Poster Presentation

BM.P44

PROXIMA 2A: A New Micro-focus Beamline for Macromolecular Crystallography

D. Duran[1], S. Le Couster[1], G. Fox[1], R. Fourme[1], R. Meijers[1], J. Samama[1], M. Savko[1], W. Shepard[1]

[1]*Synchrotron SOLEIL, Experimental Division, Gif-sur-Yvette, France*

PROXIMA 2A is a new micro-focus and energy tunable beamline dedicated to biological macromolecular crystallography at Synchrotron SOLEIL. The beamline officially opened in March 2013, and its first year of user operation has yielded excellent results. The X-ray source is a powerful in-vacuum U24 undulator coupled to a cryo-cooled Si[111] channel-cut monochromator and a pair of focussing bimorph mirrors in Kirpatrick-Baez configuration. This combination delivers a photon flux of over 10**12 ph/s into a focal spot of 10 µm × 5 µm (H×V FWHM), which is tunable over 6 – 15 keV. The supports of the optical elements have been designed to minimise the effects of vibrations and thermal dilations on the X-ray beam position, which is stable to within 5 microns over a day. The experimental station consists of a high performance micro-diffractometer, a cryostream, an area detector (ADSC Q315r), and an X-ray fluorescence detector. The X-ray energies for MAD experiments are directly calibrated on the sample. A robot equipped with a large 9 uni-puck dewar (CATS Irelec) is available to users for the automated transfer and screening of cryo-cooled samples. The users launch their experiments via an MXCuBE interface [1], which permits the centering of the sample, collecting of diffraction images, recording of X-ray spectra and the transfer of samples. The X-ray diffraction data are of an excellent quality, and the users readily exploit the micro-focused X-rays to select the best zones of their crystals. The first year of results from users has yielded a variety of success stories including novel protein structures resolved from crystals as small as 5 microns, as well as those solved by SAD & MAD methods. The future perspectives include automated helical and grid scans, in situ plate screening and multi-crystal merging techniques.

[1] *Gabadinho et al., J. Synchrotron Rad. 2010, 17, 700-707.*

Keywords: microcrystallography, macromolecular crystallography, beamline