2SBP-06

超遠心分析と質量分析による溶液中での蛋白質間相互作用解析

In solution characterizations of protein-protein interactions by analytical ultracentrifugation and mass spectrometry


Recent advancements in methods for quantitative protein-protein interaction analysis will be introduced. Analytical ultracentrifugation (AUC) is a powerful method to clarify behaviors of proteins and protein assembly in solution. Size distribution with shape information, molecular weight and interaction parameters are estimated by AUC. The sizes and shapes of each component in highly complicated solution system can be clearly identified by the combination of AUC with native mass spectrometry. Meanwhile, the detailed structural information on large protein complexes and protein aggregates can be efficiently acquired by hydrogen deuterium exchange mass spectrometry (HDX-MS). Several examples of HDX-MS will be introduced in this presentation.

2SCP-02

From Personal Genome to Personal Proteins: Connection between the Reference sequences of genomic DNA and Proteins

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The human reference genome sequence is a fundamental resource to describe a variety of data on human. In the similar way, UniProt provides the basic resources of the reference proteins with a lot of functional annotations. Literally speaking, the two “references” should be same and functional annotation in each reference should be transferred to the other reference, but they are different because the different biological resources are used. To clarify the differences and to connect the functional information in both references, we compared two references at a single base (or residue) level, and developed a method to map each genome position onto a protein residue to interpret the personal genome difference by using protein knowledge.

2SCP-04

アミノ酸配列基間距離予測に基づくタンパク質立体構造モデルの評価

Model quality assessment method based on a residue-residue distance matrix prediction

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Protein structure prediction methods using computers are very useful and essential in structure based drug design, function analysis and so on. At present, various prediction methods have been developed. Many of the methods are fully automated, and researchers can get protein models easily only by preparing amino acid sequences as input. When using models, the most important thing is to know their quality. Therefore, model quality assessment methods play important roles. Recently, we developed some model quality assessment methods. In this presentation, I introduce our methods and discuss about the performance of them.