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X-ray Microbeam Diffraction for Protein Crystallography Using FZP. K. Miura, A. Takeuchi, H. Takano, K. Uesugi, N. Shimizu, Y. Suzuki, Life & Environmental Science Division, Japan Synchrotron Radiation Research Institute, Kouto, Mikazuki, Sayo, Hyoto 679-5198, Japan.

X-ray structure analysis for micrometer-size crystal and local area of microscopic specimen will be powerful tool for protein crystallography and/or material science by utilizing fine focus X-ray beam. Recently, large progress has been achieved in X-ray optics and light source. Now, sub-micrometer probe size becomes routinely available in hard X-ray domain. We will report the application of microbeam to X-ray diffraction experiment using protein crystals.

Experiment has been done at BL20XU / SPring-8. Fresnel zone plate (FZP) with 197 mm focal length at 9.85 keV and 0.25 μm outermost zone is used as an X-ray focusing device. Measured spot size at the sample position is about 0.3 μm , and total flux of focused beam is estimated to be around 4×10^9 photons/s. The diameter of the FZP is 100 μm , and the convergent angle of focused beam is 5-4 rad. Diffraction data has been taken by means of conventional oscillation camera method with Φ -axis goniometer and Imaging Plate detector (RIGAKU R-AXIS IV). By considering the divergent angle of incident X-ray beam, the broadening of the diffraction spot is estimated to be about 100 μm . That is the same as the pixel size of R-AXIS IV.

Test of the micro-diffraction instrument is done by using a lysozyme single crystal as a standard sample. The thickness of crystal is around 20 μm . Fully diffraction data up to 2.0 \AA are collected at 298 K or 100K and its R-merge is 0.089. With these data, refinement statistics appears good, with R free of 25 %. These experimental results indicate that structure analysis of protein crystal with sub-micrometer probe size is promising.