Scanning X-ray Micro Diffraction Capabilities at GM/CA@APS

Nagarajan Venugopalan[1], Ruslan Sanishvili[1], Mark Hilgart[1], Shenglan Xu[1], Craig Ogata1, Michael Becker[1], Oleg Makarov[1], Sergey Stepanov[1], Steve Corcoran[1], Janet Smith[2], Robert F. Fischetti[1]

[1]GM/CA@APS, XSD, Argonne National Laboratory
[2]Life Science Institute, University of Michigan

GM/CA@APS operates canted-undulator beamlines, 23ID-B and 23ID-D, at the APS. The GM/CA beamlines provide intense and homogeneous X-ray beams down to 5μm in size, a precise goniometer, on-axis visualization and sample mounting robotics. Software tools such as raster, vector, automated scanning, variety of data acquisition modes, automated strategy and data reduction capabilities have been integrated into an all-in-one user interface, JBluice-EPICS [1]. These hardware and software capabilities have greatly contributed to the publication of many structures from challenging projects in structural biology.

Advances in lipidic cubic phase (LCP) methods have successfully yielded crystals of many membrane proteins, but most crystals grown by this method are small, weakly diffracting, inhomogeneous, radiation sensitive, and optically invisible when mounted on a loop and cryo-cooled. The Raster tool was initially developed to search for such invisible crystals grown in LCP, but turned out to also be helpful with assessing quality and identify better ordered regions of a large crystal, select a single crystal from a crystal heap, etc... An individual hit or a list of positive hits can then be passed on for data collection. This technique was streamlined and completely automated, from sample mount to centering crystal in two orthogonal directions and to pass on positions of diffracting regions directly for data collection. Although the Raster tool was initially developed for crystallography, it has proved to be a very useful tool for scanning microdiffraction of various plant and human tissues.

As rastering requires exposing radiation sensitive samples to x-rays, reducing instrumental x-ray background in an image can considerably reduce the dose required for raster. Two main sources of X-ray scattering (in addition to the sample) that reach the detector are: scattering within the collimator that escapes the exit aperture, and air scattering of the direct beam before it terminates in the beamstop. Scattering from the collimator can be reduced by decreasing the size of the exit aperture. Collimators with considerably reduced exit aperture size in combination with a collimator-positioning system with motorized translational and angular adjustments have been installed on the beamlines for improved Signal-to-Noise ratio (S/N) in a diffraction image.
Raster capabilities and raster automation, efforts to reduce instrumental background in an image and future plans at GM/CA beamlines will be presented.

References

[1] Stepanov S et al. JBluice-EPICS control system for macromolecular crystallography. Acta Crystallogr D Biol Crystallogr. 2011 Mar;67(Pt 3):176-88.