

Automatic Biological Structure Determination at the Advanced Light Source

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In an effort to realize high-throughput data collection for macromolecular crystallography, we have developed and installed an automatic cryogenic sample alignment and mounting system at the Berkeley Center for Structural Biology at the Advanced Light Source. Rapid mounting and unmounting of the samples increases the efficiency of the crystal screening process, where many crystals have to be tested for the quality of diffraction as rapidly as possible. The automounter has random access to 112 samples, stored in liquid nitrogen. Mounting of a crystal takes approximately 10 seconds, during which the crystal temperature is maintained at ~100 K. Centering of a crystal can be done by the user through the remote controlled xyz goniometer stage or automatically by a centering algorithm. To further increase throughput, we have also developed a sample transport/storage system based on "puck-shaped" cassettes, which can hold 16 samples each. We are currently coupling the robot to smart software to automatically screen and analyse crystals and then determine and enact optimal data collection. A database tracks crystals, experimental and beamline parameters, as well as follows project status.