## A Comprehensive Environment for doing Macromolecular Crystallography at SSRL

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The Macromolecular Crystallography (MC) group at Stanford Synchrotron Radiation Laboratory is currently developing, maintaining and providing support at 5 experimental stations, with 2 more under construction. A considerable effort is put into designing an efficient and intuitive environment that makes the experiment as productive as possible for the visiting scientists.

All MC beam lines now provide automated mounting and screening of samples, a feature, largely driven by the high throughput crystallography and structural genomics projects, that is now made available to all users. New tools for accessing resources at SSRL remotely have been added recently. A Linux based terminal server, NX by NoMachine, allows for secure and responsive remote graphical sessions in which the data collection and processing environment is nearly identical to that locally on the beam line. Several new and improved web based applications for diffraction image viewing, analysis, auto-indexing and strategy calculation are provided under the umbrella of the WebIce project. Many enhancements have been made to the beam line control software, BluIce, to make screening and sample robot operation easy and safe to use. More data backup options and tools make it easier for each user to find the best option.

The combination of advanced automation at the beam lines and remote access to all data collection resources provide users with the choice of just sending a cassette with samples to SSRL and conduct the experiment entirely from their home lab.

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