Analyzing Mosaic Domain Changes Induced by Cryo-Cooling with Digital Topography

Jeffrey J. Lovelace[a], Cameron R. Murphy[a], Reinhard Pahl[b], Keith Brister[b], Gloria E. O. Borgstahl[a], *[a]Eppley Institute for Cancer Research and Allied Diseases, Omaha, NE, USA. [b]BioCARS - The University of Chicago, Argonne, IL 60439, USA*. E-mail: gborgstahl@unmc.edu

To better understand how cryo-cooling affects the mosaic domain structure of protein crystals a complex experiment was undertaken. Super fine φ slicing was coupled with digital topography to study diffraction at two temperatures (RT and 100K) on a single crystal, keeping the same orientation and on the same set of reflections.

For the experiment, a single lysozyme crystal was immobilized in a capillary with epoxy to eliminate slippage. The orientation was adjusted until a group of reflections were positioned to minimize Lorentz effects. The reflection group also had an arrangement that allowed them to be collected on a digital topography system in one pass. For the first part of the experiment a super fine φ slicing run was collected followed by a digital topography run at room temperature. Next the crystal was cryo-cooled in the capillary maintaining the same orientation. After cooling, a run of digital topography followed by a super fine φ slicing run was carried out on the same reflections. After processing, the sequences were analyzed to determine how the cryo-cooling had affected the mosaic domains.

The crisp mosaic domains visible in the room temperature data were shattered during cooling, the domain borders became highly irregular and some regions failed to diffract at all. Although exaggerated, the angular relationships between the major domains appeared to be conserved.

Keywords: cryo-cooling, digital topography, fine phi slicing