

High Resolution X-ray Powder Diffraction Study of Macromolecular Crystals with a Large Guinier-type Camera at SPring-8

Miura K.

Japan Synchrotron Radiation Research Institute (SPring-8/JASRI)

We developed a Guinier camera at structural biology beamline BL40B2 in SPring-8 for powder diffraction experiments of macromolecule crystals [1].

The camera has a maximum specimen-to-detector distance of 1000 mm with a vacuumed path, and its maximum angular resolution is 0.006° with a Blue Imaging Plate. Therefore it can separate adjacent peak at high angle in a powder diffraction data of lysozyme for over 10 minutes exposure.

The secondary study has been continued at high flux beamline BL40XU [2]. X-ray beam for protein powder diffraction was monochromized by channel-cut monochromator after focused by two mirrors system. Its stronger parallel beam was useful in lysozyme diffraction data for only 30 sec exposure with 1Å of wavelength.

In addition, we have modified an optical equipment of a pinhole system to make a smaller sized X-ray incident beam. With a diameter 25 micron pinhole, we have been able to collect fine powder diffraction data of microcrystalline materials with large unit cells near 130 Å. As a example we used powdery microcrystals of Thermolysin from *Bacillus thermoproteolyticus*, which MW is 34kDa with 316 atoms. The powder diffraction data with 120 sec exposure time was efficient with the average of peak width of 0.006 degrees. [3] Further several data of macromolecule crystals from this camera system will be presented.

References

- [1] K. Miura et al, AIP Conference Proceedings 705, 989-992 (2004)
- [2] K. Inoue et al AIP Conference Proceedings, 705, 336-339 (2004)
- [3] SPring-8 User Experiment Report: 2004A0176-NL2a-np, 2004B0759-NL2a-np