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SAS Phasing Using Home Source and Synchrotron X-rays: An Optimal Combination for Cost-Effective High-Throughput Structure Determination. L.R. Chen, Z.-J. Liu, D. Lee, W. Zhou, W. Tempel, J.P. Rose, B.C. Wang, Southeast Collaboratory for Structural Genomics, Dept. of Biochemistry & Molecular Biology, Univ. of Georgia, Athens, GA, USA.

Single wavelength anomalous scattering (SAS) phasing has become a common tool for macromolecular structure determination and offers the advantage of phasing from in-house data that is impossible for the MAD experiment. The Southeast Collaboratory for Structural Genomics (SECSG), has developed methods and procedures for automated, efficient, cost-effective SAS structure determination using both home source (Chromium/Copper) and synchrotron (SER-CAT) X-rays. This mixed-source approach together with a focus on SAS structure determination reduces SECSG's requirements on valuable synchrotron X-rays and allows SECSG to best use its data collection resources. In our experience, SAS structure determination from home source data has proven to be a robust and powerful tool for high-throughput structural genomics applications.

The SECSG mixed-source approach for SAS structure determination including examples of high throughput structure determination from home source data will be presented.

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