Current Status of Serial Crystallography at Spring-8 MX Beamlines

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In this decade, we have advanced the efficient high-resolution crystal structure analysis of membrane proteins using microcrystals at the beamline BL32XU at SPring-8 in Japan, by developing beamline hardware and software. Our approach has revealed that the signal-to- noise ratio can be significantly improved using dozens or hundreds of such crystals, even they are low-diffracting or challenging. Consequently, we have successfully determined the numerous high-impact crystal structures of a wide range of membrane proteins. The developed 'serial' data collection protocol had been implemented our automated data collection system, ZOO, and enabled un-attended experiments at MX beamlines.
Recently, we achieved 1.8Å resolution crystal structure determination using 600 nm sized polyhedra crystals grown in cell-free protein crystallization technique. The serial synchrotron rotation crystallography (SSROX) implemented in ZOO opened a new window for protein nano-crystallography with synchrotron radiation. We will discuss the experimental limitation coming from crystal size and dose for the synchrotron experiments by comparing results in some literature from SR and XFEL projects.