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COVID-19 Research at Light Sources[1]

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The COVID-19 pandemic has prompted a rapid and multifaceted response from the global scientific community. As part of this response, the tools of structural molecular biology available at synchrotron and x-ray free electron laser light sources have played a critical role in resolving angstrom-scale details of the SARS-CoV-2 virus that determine its interactions with antibodies and cells. In particular, the structure of the main protease and spike proteins of the virus have been the focus of attention for the development of vaccines and antiviral drugs. As of early 2021, one year after the first report on the structure of SARS-CoV-2, macromolecular crystallography (MX) experiments performed at light sources world-wide have produced many hundreds of protein data bank deposits and have contributed to numerous drugs and vaccines in clinical trials. The rapidity of this scientific response was made possible in part by many years of development of highly-automated MX experimental capabilities that support remote-access by users. This has allowed light sources to remain operational for COVID-19 research when local health orders and travel restrictions do not permit the physical presence of users on-site. Innovations in sample delivery, controls and remote data collection at light sources have occurred in parallel with advances in data analysis and structure validation that make rapid, automated access to MX experimental stations and structure determination even more impactful. These capabilities continue to be refined for structural molecular biology and, as a consequence of the pandemic's effects on light source operations, they are increasingly being adopted for many non-biological experiments at light sources around the world.

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