116g Mitigation of Radiation Damage to Protein Crystals Using a Helium Cryostream

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X-ray data collection for protein crystals is typically performed at cryogenic temperatures to mitigate radiation damage by ionizing X-rays. Most common method of data collection is using a cold nitrogen stream at a temperature of around 100 K. Even when using cryogenic temperatures for data collection, the radiation damage to protein crystals can only be reduced, but not completely eliminated. In order to assess the effect of cryogenic stream temperature on radiation damage to protein crystals, data were collected on D-xylose isomerase crystals using synchrotron radiation (APS Beamline 14 BM-C) at stream temperatures of 15 K, 50 K and 100 K. The 15 K and 50 K data were collected using cryogenic helium (Pinkerton Device). 100 K data were collected using nitrogen stream for comparison. Helium has a lower boiling point (4 K) than nitrogen (77 K), which allows data collection at lower temperatures. Multiple crystals of similar quality and giving similar diffraction resolution were used at each temperature. Initial data were collected on the crystal followed by a 10 minute beam exposure with detector covered. Data collection and exposure cycles were completed at least 6 times for each crystal and diffraction data were analyzed at each stage. Crystal statistics showed significant reduction in radiation damage at the lowest data collection temperatures (15 K helium stream). In particular, the signal-to-noise estimate, $I/\sigma(I)$, of the highest resolution shell showed progressively less deterioration as temperature of the cold stream decreased. The results indicate that manifestations of radiation damage appear less rapidly at lower temperatures and the effects of radiation damage can be partially mitigated at very low temperatures particularly for high resolution data.