

## E0023

**Experimental Aspects of High Resolution Data Collection.** Stephan L. Ginell<sup>1</sup>, Andre Mitschler<sup>2</sup>, Andrzej Joachimiak<sup>1</sup>, Alberto Podjarny<sup>2</sup>, <sup>1</sup>Bioscience Div., Argonne National Laboratory, 9700 South Cass Ave., Argonne, IL 60439 USA, <sup>2</sup>IGBMC, 1 rue Laurent Fries, Illkirch, France.

Macromolecules that diffract to resolutions of 0.6Å to 0.9Å allow us analyze molecular details that in the past could only be observed in small molecules. The refinement and analysis of macromolecular structures at these resolutions requires that the experimental data be of the highest quality. The need to minimize radiation damage while maximizing the intensities for the weak high-resolution reflections is ever present. One structural characteristic found in high-resolution structures are multiple conformations. To lower the temperature factors and better define structural elements data is collected at 15K. Aldose Reductase (AR) a 36 KDaltons enzyme involved in diabetes complication will be used as an example to provide the details of collecting high-resolution data.