LIFE SCIENCE

During the last decade, synchrotron radiation has brought on enormous changes in the field of structural biology. Several thousand new structures of biological macromolecules have been determined through use of synchrotron radiation. It is therefore no longer expected that researchers in this field will attempt to study functions of macromolecules without referring to their three-dimensional structures.

The advent of the third generation synchrotron radiation source will clearly accelerate the development of research in this field. The third generation source will make it possible to analyze the structures of supramolecular complex crystals and microcrystals, that have very weak diffraction power. Furthermore, the use of anomalous scattering makes it possible to analyze these structures more rapidly.

The demand for beam time is larger than those available at SPring-8, especially in the life science field. This demand is not likely to decrease, particularly at a time when genome projects are expected to elucidate many unknown genes whose structures have yet to be analyzed. This new scientific field is referred to as structural genomics; in this field, the functions of unknown genes are studied by analyzing the three-dimensional structures of the products of particular genes. Such projects are expected to yield great benefits in a variety of fields, including biology, medicine, pharmacology and agriculture. The current report covers only a limited number of results from studies in this rapidly expanding field.

A beamline dedicated to the MAD method is in operation at SPring-8. This beamline was constructed on the basis of the trichromatic concept. In the trichromatic concept, three data sets using three different wavelengths are collected quasi-simultaneously. Several new structures have already been solved using this beamline. Among these, the structural analysis of blasticidin S deaminase, a Zn-binding protein, is provided in this report. The high intensity is also beneficial for atomic resolution structural analyses. The structure of the catalytic domain of chitinase, one of the multidomain proteins from Bacillus circulans, was refined at an atomic resolution (1.13 Å) using anisotropic displacement parameters.

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