

## LIFE SCIENCE:



Brilliant synchrotron X-ray is continuously shedding light on the structural aspects of biological macromolecules. As a result of completing the first phase in structural genomics research projects throughout the world, the monotonic increment of the number of determined structures by year was stopped in 2008. However, by last year, the number was recovering. This might be caused by the advancement of the research techniques under the former projects and the start of the next phase of structural genomics research. This affects studies in structural biology not only quantitatively but also qualitatively. Within this background, we select ten topics among the variety of fruitful research conducted in 2009. Their brief summaries are described below.

Ion transport is a key function in signaling and action driven by a concentration gradient. Ca-ATPase works as a pump to recover the ion gradient after muscle contraction. Toyoshima and colleagues successfully determined its structures in the nine reaction steps and revealed its dynamical properties, as briefly summarized in the overview, "A place in the "X-ray" sun." His group also investigated another ion pump protein, Na, K-ATPase, which produces ion gradient for nervous stimuli and so on. The structure revealed the action of a heart stimulant drug, ouabain. In contrast to the pump proteins, channel proteins passively transport molecules using the concentration gradient. Connexin acts as a bridge between the cytoplasm of adjacent cells and controls the permeation of ions

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or small molecules. Its characteristic *tsuzumi*-like structure and gating mechanism were revealed by Tsukihara and colleagues. Its initial model, obtained using electron microscope, was improved using high resolution X-ray diffraction data.

For environmental and agricultural applications, plant biology is an important research. Photosystem II is a large membrane protein and contains a metal ion cluster and chloride ions needed to recycle atmospheric oxygen by water oxidation. Shen and colleagues revealed previously undiscovered but essential chloride binding sites using anomalous signals from substituted bromine and iodine. Gibberrelin is a key hormone in plant growth stimulation. Its discovery and major research progress were accomplished by Japanese researchers. Last year two Japanese groups independently determined its receptor protein structures (Hakoshima *et al.* and Kato *et al.*). The analyses reveal clearly the stimulation mechanism by which the gibberellin binding to the receptor induces a direct interaction with the repressor protein, leading to the degradation of the receptor by ubiquitin ligase.

In supramolecule research, the structure of the largest cytoplasmic protein, vault, was determined by Tsukihara and colleagues. Its rugby-ball-like structure is an assembly of 78 monomers and its long axis reaches 65 nm. A fine and parallel X-ray beam produced from an X-ray undulator enabled data collection from crystals with a large lattice length of 700 Å.

The next topic is protein transport. A cell is not a simple mixture of biological molecules and their subcellular localization is essential to maintain its system. The membrane protein SecYE plays a role in the secretion of proteins produced in cytoplasm to the extracellular region. Its structure, determined by Nureki *et al.*, revealed its dynamical open-close conformational change induced by binding SecA protein. Peroxisome is an organelle that participates in fatty-acid metabolism. Its contents are imported from cytosol across the membrane by a protein import machinery. Miki *et al.* determined the structure of the machinery component Pex14p. This result clearly showed the high affinity of Pex14p to a specific motif observed in the machinery components.

Dynamic motion is characteristic of living organisms. Even small bacteria can swim in some species by flagellar rotation with a screwlike motion. This action is achieved by a protein biomotor driven by the energy of an ion gradient. Imada's group recently determined two proteins located in the motor stator, and added new lines to the blueprint of the biomotor.

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