Socially-distanced Crystallography in the time of COVID: Remote capabilities at SSRL

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The SSRL Structural Molecular Biology group operates 5 protein crystallography (PX) beam lines on the SPEAR3 storage ring, BL7-1, BL9-2, BL12-1, BL12-2 and BL14-1. All of the PX beam lines are MAD-capable, with one station (BL7-1) using a single-crystal side-scattering monochromator with a limited energy range (typically 3000-4000 eV), and the other four using liquid nitrogen-cooled double crystal monochromators giving a much wider energy range capability (over 10000 eV). Two of the beamlines (BL12-1 and BL12-2) are in-vacuum undulator microfocus beamlines ideal for collecting data from small crystals. The SSRL PX beam lines are fully automated, with samples being mounted by the Stanford Automated Mounting system (SAM) from either Uni-Pucks or SSRL 96-port cassettes. Data collection is controlled with the Blu-Ice/DCS software system. Images collected during sample screening are automatically analyzed and processed, and the results, including the number of spots, Bravis lattice, unit cell, estimated mosaicity and resolution, are visible almost immediately through Blu-Ice, and also via the internet through Web-Ice. In the mid-2000s, the SSRL PX beamlines became the first in the world to offer fully remote access to users, who connected to the beam line computers via the highly responsive NX client. Since the ultimate goal of synchrotron data collection is to get the best possible data from the best available crystals, the combination of high-throughput automation and remote access at SSRL revolutionized the way in which scientists interacted with synchrotron beam lines to achieve this goal. In this past experimental run, our fully evolved remote access capability meant that we were able to open the SSRL PX beamlines for critical COVID-19 related research.