

Macromolecular Crystallography at SSRL and LCLS

Aina Cohen and Clyde Smith, representing the SSRL Macromolecular Crystallography Group

The SSRL Structural Molecular Biology (SMB) group currently operates 4 fully automated macromolecular crystallography beamlines at SSRL, BL7-1, BL9-2, BL12-2 and BL14-1 for local or fully remotely controlled experiments. At the LCLS goniometer-based femtosecond diffraction experiments are supported at the new MFX experimental station. MFX saw first light in January 2016 and supported the first experiments in July 2016. The SMB group also is partnering with Stanford University and the Scripps Research Institute to build a next generation undulator microfocus beamline, BL12-1 to be completed in 2017. BL12-1 has been designed for investigations of the most challenging macromolecular crystallography systems confronting scientists today, including cases where crystals can only be grown to a few microns in size. All SMB crystallography beamlines support fully automated sample mounting, accomplished with the Stanford Auto-Mounting System (SAM). At SSRL samples may be automatically screened for diffraction quality and the data obtained is automatically analyzed to provide information on the number of diffraction spots, the Bravais lattice, unit cell, estimated mosaicity and resolution. Data collection strategies for native, SAD, or MAD data sets can be requested from the web-based program, Web-Ice. Recent developments have decreased the cycle time of SAM (dismounting one sample and mounting the next) to under 30 seconds, and the time for automated loop centering has been decreased to under 15 seconds, greatly increasing the throughput and efficiency of the beamlines. For information regarding MFX access and beamtime, contact Aina Cohen (acohen@slac.stanford.edu). For access to SSRL beamlines, contact Lisa Dunn (lisa@slac.stanford.edu)