Res. Rev. J Mat. Sci. 2018, Volume 6
DOI: 10.4172/2321-6212-C8-036

The Berkeley Center for structural biology suite of crystallography beamlines at the advanced light source

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Structural biology continues to revolutionize the way we understand life sciences at a molecular level. Critical to structural biology is macromolecular crystallography and the absolute requirement of acquiring X-ray diffraction data from increasingly challenging samples. The Berkeley Center for Structural Biology (BCSB) brings 20 years of experience to beamline management and innovation. We operate five high-throughput protein crystallography beamlines at the Advanced Light Source at Lawrence Berkeley National Laboratory and are complementing our portfolio with the addition of a new microfocus beamline. Our vision is to provide state-of-the-art beamlines through continual development and outstanding service for crystallographers around the world, enabling structure solution on even the most complex biological systems. BCSB innovations include the pioneering of the automatic robotic sample changer, the development of a compact variable collimator to define the size of the beam and the measurement of the sample flux through a compact diode beam stop. To facilitate the beamline experience a graphical user-friendly interface was developed and over the years refined and streamlined to fit the needs of the crystallographers. The majority of the BCSB users are now shipping their samples and using the beamlines remotely from their home institutions. In recent years a series of new tools were implemented taking advantage of BCSB innovations and fast-framing detectors. Now crystallographers can use a queuing approach to speed-up sample screening, diffraction-based raster search to locate micron-size crystals in a sample and vector/helical data collection to minimize radiation damage. In the last year, we have implemented a user-free automatic approach for sample screening and full data collection. Quite often the automated approach identifies good quality data from samples that would otherwise have been missed. The automatic data collection approach has proven valuable to fragment-based screening and drug design. Together with the automatic processing of datasets, users can focus on structural biology rather than details of data collection.

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