Poster

Development of time-resolved structural analysis environment at SPring-8 BL41XU

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Time-resolved structural analysis allows us to understand the detailed reaction mechanism of proteins. At SPring-8 BL41XU, we are proceeding with the development of time-resolved structural analysis using serial crystallography targeting reactions slower than milliseconds, which is complementary to the serial femtosecond crystallography at SACLA.

So far, we have completed the introduction of a high-viscosity cartridge injector, which was developed at SACLA for serial femtosecond crystallography [1] and have also created an environment that allows us to know the hit rate and index rate in real-time. In addition to a nanosecond wavelength tunable laser, a continuous wave laser was also used as an excitation laser to initiate the reaction. Currently, we are constructing an excitation laser optical system and setting up a timing control system for time-resolved structural analysis of photoreceptive protein.

In addition to this, we are also launching time-resolved experiment using the fixed target serial method. In this method, microcrystals are captured in a sample holder with a lattice of tapered holes, transported onto the X-ray optical axis by a high-speed two-dimensional automated stage, and diffraction data is collected. Since diffraction data is measured using only the crystals captured in the holes, it is expected that the amount of sample consumed can be suppressed. So far, prototype sample holders with 10,000 holes have been manufactured, and a control system that scans it two-dimensionally at high speed while reading out the detector with sub-millisecond timing accuracy has been completed. In the future, we will proceed with static diffraction data measurements and structural analysis using standard samples, and we will launch an inkjet system to initiate reactions by applying a substrate solution.

In this presentation, we will report on the current status of time-resolved experiment at SPring-8 BL41XU.

[1] Shimazu *et al*., (2019). *J. Appl. Cryst*., **52**, 1280–1288.