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TPS-05A1 Protein Microcrystallography Beamline at the National Synchrotron Radiation Research Center

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The routine use of synchrotron radiation for single crystal diffraction study in the past decades has revolutionized macromolecular structural biology. However, crystals of important macromolecules, such as membrane proteins and viruses, are usually small in sizes and have poor diffraction quality. Advances in synchrotron radiation sources, detectors, and software are necessary to tackle these challenging problems. This beamline aims to provide such a tool for difficult structures as well as routine data collection. The X-ray source of TPS-05A1 is a three meters long in-vacuum undulator (IU22), producing a high-brilliant X-ray beam. The X-rays are monochromated by a liquid-nitrogen-cooling Si double-crystal monochromator, and focused by a pair of Kirkpatrick-Baez mirrors. The focused beam size at the sample is 50 μm (H) $\times$ 20 μm (V) with a photon flux of 6×10^{12} photons/s. Apertures are used to collimate the beam in the range of 50–5 μm . The beam divergence at the sample is less than 500 μrad (H) and 100 μrad (V), and the energy range is from 5.7 to 20 keV (wavelength 2.175–0.62 $\text{\AA}$). TPS-05A1 will be equipped with a high speed CCD area detector and a robotic sample changer for automatically sample mounting and centering, making the data acquisition more efficient. The optional mini- goniometer of the high precision micro-diffractometer enables crystal reorientation for challenging experiments. The design and constructing status of this beamline is given in this article.

Keywords

TPS-05A1, difficult structures, protein crystallography, remote access, beamline automation

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