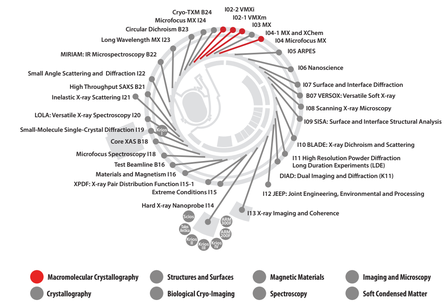
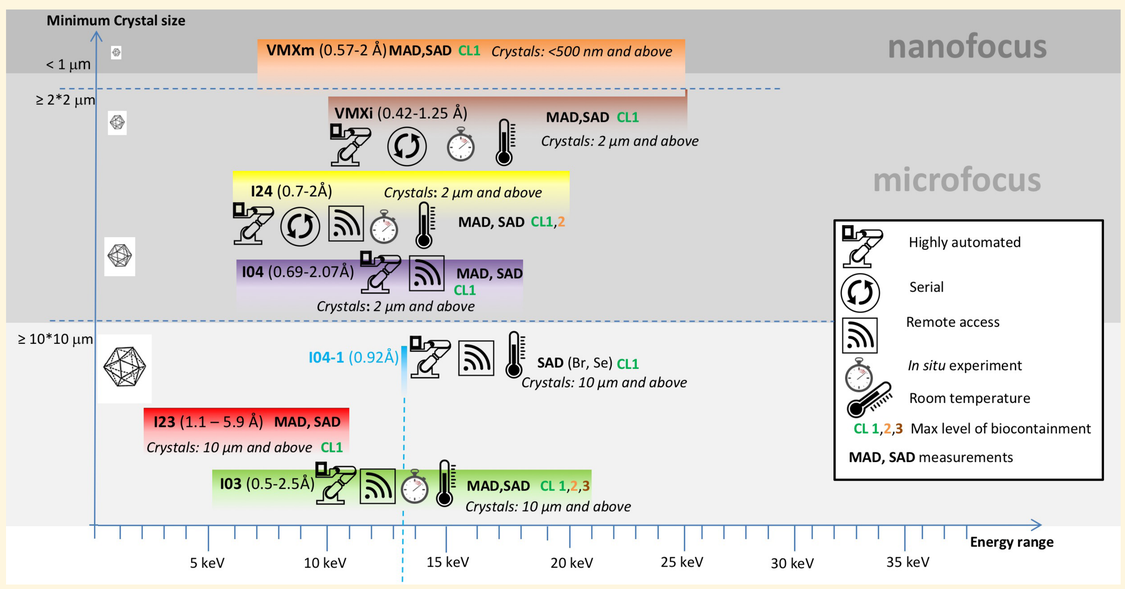
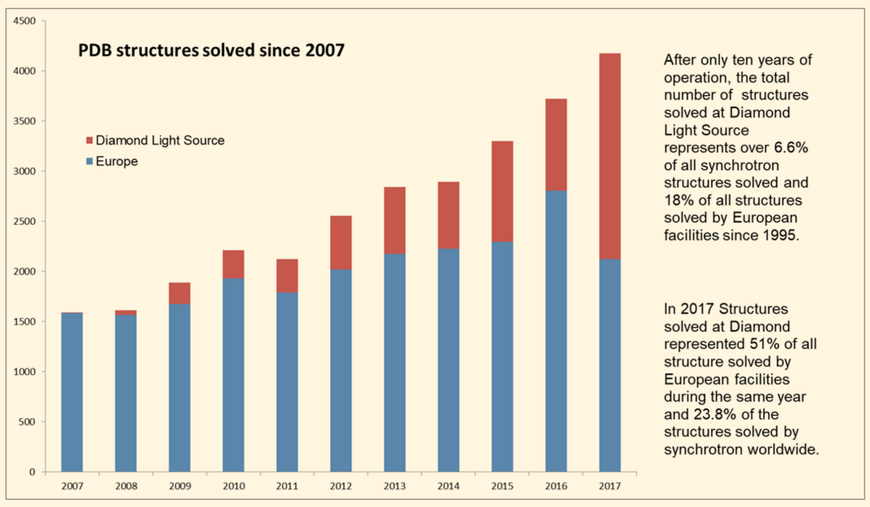


