

The Berkeley Center for Structural Biology: A suite of macromolecular crystallography beamlines at the Advanced Light Source

Daniil Prigozhin¹, Jeff Dickert², John Taylor³, Randall Cayford⁴, Kevin Royal⁵, Anthony Rozales⁶, Stacey Ortega⁷, Adrian Spucces⁸, Jay Nix⁹, Marc Allaire¹⁰

¹*Lawrence Berkeley National Laboratory* ²*Lawrence Berkeley National Lab*, ³*Lawrence Berkeley National Lab*, ⁴*Lawrence Berkeley National Lab*, ⁵*N/A*, ⁶*Lawrence Berkeley National Lab*, ⁷*Lawrence Berkeley National Lab*, ⁸*Lawrence Berkeley National Lab*, ⁹*Molecular Biology Consortium*, ¹⁰*N/A*
daniilprigozhin@lbl.gov

The Berkeley Center for Structural Biology (BCSB) manages a suite of seven complementary macromolecular crystallography beamlines at the Advanced Light Source (ALS). Three of the BCSB beamlines under operations use the wiggler insertion device source on ALS sector 5.0, beamlines 5.0.1, 5.0.2 and 5.0.3. Two additional operational beamlines 8.2.1 and 8.2.2 utilize the superbend source on ALS sector 8.2. BCSB is currently commissioning a new microfocus macromolecular crystallography beamline 2.0.1 using an undulator insertion device on ALS sector 2.0. A branchline to beamline 2.0.1 is under development and will bring a second beam and end-station in the 2.0.1 hutch, an effort known as GEMINI. All BCSB beamline controls use the recently deployed B4 Graphical User Interface. The B4 GUI is easy-to-use and supports automation in data collection and on-the-fly data analysis. B4 Autocollect, a fully automated pipeline for data collection, is now available on all beamlines. A large number of samples can be characterized automatically in a high-throughput manner without human interventions. Structural biologists can benefit from B4 Autocollect especially for highly repetitive large volume applications such as fragment-based drug design campaigns.