

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 for studies of very small crystals (BL12-1 and BL12-2) are equipped with EIGER PAD detectors, and offer shutterless helical collection and dose mode calculations built into the data collection software interface. All SSRL MC beamlines offer the option to collect data remotely using cryo-cooled crystals, including fully autonomous crystal screening, data collection and data processing. In 2020, remote data collection schemes under humidity-controlled or temperature-controlled conditions were released supporting crystal handling and transport of crystals 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 or temperature 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, further support the study of metalloenzyme structure, and verify the chemical state of the crystal's components, 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 crystallography (SX) techniques. Our capabilities also include the use of crystal injectors for SX at SSRL, and anaerobic setups for crystal growth, characterization, and mounting. To learn how to become an SSRL SMB user, visit our webpage or contact Lisa Dunn (<https://smb.slac.stanford.edu/forms/becominguser/>, lisa@slac.stanford.edu) and submit your proposals for Rapid Access, Block Allocation Groups (BAG) or Standard MC and extensions.

Similarities in instrumentation, existing and new sample delivery systems, and software environments form the foundation of a synergistic relationship between micro-focus beam line 12-1 at the SSRL synchrotron and the Macromolecular Femtosecond Crystallography (MFX) instrument at the LCLS XFEL. General user facilities for serial femtosecond crystallography (SFX) at MFX include equipment for liquid-crystal injector-based sample delivery and a goniometer-based setup, which supports fully automated sample exchange and data collection at room temperature and controlled humidity or at cryogenic conditions. The goniometer setup provides a suite of efficient automated experimental 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 using only 100 to 1000 still diffraction images.