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High Throughput Protein Crystallography at the NIGMS East Coast Structural Biology Facility. Anubhav Jain², Jean Jakoncic¹, Marc Allaire¹, Alec Berntson², Kun Qian¹, Fabiano Yokaichiya¹, Vivian Stojanoff¹,
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High-throughput protein crystallography using industrial automation techniques have reduced the time needed to conduct protein structure experiments at many facilities around the world. The X6A beamline at the National Synchrotron Light Source (NSLS) has been dedicated to studies concerned to bio-molecular crystallography and the developments of automation techniques to help the biological-, biochemical- and biophysics- communities to explore all aspects of structural biology. The facility serves experts and non-experts crystallographers from protein purification to structural determination coordinates. For high sample throughput an automated sample changer has been commissioned allowing quick sample screening and high throughput data collection. Key to the operation is a new package for precise protein crystal centering based on expert system codes. Sample screening is performed according to protocols and a sample database automatically uploaded at the time users schedule their beam time on a electronic calendar available to the User at the Facility website (<http://protein.nsls.bnl.gov>).