

## W0304

**From Sample to Structure: Automation at SER-CAT.** James Fait<sup>1,2</sup>, John Chrzas<sup>1,2</sup>, John Goczy<sup>1,2</sup>, Andy Howard<sup>3</sup>, Zhongmin Jin<sup>1,2</sup>, John Rose<sup>2,1</sup>, B. C. Wang<sup>2,1</sup>,<sup>1</sup>SER-CAT, Bldg. 436 B, APS, ANL, 9700 S. Cass. Ave., Argonne, IL, <sup>2</sup>Dept. of Biochemistry and Molecular Biology, The Univ. of Georgia, Athens, GA, and <sup>3</sup>Biological, Chemical, and Physical Sciences Dept., Illinois Inst. of Technology, Chicago, IL.

Automation has been extended to all aspects of the synchrotron experiment for biological macromolecular structure determination. At SER-CAT, beamline setup, sample handling, sample alignment, strategy, data collection, data reduction, structure solution and data archive have all been automated or are in the process of being automated. Use of robotics, image processing, and multiprocessor computing all contribute to the ease of completing the synchrotron experiment, with the user able to attempt the phasing of the sample on site, while it is still possible to augment the collected data, if necessary. Details of the implementation of various aspects of the automation process will be presented, along with several case studies.