

The Structural Molecular Biology Program at the Stanford Synchrotron Radiation Lightsource

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The Structural Molecular Biology (SMB) program at the Stanford Synchrotron Radiation Lightsource (SSRL) provides an integrated suite of macromolecular crystallography (MC) and small angle X-ray scattering (SAXS) beam lines enabling studies on the most challenging problems in structural biology. Two state-of-the-art microfocus MC beamlines with exceptional brightness (BL12-1 and BL12-2) are equipped with high-frame-rate (100+ Hz) EIGER-16M pixel array detectors for rapid shutterless data collection using very small crystals. All SSRL MC beam lines offer the option to collect data remotely using cryo-cooled crystals, including fully autonomous crystal screening, data collection and data processing. More recently, in situ crystallization and remote data collection schemes under humidity controlled conditions have been released that simplify crystal handling and transport at near-physiological temperatures. These tools avoid direct manipulation of crystals, support robotic sample exchange, and allow full rotational access of the sample in a controlled humidity environment. All MC beam lines support MAD and SAD data collection, including automated X-ray fluorescence scans around the metal absorption edges and software to optimize the data collection strategy. To monitor radiation damage and further support the study of metalloenzyme structure, BL9-2 includes a remote-accessible single crystal UV-visible microspectrophotometer. Advanced data analysis tools provide rapid feedback during fast-paced experiments including support of serial diffraction techniques. To learn how to become an SSRL-SMB user, visit this webpage: <https://smb.slac.stanford.edu/forms/becominguser/>

Similarities in instrumentation and software environments form the foundation of a synergistic relationship between the SSRL BL12-1 and the Macromolecular Femtosecond crystallography instrument (MFX) at LCLS, through a Gateway approach. The MFX instrument includes a highly automated goniometer setup for diffraction experiments, developed and supported by the SMB group. The experimental front-end is based on developments at SSRL and LCLS XPP to provide an efficient framework to carry out goniometer-based experiments using automated strategies tailored to handle a variety of sample requirements, crystal sizes and experimental goals. These developments coupled with improvements in data processing algorithms make it possible to derive high-resolution crystal structures at the LCLS XFEL using only 100 to 1000 still diffraction images.