

## Poster Presentation

**BM.P56**

### *IPR Beamline for Macromolecular Assemblies at SPring-8 (BL44XU)*

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Biological macromolecular assemblies play significant roles in many biological reaction systems, including energy transfer, protein synthesis, protein degradation and signal transduction. A detailed understanding of the functions of the macromolecular assemblies requires information derived from three-dimensional atomic structures. X-ray crystal structure analysis is one of the most powerful methods to determine the three-dimensional structures of macromolecular assemblies at atomic level. Since features of crystals of biological macromolecular assemblies are extremely weak diffraction power and narrow space between the diffraction spots, it is essential to use high brilliance and high paralleled synchrotron radiation for diffraction data collection from crystals of biological macromolecular assemblies. The Institute for Protein Research (IPR) of Osaka University is operating a beamline for crystal structure analysis of biological macromolecular assemblies at SPring-8 (BL44XU). This beamline is designed to collect high quality diffraction data from biological macromolecular assembly crystals with large unit cells. The light source of this beamline is a SPring-8 standard type in-vacuum undulator. Liquid nitrogen cooled double crystal monochromator and horizontal focusing mirror are used as the optical components. BSS (Beamline Scheduling Software), which is SPring-8 protein crystallography beamline standard GUI, is installed to unify user operation throughout protein crystallography beamlines in the SPring-8. We have recently upgraded to a high speed air-bearing goniostat and installed a high performance CCD detector, MX-300HE. Present status and future plan of the beamline will be presented.

**Keywords:** X-ray crystallography of biological macromolecules, biological macromolecular assemblies, synchrotron structural biology research