Evaluation of Biocrystallography Experimental Hutch of Hyogo Beamline (BL24XU)

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The branched experimental hutch A of Hyogo beamline (BL24XU) was constructed for ordinary crystal structure analysis of biological molecules. The monochromatized 1.5th harmonics from figure-8 undulator of BL24XU are introduced in the hutch. A conventional powder diffractometer Rigaku RINT and an imaging plate diffractometer Rigaku R-AXIS4 were installed in the hutch. The hutch was opened for users from last October.

To determine the wavelength of incident X-rays, we carried out powder diffraction experiments on silicon and α-Fe_2O_3 samples. Finally, the wave length determined from 2θ angles of diffraction peaks is 0.834 Å (14.9 keV).

Sample protein crystals employed for the test were hen egg white lysozyme (HEWL) and FMN binding protein. The diffraction patterns from these protein crystals are very clear and sharp. Diffraction spots from a HEWL crystal were recorded at least up to 1.4 Å resolution. Summary of the data collection from the HEWL crystal is shown in Table 1. Diffraction spots from a FMN binding protein crystal were recorded at least up to 1.2 Å resolution.

We inspected the relationship between S/N ratio and the distance from sample crystals to the detector. We confirmed that the background noise is in inverse proportion to the square of the detector distance, however, integral intensity and the peak top value of the reflections from crystals are in inverse proportion to detector distance.

For the purpose of reducing X-ray damage on sample crystals a cryo-cooling system was installed in the hutch. We carried out an experiment to observe X-ray damage on a HEWL crystal at 100 K. Comparing a diffraction image from a crystal irradiated 2 hours by X-ray with the one before 2 hours' irradiation at the same orientation, we found that the former is about 10% weaker than the latter without ring current decay. This result means that damage caused high flux X-ray beam from figure-8 undulator is not negligible even at 100 K and cryo-cooling is indispensable to almost all protein crystals except tough crystals such as FMN binding protein.

Some improvement as mentioned below remain to be introduced in the hutch. Since the present beam stop casts a large shade on diffraction images, we cannot observe low resolution reflections. We have a installation plan of a smaller beam stop with fine positioning mechanism.

Table 1. Summary of the data collection

Crystal to detector distance	200 mm
Exposure time	90 sec/deg
No. of observed reflections	109,337
No. of independent reflections	20,419
Completeness	95.2%
R_{merge}	6.04%