

Poster Presentation

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Processing of Protein Crystals using by Deep-UV Pulsed Laser

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The absorption of X-rays which pass through the protein crystal is possibly the largest source of systematic errors in macromolecular crystallography. Therefore we are developing protein crystal processing system using Pulsed UV Laser Soft Ablation (PULSA) technique [1] to reduce the systematic error as well as background scattering from cryoprotectant agents. For high-quality diffraction data collection from organic material, crystals are usually processed to spherical shape in order to keep X-ray path length in crystal constant. This dramatically reduces systematic errors caused by 'absorption of X-rays'. Although shaping crystal was thought to be effective for protein crystallography, there was no usual technique to achieve this because protein crystals are exceedingly fragile against mechanical stress. We are developing protein crystal processing system using PULSA technique. In this system, short pulsed UV-laser (maximum power: 1.0 $\mu\text{J}/\text{pulse}$, wavelength: 193.4 nm, duration: less than 1.3 nsec) is raised by NSL-193L (Nikon Corporation) and focused on 4 $\mu\text{m}\phi$ (FWHM). The focused laser is controlled by galvanomic mirror system and irradiates a sample. Combining this mirror system with four-axis goniometer enables to process crystal to arbitrary shape that is easily defined on GUI. Several protein crystals have been successfully processed into spherical, column and square pole shape, etc. In the case of crystal processed into column shape (diameter is 50 μm), in addition to reducing absorption effects, signal-noise ratio of diffraction data can be increased by removing cryoprotectant agent surrounding the crystal. This work was supported by "Platform for Drug Discovery, Informatics, and Structural Life Science" from MEXT, Japan.

[1] Kitano H. et al., *Jpn. J. Appl. Phys.* 44 (2004) L54.

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