## SR Beamline for Macromolecular Assembly Crystallography Operated by IPR at SPring-8

Atsushi Nakagawa<sup>a</sup>, Eiki Yamashita<sup>a</sup>, Masato Yoshimura<sup>a</sup>, Mamoru Suzuki<sup>a</sup>, Masaki Yamamoto<sup>b,c</sup>, Tomitake Tsukihara<sup>a</sup>, <sup>a</sup>Institute for Protein Research, Osaka University, Japan. <sup>b</sup>RIKEN/SPring-8, Japan. <sup>c</sup>JASRI/SPring-8, Japan. E-mail: atsushi@protein.osaka-u.ac.jp

Biological macromolecular assemblies play significant roles in many biological reactions systems. To reveal the function of the macromolecular assemblies at atomic level, three-dimensional structure of the complex molecules is essential. A synchrotron radiation beamline for biological macromolecular assemblies at SPring-8 is operated by the Institute for Protein Research, Osaka University. Since crystals of biological macromolecular assemblies are often x-ray radiation sensitive and extremely weak diffraction power, it is essential to use high-brilliance and highly paralleled synchrotron radiation for diffraction data collection. This beamline is designed to collect high resolution and high quality diffraction data from macromolecular assembly crystals with large unit cells. A newly designed detector, DIP6040, which is a hybrid-type of image plates and a CCD, is installed

Diffraction data from crystals with large unit cell (a=b=630, c=350Å) has been collected above 3.6 Å resolution. The present status and recent results of the beamline will be presented.

Keywords: biological macromolecular crystallography, synchrotron radiation crystallography, biological macromolecular assemblies