An Open Flow Helium Cryostat for Macromolecules

B. Leif Hanson[1], Anthony Martin [2], Joel M. Harp[1], Damon A. Parrish[3], Christopher G. Bunick[3], Kristin Kirschbaum[2], A. Alan Pinkerton[2] and Gerald J. Bunick[3]

[1]University of Tennessee/Oak Ridge Graduate Program in Genome Science and Technology
[2]Chemistry Department, University of Toledo, Toledo, OH 43606
[3]Life Sciences Division, Oak Ridge National Laboratory, Oak Ridge, TN 37831-8080

A helium cryostat developed at the University of Toledo (described in the Journal of Applied Crystallography 31: 815-817), has sufficiently low liquid He consumption to allow the acquisition of complete diffraction data from a protein crystal on a single 250 L tank of liquid He. This helium cooling system has been tested on macromolecules, using crystals of chicken egg lysozyme, sperm whale myoglobin, and the human light chain dimer, Mcg. The device was calibrated using phase changes in terbium vanadate crystals, which indicate that temperatures delivered by the cryostat were <33 K at the crystal position. The observed unit cell dimensions in the macromolecular crystals were consistent with temperatures <77 K.

Large crystals approaching suitability for neutron diffraction studies were successfully flash-cooled and a large crystal of lysozyme was rescued for data collection after undergoing a cycle of macromolecular crystal annealing (MCA) following poor flash cooling. Comparative data from myoglobin crystals collected using nitrogen and helium cryostats showed demonstrable improvement in the electron density map of selected residues and an overall improvement in the B factor. The results of these studies show that this device might be an especially useful adjunct both for neutron diffraction studies and at high intensity synchrotron X-ray sources, in addition to its use in the standard macromolecular repertoire.