

Evaluation of Biocrystallography Experimental Hutch of Hyogo Beamline (BL24XU)

Yoshio Katsuya¹ (0003395)*, Yoshihiro Mezaki¹ (0003397), Nobuyuki Mouri¹ (0004216), Yukio Morimoto² (0003007), Kazuya Nishio² (0004148), Tadatsugu Miyazaki² (0003042), Motohiro Koguchi² (0003043), Kyoko Suto² (0003016) and Kensaku Hamada³ (0001241)

1) Hyogo Prefectural Institute of Industrial Research, Yukihiro-cho, Suma-ku, Kobe 654-0037, Japan

2) Faculty of Science, Himeji Institute of Technology, Kouto, Kamigori, Hyogo 678-1205, Japan

3) Interdisciplinary Faculty of Science and Engineering, Simane University, Matsue, 690-1201, Japan

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 imaging plate diffractometer Rigaku R-AXIS4 was installed in the hutch.

To determine the linear polarization factor of incident X-ray, we carried out powder diffraction experiments on α -Fe₂O₃ samples. Finally, the determined polarization factor is -0.54.

Sample protein crystals employed for the test were aspartate aminotransferase (AspAT) from *Phormidium lapideum*, Chitinase from *Matsuebacter chitosanotabidus*, and FMN binding protein from *Desulfovibrio vulgaris* Miyazaki F.

The crystals of AspAT belong to the tetragonal space group $P4_32_12$ with unit cell dimensions of $a=b=133.4\text{\AA}$ and $c=125.8\text{\AA}$. Diffraction spots from an AspAT crystal were recorded at least up to 2.5\AA resolution. For an AspAT crystal, 256,270 reflections were observed and 39,537 independent reflections were obtained with a merging R-value of 0.102. The diffraction data set was 99.0% complete at the resolution of 2.5\AA .

Diffraction spots from a FMN binding protein crystal were recorded at least up to

1.05\AA resolution. Total 64,936 reflections were observed and 36,511 independent reflections were obtained with a merging R-value of 0.031. Summary of reflections intensities and R-factors by shells is shown in Table 1.

These results show that incident X-ray and our equipment installed in the hutch A of BL24XU have sufficient performance for ordinary protein crystallographic studies.

Table 1. Summary of reflections intensities and R-factors by shells

Resolution	I	error	R
20.00-2.26	6398.7	445.6	0.030
2.26-1.80	2093.5	151.9	0.028
1.80-1.57	788.6	65.2	0.037
1.57-1.42	453.2	45.3	0.032
1.42-1.32	312.7	38.6	0.050
1.32-1.24	263.5	37.8	0.033
1.24-1.18	223.8	37.3	0.073
1.18-1.13	199.5	37.5	0.098
1.13-1.09	145.7	35.6	0.136
1.09-1.05	111.5	31.7	0.095
total	1286.1	104.4	0.031