Evaluation of Laue diffraction data from the crystal of FMN binding protein

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FMN binding protein is a protein found in a sulfate reducing bacterium, *Desulfovibrio vulgaris* Miyazaki F. The native protein is characterized as a soluble, 14,000 Da protein with a FMN. A sequence study of FMN binding protein suggests that FMN binding protein has no similarity to other proteins containing FMN.

Redox potential of FMN binding protein is very negative (-370 mV) and a semi-quinone state of FMN is unstable. There is no evidence of a relationship between the redox properties and its function, but the unique redox properties may be important to the function of FMN binding protein *in vivo*.

We have determined the crystal structure of FMN binding protein by the multiple isomorphous replacement method. Two native data sets were measured at Photon Factory, KEK, Japan, using the Weissenberg camera for macromolecule. The crystals used for second data set diffracted to 1.3 Å, which were suitable for structure refinement at atomic resolution.

Apart from the experiments by the monochromatic methods, we have measured Laue data at BL-18B beam line, Photon Factory. The crystals gave excellent Laue diffractions and all diffraction spots were not streaked during the experiments. Thus, FMN binding protein crystal is suitable for Laue experiment.

A data set for FMN binding protein crystal was collected at BL44B2 beam line equipped with the Rigaku R-AXIS IV imaging plate detector system. A crystal-to-detector distance was 150 mm. The crystal diffracted up to 1.0 Å with a high signal noise ratio at room temperature. Though diffraction at the highest resolution shell gradually became weak due to radiation damage, we could complete the data collection. We also tried data collection at 100 K using the Oxford Cryosystems, but we could not complete the experiments since every crystals gave streaked diffractions.