M05.0B Preservation and Decay at Cryo. Temperatures|

Chair: D. Theil
Co-Chair: E. Garman

Attendance: 220

This session addressed the related issues of developments in cryo-preservation methods and the current understanding of radiation damage.

The chair, D. Thiel (Cornell), opened the session explaining that even at cryo temperatures all crystals are mortals, that fully focused undulator radiation is lethal, that determination of cryo conditions can still be problematic particularly for membrane protein and virus crystals, and that damage mechanisms are not completely understood.

G. Bunick (Oak Ridge) then described the technique of crystal annealing. Where cryo cooling has not reproduced room temperature mosaicity, crystals may be warmed to room temperature by returning them to their drops for 3 minutes and then flash cooled again with partial recovery of the original mosaicity.

S. McSweeney (EMBL-Grenoble) presented a detailed systematic study of the structural changes induced in acetylcholinesterase by radiation damage. Successive data sets were collected from the same crystal and the structures from each were refined. The unit cell gradually increased and the molecules in the cell rotated and tranlated as damage increased. Di-sulphide bonds broke first. The study raised important questions particularly our need to understand dose rate effects and the possible use of free-radical scavengers.

C. Nave (Daresbury) reviewed our current knowledge of the physical processes involved when an x-ray loses energy in a crystal, and he presented some model calculations on beam heating of frozen crystals. Initially, the temperature rises a few degrees but quickly levels off.

T. Tsukihara (Osaka) reported the cryo-conditions and structure determination of the membrane protein cytochrome c oxidase. A combination of 5% PEG 4000 and 35% glycerol and a slow cooling protocol were used with the crystal mounted in a sealed capillary tube. This resulted in lower mosaic spread and higher quality diffraction than fast cooling in a loop.

Last, L. Liljas (Uppsala) reported the successful solution of the structure of cricket paralyis virus from a frozen crystal despite significant problems in scaling the data due to a sudden decrease in the unit cell during data collection.

Elspeth Garman (Oxford), co-Chair