

Poster Presentations

[MS10-P26] **The Crystallography Endstation at Beamline P11 at PETRA III.** Anja Burkhardt,^a Bernd Reime,^a Tim Pakendorf,^a Jan Roeber,^a Nicolas Stuebe,^a Jan Meyer,^a Pontus Fischer,^a Saravanan Panneerselvam,^a Alke Meents,^a

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Beamline P11 at PETRA III is dedicated to imaging and diffraction experiments of biological samples. The beamline provides two experimental endstations: an X-ray microscope and a crystallography experiment. The P11 X-ray optics consist of a LN₂ cooled double crystal monochromator and two horizontal deflecting and one vertical deflecting X-ray mirrors. The mirrors are dynamically bendable and are used to generate an intermediate focus at 65.5 m from the source with a size of $16 \times 96 \mu\text{m}^2$ rms ($v \times h$). The crystallography endstation is installed on top of a 8 meter long granite block which is the key element of the P11 experimental hutch. The sample position is located at 72.9 m from the source. A CVD diamond based X-ray feedback system provides a long term beam position stability of better than 1 μm . The crystallography experiment is equipped with a high precision single axis goniometer with a combined sphere of confusion of smaller than 100 nm. The instrument provides an on-axis microscope for easy crystal centering and beam alignment. Diffraction experiments can be performed at energies between 4 and 30 keV. The beamsizes can be adjusted between $6 \times 12 \mu\text{m}^2$ FWHM ($v \times h$) with a photon flux of about 2×10^{12} ph/s and $300 \times 300 \mu\text{m}^2$ FWHM ($v \times h$) with 1×10^{13} ph/s. Due to the very small beam divergence P11 is ideally suited to measure large unit cell systems, such as viruses or large molecular complexes. The beamline is equipped with a Pilatus 6M-F detector which allows fast data collection with frame rates of up to 25 Hz. In addition to the standard

data collection features the beamline control software at P11 provides a grid scan capability for crystal centering and measurement of micro crystals (with and without crystal rotation) and an interface for serial crystallography. An automatic sample changer is under construction and will be available to users in 2014. The robot will be able to mount samples within 10 s and the large dewar will allow storage of more than 300 samples.

Keywords: Synchrotron X-ray Instrumentation; Macromolecular Crystallography; Diffraction