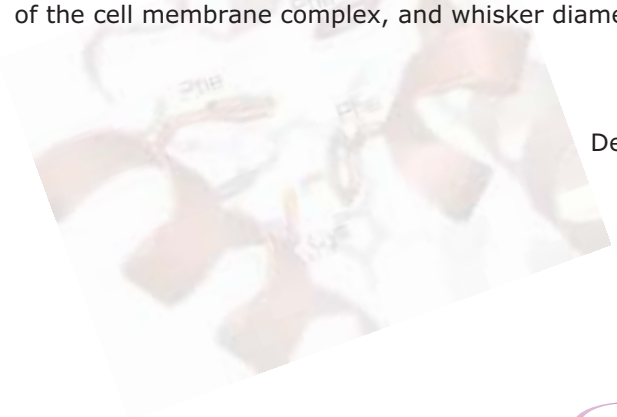
Life Science
Structural Biology

Many exciting structures of biological macromolecules were determined using beamlines for Life Science at SPring-8 in 2005. The determination of precise three-dimensional structures had great impact on studies in structural biology by revealing the molecular mechanisms of the biological functions. Protein crystallography and small-angle X-ray scattering (SAXS) become increasingly powerful methods using synchrotron radiation. The Protein 3000 project, which aims at determining a number of protein structures with biological significance, has been promoted with the use of the beamlines at SPring-8. For efficient operation, the functions of beamlines BL38B1 and BL40B2 were rearranged; BL38B1 was renamed Structural Biology III fully dedicated to protein crystallography and BL40B2 Structural Biology II focussing on SAXS.

All the beamlines for Life Science operated satisfactorily last year, and a number of new structures of biologically important molecules were reported. Here selected are representative papers published by SPring-8 users. The first three papers focus on the assembly of proteins or complexes. The structure of the bacterial flagellar hook and its joint mechanism are presented on the basis of the accurate crystal structure of its fragment protein and electron cryomicroscopic analysis. The structure of giant hemoglobin from beard worm (400 kDa) reveals a hierarchic assembly of four globin chains whereas that of P-protein of the glycine cleavage system (200kDa) shows how the active site is constituted in the a_2b_2 tetramer. The subsequent three papers describe the structures of DNA and proteins that interact with DNA/RNA. Using the Z-DNA binding protein, the structural analysis of a designed 15 base pair dsDNA successfully showed the junction structure between Z-DNA and B-DNA. In the FEN1-PCNA complex, an interesting motion of the protein is observed, which may be necessary for DNA processing whereas the structure of leucyl-tRNA synthetase-$tRNA^{Leu}$ complex provides the basis for proofreading between amino acid and tRNA. The precise structures of phytobilin synthesis enzyme and glucooligosaccharide oxidase enabled the clarification of the mechanisms of catalytic reactions. In acyl-coa thioesterase PaaI, an interesting structural change is discussed in relation to the reactivity of oligomeric enzyme. Taking advantage of *in situ* observations of SAXS, the last paper deals with the influence of humidity on the thickness of the cell membrane complex, and whisker diameter analyzed using the microbeam of BL40XU.



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