

## W0181

**Structure of Aldose Reductase-Inhibitor Complexes at Ultra-High Resolution From Helium Cooled Crystals.** S. Ginell<sup>1</sup>, T. Petrova<sup>2</sup>, I. Hazemann<sup>2</sup>, A.Cousido<sup>2</sup>, A. Mitschler<sup>2</sup>, F. Ruiz<sup>2</sup>, M. Van Zandt<sup>3</sup>, A. Joachimiak<sup>1</sup>, A. Podjarny<sup>2</sup>, <sup>1</sup>Argonne National Laboratory, Argonne, IL, <sup>2</sup>IGBMC, Illkirch, France, <sup>3</sup>IDD, Branford, CT.

Ultra-high resolution diffraction data of 0.9Å were collected at 19 KeV on human Aldose Reductase-inhibitor complexes at 15K and 60K at the APS beamline 19ID. Aldose Reductase (AR) is a 36 KDaltons enzyme involved in diabetes complications. For the AR IDD 676 complex, data were collected at 15K, while for the AR IDD 594 complex, data were collected at 15K and 60K for a hydrogenated crystal and 15K for a perdeuterated crystal.

The AR IDD 676 complex structure with 15K data shows a double conformation for the carboxylate head of the inhibitor, this was not resolved with the 100K data. This double conformation is also seen in a crystal structure at pH=8 and appears to be important for the proton donation mechanism. The current refinement of the AR IDD 594 complex at 15K and 60K give R-factors of 7.9 and 7.6 and show a decrease in B-factors with temperature. Comparison of hydrogens, bonding electron density and 'lone pairs' for the models at 15K, 60K and 100K is currently under study.

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