MS1-P2 Current status of sample exchange robots at the photon factory macromolecular crystallography beamlines

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The Structural Biology Research Center at the Photon Factory (PF) has developed sample exchange robots PAM (PF Automated Mounter) to achieve fully automated data collection in high-throughput X-ray experiments and/or remote experiments. The PAM was based on the robots SAM developed by SSRL macromolecular crystallography group, but the PAM has double tongs for rapid sample exchanging. The PAM has been installed at the PF macromolecular crystallography beamlines BL-5A, BL-17A, AR-NW12A and AR-NE3A. A beamline BL-1A was built for low energy experiments and operated since 2010. We have firstly installed the PAM modified to fit the BL-1A. For effective lower energy experiments, we covered whole diffractometer with a helium chamber recently. In parallel with development of the helium chamber, we developed a new sample exchange robot in order to minimize a leak of helium gas, named PAM-HC (PAM for Helium Chamber). Cryo-pins are grasped by a collet chuck that is placed on a tip of a slim robot arm. The PAM-HC can access a sample rotation axis of the diffractometer in the helium chamber through a tunnel in a side of the chamber. In addition, we are now developing an offline sample storing system based on PAM, which can automatically store the flash-cooled samples into the cassettes. Current status of the PAM and the PAM-HC will be presented.

Keywords: Robot, Automation, Macromolecular crystallography

MS1-P3 The crystallography endstation at beamline P11 at PETRA III

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The "Bio-Imaging and Diffraction Beamline" P11 at PETRA III is dedicated to structure determinations from periodic (crystalline) and aperiodic biological samples (*e.g.* entire cells). For this purpose two state-of-the-art experiments are available: an X-ray microscope utilizing tender X-rays between 2.4 and 10 keV [1] and a crystallography endstation operated between 5.5 and 30 keV.

The flexible P11 X-ray optics allow to tailor the beam properties to the needs of the experiment: A large parallel beam is available for investigations of large unit cell systems, such as viruses and large molecular complexes. For structure determinations from microcrystals a highly intense microbeam can be generated. With this serial crystallography experiments using liquid delivery systems [2] or silicon chips [3] can be realized.

The X-ray optics comprise an LN_2 cooled double crystal monochromator, followed by a first Kirkpatrick-Baez (KB) mirror system which consists of two horizontal and one vertical deflecting mirror and is located in the P11 optics hutch. A second KB system is installed very close to the crystallography endstation at 73 m. All KB mirrors are dynamically bendable. The first KB system can be used to generate a secondary source at 65.5 m. With this beam sizes down to 300 × 300 μm2 FWHM (v × h) can be realized at the sample position. The second KB system allows for further refocusing the X-ray beam into a spot of $4 \times 9\ \mu m^2$ FWHM (v × h) with full flux from the source (2×10^{13} ph/s at 12 keV). Smaller beam sizes down to $1 \times 1\ \mu m^2$ with more than 2×10^{11} ph/s in the focus can be obtained by slitting down the secondary source at the cost of flux.

At P11, all experiments are installed on an 8 m long granite support which provides an extremely stable setup for vibration sensitive experiments. The crystallography endstation is equipped with a high precision single axis goniostat with a combined sphere of confusion of less than 100 nm.

In addition, P11 is ideally suited for high-throughput crystallography and fast crystal screening. A Pilatus 6M-F detector allows for fast data collection with frame rates of up to 25 Hz. Crystals can be mounted in less than 10 s using an automatic sample changer and a large storage dewar provides space for 368 samples.

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