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The Structural Biology Center User Program at the Advanced Photon Source, Argonne National Laboratory. Stephan L. Ginell, R. Alkire, M. Cuff, N.E.C. Duke, Y. Kim, K. Lazarski, J. Osipiuk, F. Rotella, R. Zhang, and A. Joachimiak, Biosciences, ANL, Argonne, IL, USA.

The Argonne National Laboratory Structural Biology Center (SBC) operates a national user facility for macromolecular crystallography at the Advanced Photon Source (APS). The SBC Collaborative Access Team (CAT) located at APS sector 19 has an insertion-device beamline, 19ID, and a bending-magnet beamline, 19BM. Both beamlines are equipped with a fully tunable monochromator designed to reach most absorption-edge energies routinely used in macromolecular crystallography and x-ray optics designed to deliver a stable, intense, highly focused x-ray beam with low angular divergence onto protein crystal samples. The crystal environment includes a low noise mosaic CCD detector, Kappa geometry goniostat, high-resolution long distance microscopes, cryogenic crystal coolers, and high sensitivity fluorescence detectors. The insertion device beamline is well suited for small, weakly diffracting crystals, or projects having very large unit cells. Data can be processed with HKL2000, MOSFILM or d*TREK. Crystallographic software to analyze data is available to users.

Beamtime on the 19ID and 19BM beamlines are available to the crystallographic research community via a peer reviewed proposal system. The proposal evaluation is based upon the projects' scientific merit, need for synchrotron time at the sector 19 beamlines, feasibility of conducting the experiments at the SBC, and the probability of success of the project. Proposals with the highest ratings will receive beamtime first.

Information on the user program will be provided and can also be obtained from the SBC web site (<http://www.sbc.aps.gov>).

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