s7.m0.p1 **Synchrotron data collection of 0.66 A data for Aldose Reductase, an enzyme of MW=36 Kdaltons.** A. Mitschler[1], R. Sanishvili[2], A. Joachimiak[2], E. Howard[1], P. Barth[3] , V. Lamour[1], M. Van Zandt[4], E. Sibley[4], D. Moras[1] and A. Podjarny[1]. *[1]UPR de Biologie Structurale, 1 rue Laurent Fries, 67404 Illkirch, France. [2]Biosciences Division/Structural Biology Center, ANL, Argonne, IL, USA. [3]LCOB, ULP, 4 rue Blaise Pascal, 67008 Strasbourg Cedex, France [4]Institute for Diabetes Discovery, Inc., Branford, CT, USA.*
Keywords: instrumentation, detectors.

We will present the the cryoprotecting procedure and the collaborative measurements at the synchrotron beamline ID19,SBC,APS of a monomeric ternary complex of aldose reductase with $NADP^+$ and a selected synthetic inhibitor of therapeutic interest in diabetic degenerative complications. The cryoprotecting condition was achieved at 40% PEG6000 and liquid nitrogen giving refined isotropic mosaicity values near 0.3°. Crystal data are: space group P21, a=49.4, b=66.8, c=47.4Å, β=92.4°, with one complex of MW=36KDa per a.u.. X- ray diffraction data at 100°K could be measured up to 0.62 Å (3x3 array CCD detector, offset 30°, λ=0.65256Å) and the treatement with the programs Denzo-HKL2000 and Scalepack gave a data set of extremely high quality up to 0.66Å. To overcome geometric limitations, two crystals of similar shape (600x400x300 μm) were used (Rmerge(I)=2.9%, redundancy of 1.85) giving an overall completeness of 89.1% (74.7% in the outermost shell 0.67 to 0.66Å). This sub-atomic resolution data has been used to refine the structure and develop a model for the catalytic mechanism, to be presented at this meeting.

s7.m0.p2 **Wavelength-Modulated Diffraction.** H. Iwasaki, T. Koganezawa, Y. Yoshimura and N. Nakamura, *Faculty of Science and Engineering, Ritsumeikan University, Kusatsu, Shiga 525-8577, Japan.*
Keywords: synchrotron radiation, anomalous dispersion, phase determination.

We have developed a new diffraction method, in which the wavelength of the incident synchrotron radiation is continually and repeatedly changed over a definite range by rocking a couple of monochromator crystals while rotating a sample single crystal. With the angular velocity of the sample crystal rotation set to be larger than that of the monochromator crystal rocking, diffraction pattern is recorded on a moving imaging plate detector. Bragg reflections appear as elongated spots and, if the wavelength range is chosen in the immediate vicinity of the absorption edge of an atom in the crystal, direct information on the phase of Bragg reflections can be derived from the intensity gradient with respect to the wavelength of the elongated spots. This method of phase determination is simpler than other methods and free from the problem of intensity scaling encountered in the multi-wavelength diffraction method.

The method can be used with a crystal and the detector kept stationary while changing the wavelength. Patterns, similar to Laue pattern, are obtained, but it is possible to assign without ambiguity the wavelength of the radiation giving rise to each spot and measure diffracted intensity from the known spectrum of the incident radiation. This is applicable to the structure determination of a sample of a particular shape or in an extreme environment.