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Characterization of dislocations in monoclinic hen egg-white lysozyme crystals by synchrotron monochromatic-beam X-ray topography

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Introduction

Protein crystals include a variety of crystal defects that limit the accuracy of structure analysis and the interpretation of physical properties. An important objective for fundamental studies of protein crystal growth and physical properties is to identify and reduce these crystal defects. X-ray topography is one of the most powerful methods for the characterization of crystal defects, especially dislocations, in crystals. We succeeded in the clear observation and identification of dislocations in protein crystals by synchrotron X-ray topography [1].However, almost all studies have been limited in tetragonal and orthorhombic hen egg-white lysozyme(HEWL)crystals [2]. For the comprehensive understanding of dislocations in protein crystals, other protein crystals and polymorphisms need to be examined. In this paper, we report the characterization of dislocations in monoclinic HEWL crystal, which is one of multiple polymorphisms in lysozyme and is not sufficiently understood yet.

Experiment

Monoclinic HEWL crystals were monoclinic with space group $P2_12_12_1$, lattice constants of a=28.0Å, b=62.5Å, c=60.9Å, and four molecules per unit cell. Xray topography was carried out with synchrotron radiation in BL15B1 and BL15C at the PF. The monochromaticbeam of 1.2Å was selected by adjusting the monochromator. Thr synchrotron radiation was strongly scattered in the test tube or glass bottle in which HEWL crystals were grown. The crystal in the test tube or glass bottle was gently transferred into a thin container, e.g. a short straw, which is transparent for the synchrotron radiation. To avoid the evaporation of water contained in the crystal, it was surrounded in the growth solution and both sides of the straw were sealed with parafilms. The sealed straw was mounted on the goniometer. A habit crystallographic face of the crystal was adjusted to be almost normal to the incident beam. For X-ray topography, an X-ray flat panel sensor was employed to find target reflections. This sensor with high sensitivity in the low energy range is very useful for monochromaticbeam X-ray topography for protein crystals. After finding the target reflections, X-ray films or nuclear plates were set and X-ray topographs were provided.

Results and Discussion

Clear dislocation images were observed by synchrotron X-ray topography. Almost all of shapes of dislocations were curved or loop ones [3]. These shapes are quite different from straight one in tetragonal and orthorhombic ones reported previously. Furthermore, the distribution of dislocations was stereoscopically observed. The Burgers vectors were also identified from the invisibility condition of topographic images. These results are discussed in the light of growth mechanism and dislocation energy.

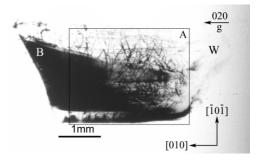


Fig.1 Synchrotron monochromatic-beam X-ray topograph of an monoclinic HEWL crystal in 020 reflection, taken with the incident beam almost normal to the (110)face.

References

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