## LIFE SCIENCE

Synchrotron radiation, especially that from third-generation light sources, is now indispensable for the structural studies of biological macromolecules and the requirement of synchrotron radiation is rapidly growing. To fulfill this, at SPring-8, five undulator beamlines and seven bending magnet beamlines have been constructed for Life Science research. The beamlines for structural genomics, BL26B1 and BL26B2, are most recently in operation, at which mounting crystals and diffraction measurements are automated in cooperation with the sample mounting robot. In addition, various new equipment and software for beamlines have been developed. A new monochromator crystal was set up at BL41XU, which gives much higher brilliance with a higher energy resolution than before and a new imaging-plate detector system in BL44XU, which allows data collection for crystals with a very large unit cell (>1000 Å). Also the use of a user-friendly beamline control system as well as a high-speed data collection system has facilitated more efficient data collection at BL38B1, particularly for application to the MAD technique.

At SPring-8, a number of new structures of biologically important molecules were determined last year. The structure of the cytochrome  $b_6 f$  complex, a membrane protein complex that functions in electron transfer and proton pumping in photosynthesis, was elucidated at 3 Å resolution. The structures of human cardiac troponin and the c-Myb-cEBPβ-DNA complex brought breakthrough in the fields of bioenergetics and transcription, respectively. The structures of the importin- $\beta$  complex with a transcription factor showed how the factor is imported into nuclei while the structures of LoIA and LoIB proteins reveal the transport mechanism of lipoproteins. The structural information of cytosine deaminase and phosphodiesterase may lead to the clinical applications. The dynamic aspects of proteins clarified using laser were presented for hemoglobin and bacteriorhodopsin, which gave insight into the mechanisms of respective biological functions.

The National Project on Protein Structural and Functional Analysis by MEXT of Japan (Protein 3000 Project) is in the second year at SPring-8, and a number of structures has been solved and registered progressively using five beamlines.

Keiichi Fukuyama