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**Optimal Data Collection Strategies for SAD Datasets in the Home Laboratory.** Cary B. Bauer, Matthew M. Benning, Michael Ruf, Joerg Kaercher, Bruker AXS Inc., 5465 East Cheryl Parkway, Madison, WI 53711 USA.

The importance of using an optimized data collection strategy to collect MAD, and later SAD datasets has long been recognized. Historically, the goal was to minimize radiation decay at synchrotron sources. As a result, complex data collection strategies such as “inverse-beam “ and “mirror” became common to insure Friedel mates were collected close to one another in time. Recently, structure solution of macromolecules via the SAD method has been shown to be a real possibility in the home laboratory. The most challenging example of this method is to use only the anomalous signal from sulfur atoms present in proteins. While radiation decay is usually not a concern in the home lab, the extreme accuracy of data required has caused debate whether it is better to use a complicated strategy such as inverse-beam as opposed to a standard strategy which simply stresses redundancy. COSMO, the strategy calculation program that is part of the Proteum software suite provides a simple method to automatically plan a data collection by entering only a few target parameters such as resolution and redundancy. This presentation will focus on how the different data collection strategy methods mentioned above influence the results of phasing via the sulfur SAD method.