

## **Characterization of Dislocations in Protein Crystals using Synchrotron White-beam Topography**

Kenichi Kojima<sup>a</sup>, Haruhiko Koizumi<sup>a</sup>, Miki Shimizu<sup>a</sup>, Masaru Tachibana<sup>a</sup>, Kentaro Kajiware<sup>b</sup>, Hiroshi Sugiyama<sup>c</sup>, <sup>a</sup>*Graduate School of Integrated Science, Yokohama City University.* <sup>b</sup>*Spring-8/JASRI.* <sup>c</sup>*PF/KEK.* E-mail: kojima@yokohama-cu.ac.jp

To determine three-dimensional structure of protein molecules using X-ray diffraction method and neutron diffraction method, various protein crystals are grown. In particular, large protein crystals (~2 mm) are required for neutron diffraction method since the brilliance of neutron radiation is weak. Moreover, the characterization of crystal defects, especially dislocations, in protein crystals is important for an understanding of their crystallization. Therefore, it is important to establish synchrotron white-beam topography of protein crystals, which is one of the most powerful methods for characterization of dislocations in the large protein crystals. The application of X-ray topography to protein crystals has been carried out by some groups. However, the topographic contrasts observed in protein crystals were poor compared with those in organic crystals of small molecules reported previously. We found that the thickness of protein crystals should be more than  $0.4\xi$  ( $\xi$ : the extinction distance) to observe the clear images. Thus, we have succeeded in observing clear topographic contrasts not only in tetragonal hen egg-white (HEW) lysozyme crystals [1] but also orthorhombic HEW lysozyme crystals using large protein crystals (~2 mm). These dislocations structures will be discussed at the conference.

[1] Tachibana M., Koizumi H., Izumi K., Kajiware K., Kojima K., *J. Synchrotron Rad.*, 2003, **10**, 416.

**Keywords:** x-ray topography, protein crystals, dislocations