

Protein Crystallography with the PILATUS 1M Detector

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The PILATUS 1M detector (Pixel Apparatus for the SLS, 1 Million pixels) is a large area X-ray detector, constructed in 2003. X-rays are detected in single photon counting mode leading to excellent and noise free data. The main properties of the device are an energy range of 6 to 30 keV, no leakage current, no readout-noise, a fast read-out time of 6.7 ms and a PSF of one pixel.

Several proteins were measured at the protein crystallography beamline X06SA of the SLS (Swiss Light Source). The properties of the detector enable fine Φ -sliced experiments with continuous sample rotation using the electronic shutter of the camera. This leads to datasets as large as 9000 images. The data are first corrected for flatfield inhomogeneity. The main spatial distortion comes from the tiled assembly of the detector. We have developed a dedicated correction algorithm, which leads to a precision of fraction of a pixel. The corrected data could be processed using a standard crystallographic software package (XDS), leading to reasonable R_{tot} -factors of around 10%. This enabled us to calculate the first refined electron density map ever measured with a pixel detector.

Keywords: data processing, protein crystallography, area detector