Poster Presentation

MS073.P03

Gentle data collection at laboratory X-ray sources

Andreas Foerster[1], Marcus Müller[1], Alastair McEwen[2], Jean Cavarelli[2], Clemens Schulze-Briese[1]
[1]*DECTRIS Ltd., Baden-daettwil, Switzerland,* [2]*Department of Integrated Structural Biology, IGBMC, Illkirch, France*
E-mail: andreas.foerster@dectris.com

With synchrotrons producing ever more brilliant radiation, concern about radiation damage is increasingly pressing. At synchrotrons, radiation damage can be avoided by data collection fast enough to ensure completeness within the permissible dose for the crystal. Alternatively, complete datasets can be assembled from a few images collected from a large number of crystals each with insufficient survival in the beam. At free electron lasers, this second approach is taken to the extreme. Each crystal yields (at most) a single diffraction pattern while being vaporized by the absorbed photon energy.
On the other hand, radiation damage can be tackled at the source. Less absorbed energy means less damage. At a given photon energy, the absorbed energy is proportional to the photons flux hitting the crystal. By this rationale, laboratory X-ray sources with their limited flux are excellent environments to develop data collection strategies unlimited by radiation damage.
To demonstrate the power of laboratory equipment, we have solved the structure of the Thermus thermophilus 80S ribosome in complex with the antibiotic paromomycin with X-rays from a rotating anode generator. The orthorhombic crystals contained two ribosome complexes in the asymmetric unit, with unit cell dimensions of a = 209 Å, b = 449 Å and c = 620 Å. Diffraction spots could be resolved to a resolution of up to 3.2 Å on an EIGER R 4M detector. The anomalous difference maps show clear density for iron sulfur clusters and bound ions.
Radiation damage is of particular detriment to experimental phasing. While particularly accurate data is required to measure the small differences between the structure factors of anomalous pairs, data collected in single- or multiple-wavelength anomalous dispersion (SAD/MAD) experiments degrade quickly because of the high absorption of the incident X-rays by anomalous scatterers.
We will show how strong anomalous data can be collected on standard laboratory equipment, on cryo-cooled crystals as well as at room temperature. Thanks to a fortuitous combination of low dose and low photon energy, it is routinely possible to solve crystal structures in the lab from the anomalous signal native to crystals of unmodified protein, as long as the diffraction data are measured at the highest accuracy, e.g. with Hybrid Photon Counting detectors.
It is ironic that in times of abundant beamtime at technically sophisticated synchrotron facilities, the humble home source proves such a powerful instrument. Properly equipped and operated, it is a formidable tool to determine macromolecular structures from delicate crystals.

Keywords: radiation damage, home source, accurate data