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Next-Generation Automation for Biological Crystallography X-Ray Data Collection. Thomas Earnest, Carl Cork, Jim O'Neill, Physical Biosciences Div., Lawrence Berkeley National Laboratory, Berkeley CA 94720.

Automation of the structure determination process significantly benefits the structural biology community by increasing the overall speed and accuracy of data collection, and by providing the capability for the rapid screening of crystals to select those which will provide the best quality data. An automated crystal mounting and alignment system has been developed at Lawrence Berkeley National Laboratory and installed on three of the protein crystallography beamlines at the Advanced Light Source (ALS), and is currently being implemented at synchrotron crystallography beamlines at CHESS, NSLS, and the APS through a multi-institutional collaboration. There are several benefits to using an automounter system – i) optimization of the use of synchrotron beamtime, ii) facilitation of advanced data collection techniques, iii) collection of higher-quality data, iv) reduction of the risk to crystals during mounting, unmounting, and remounting, v) exploration of systematic studies of experimental protocols. Development of the next-generation automounter featuring a Cartesian geometry with three Adept motorized linear encoded stages, and smart cameras to enable a simple automated alignment procedure and state checking, is underway with improvements in robustness, simplicity of operation, and sample tracking. Supported by National Institutes of Health / National Institute of General Medical Sciences R01 GM62648.