strategies to collect dataset efficiently for the S-SAD method, (i) lowering the measurement error using high brilliant short wavelength X-ray, (ii) augmenting the anomalous signal using long wavelength X-ray. To validate these strategies, we experimented on the S-SAD method with standard samples at two synchrotron beamlines, SPring-8/BL41XU and SAGA-LS/BL15. (i)We have collected datasets from standard samples (insulin, thaumatin and lysozyme) using various wavelength between 0.71 to 1.90 Å at the SPring-8 undulator beamline BL41XU. We succeeded in the determination of the phases and building the molecular models of insulin from dataset collected in 0.9 − 1.9 Å wavelength, thaumatin from 1.5 - 1.9 Å and lysozyme from 1.5 - 1.7 Å, respectively. In addition, it ascertained that the dataset collected in longer wavelength allowed the phase determination and model building from lesser redundancy. (ii) SAGA-LS/BL15 has a bending magnet as a light source, and it is able to use X-ray between 0.54 to 5.90 Å wavelengths. The preliminary X-ray diffraction experiment of insulin crystals using 1.5, 2.3, 2.6 and 2.9 Å wavelengths was performed at this beamline. The $R_{merge}$ of the collected datasets were about 4 - 7 % in all wavelengths, and the molecular models could be built automatically from dataset in 1.5 and 2.3 Å wavelengths by S-SAD analysis. From the datasets collected using 2.6 and 2.9 Å wavelengths, we could determine the position of sulfurs and the phase but not build their models automatically due to the less of the resolution.

Keywords: protein crystallography with synchrotron radiation, anomalous dispersion methods, sulfur

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### Sulphur SAD (S-SAD) phasing using Co$K_\alpha$ radiation

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The S-SAD phasing is extremely useful for structure determination of a novel protein especially when its heavy atom derivatives are difficult to prepare. For S-SAD phasing, Cr$K_\alpha$ radiation has generally been used in a laboratory because its wavelength (2.2909 Å) is closer to the absorption edge of sulphur (~5 Å) than that of Cu$K_\alpha$ radiation. However, precise measurements of anomalous signals using X-rays with such a long wavelength is sometimes difficult due to errors originating from numerous sources such as air dispersion, absorptions by solvent around a crystal, a mounting loop, and components of an instrument such as a window material. Furthermore, with a plate detector, it is cumbersome to collect high resolution data that are necessary to reach the final structure. One can minimize the camera length to record high angle reflections, however those reflections will suffer severe errors by absorption and obliqueness. The optimal wavelength for S-SAD phasing may lay somewhere in-between Cu$K_\alpha$ and Cr$K_\alpha$. Therefore we have developed an X-ray generator producing strong Co$K_\alpha$ radiation (1.7902 Å) based on an FR-E Suberbright (Rigaku) and built a S-SAD system around it. The final system consists of an FR-E Superbright DW (Cu/Co) (Rigaku), a VariMax Co (Rigaku Americas) and an R-RAXIS VII/HTC (Rigaku). To reduce the absorption, we eliminated the black shielding film of the image plate detector. In order to evaluate the Co system, we tried structure analysis of four commercially available proteins: Insulin, HEW-Lysozyme, Glucose isomerase, Trypsin and Thaumatin. We will show these experimental data at the conference.

Keywords: SAD, protein phasing, single anomalous diffraction

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### Development of computer software for general area detector diffraction system(GADDS)

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We have developed the software which determines the orientation of the single crystal using General Area Detector Diffraction System(GADDS). The developed software is possible to determines the orientation for all kinds of crystal system and to analyze the single crystal when Detector's position was laid down at every directions against the beam direction. In case a uncertainty of the position of diffraction spots is below a millimeter, the orientation can be determined the right way by the least squares fitting. The software can previously forecast a diffraction situation by inputting the data which are a crystal system, a lattice constant and suchlike. The software offers a method that turns the single crystal determined the orientation toward the direction wanted by user. GADDS Analysis Program developed with C++ programming language can be utilized for the instruments of X-ray diffraction as well as Analysis of Laue-Film.

Keywords: Laue film, diffraction pattern, analysis software

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### Structural changes of reaction centre from Bl. viridis revealed by time-resolved Laue diffraction

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Reaction centre of Bl. viridis (RCvir) was the first membrane protein from which high resolution diffraction data was ever obtained. The structure showed three subunits and the photosynthetic pigments which were ordered in a two fold symmetric arrangement. Further, an electron pathway across the membrane was proposed, initiated by capturing a photon by the special pair, a bacteriochlorophyll dimer located on the periplasmic side. This absorption generates an electron, which migrates through the membrane to the movable ubiquinone, the final electron acceptor. After reduction to ubiquinol, it will then be released into the membrane. Even though the basic structure of RCvir is known, detailed structural information about how light gets converted into chemical energy is still missing. This lacking information is of major interest, since RCvir has high homology to photosytem II of higher plants. If one gets more insight into the photocycle of RCvir one could use this information and apply it directly to eukaryotic systems. One way of exploring the reaction path is to perform a time-resolved laue experiment where the photocycle is initiated with a laser and electron transport is monitored with a polychromatic x-ray beam. The illumination is very demanding for the crystal and thus robust crystals are an absolute requirement for the experiment. So, we crystallized RCvir using the sponge phase crystallization method and a type I crystal form