP₃ from the crystal structure, using the MARBLE and the CHARMM27/CMAP force field parameters. The resultant trajectory showed the hinge motions with breaking hydrogen bonds between the two domains. However, the interdomain salt bridge (E439-R241) near the hinge remained intact. Since a mutation (R241Q) destroying the salt bridge was shown to markedly reduce the IP₃-binding activity, it is considered that the salt bridge should be a determinant of the conformation in the ligand-free state. In the presentation, we will show the results of the simulations for the R241Q mutant, as well as the wild-type.

1P005 ドメインサイズの残基出現頻度と埋もれやすさに与える影響
○城田 松之¹、石田 貴士¹、木下 賢吾^{1,2}

¹東大・医科研、²SORST, 科技機構

1pE07 Effect of domain size on residue frequency and propensity to be buried

Matsuyuki Shirota(1), Takashi Ishida(1), Kengo Kinoshita(1,2) (1:Inst. Med. Sci., Univ of Tokyo; 2: SORST, JST)

Protein folding is mainly driven by the free energy change of bringing hydrophobic side chains out of contact with water and into contact with each other in the interior of the molecule. When proteins with the same shape but different size are compared, the fraction of the residues buried in the core would increase and the fraction of the residues exposed to the surface would decrease as the protein size increases. It is possible that the larger the fraction of the core is, the more hydrophobic residues and the less hydrophilic residues the protein would contain or the more fraction of hydrophilic residues would become buried. Tb test this hypothesis, we divided the protein domain dataset into size classes and compared the residue occurrence rates and propensities to be buried among the classes. An increase in the domain size significantly decreased the occurrence rates of lysine and glutamate. On the other hand, it increased the occurrence rates of three aromatic residues and glycine. Since lysine and glutamate are charged and hydrophilic, their decrease would be caused by the decrease of the surface fraction of domains. We also observed that the burial of hydrophilic residues in the core become frequent in large domains. The selection of residues in the core of small proteins is highly biased toward hydrophobic residues and this bias decreases as the domain size increases.