Macromolecular Crystallography

Macromolecular Crystallography (MX) is a core activity at Diamond with seven beamlines dedicated to the technique alongside the XFEL Hub, Membrane Protein Laboratory and XChem fragment screening facility for the extensive UK structural biology community as well as researchers in Europe and beyond. The MX research carried out at Diamond covers a number of structural biology themes including bacterial pathogens, virus structures and membrane transporters. There is also active research and development in algorithms and software for the treatment and analysis of crystallographic data. Alongside this, the continual design and implementation of new instrumentation is critical for the delivery of cutting edge beamlines and labs.

A routine offer to the user community





I03: High throughput and automated beamline capable of accepting biological agents in Hazard Groups 2 and 3

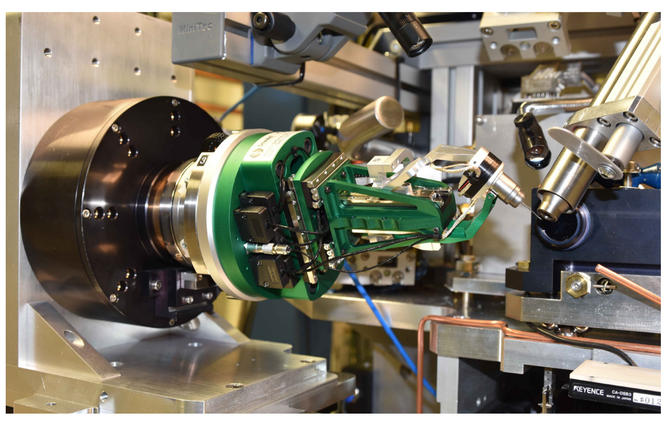
I03 is a tuneable beamline with a working wavelength range of 0.6 - 2.0 Å. The standard working wavelength is 0.976 Å (12.7 keV) with a focused beam size of 80 x 20 μm (FWHM). As with all the MX beamlines, I03 uses SPINE standard pins and Unipucks for cryo-cooled samples. I03 also offers for CL3, *in situ* experiments using SBS format plates. I03 can provide containment measures for experiments involving biological agents in Hazard Groups 2 and 3.

I04: High throughput and automated microfocus MX beamline

As with I03, I04 is a high throughput and extremely automated MX beamline now equipped with a high precision, fast SmarGon multiaxis Goniometer coupled to high capacity BART sample robots. The typical working wavelength is 0.9795 Å (12.658 keV) but it is tuneable over the wavelength range 0.69 - 2.066 Å. The beamsize can be focused from 10 x 5 to 110 x 100 microns across the available energy range. The combination of energy tuneability, choice of beam size and crystal reorientation with the multi-axis goniometer enable optimised data collections for challenging projects.

I04-1: fixed wavelength monochromatic MX beamline

I04-1 is a fixed wavelength monochromatic beamline. The beamline was originally aimed at high-throughput data collection for well-diffracting crystals, with off-the-shelf robotics and a stable beam thanks to a simple beamline design. However, it is now fully part of the routine MX user program, for both academic and industrial users alike, since the constraints (5-fold weaker beam than I03/4, fixed energy) affect only a subset of MX experiments. At Diamond beamline I04-1, the full X-ray screening experiment has now been implemented as a highly streamlined process (cf. “Crystal-based fragment Screening” poster).



VMXm: micro/nanofocus MX beamline

VMXm is a micro/nanofocus Macromolecular Crystallography (MX) beamline aimed at atomic structure determination in cases where the production of significant quantities of protein material and crystals is problematic. Indeed this is the case for many challenging protein complexes and medically important macromolecules that yield only very small crystals. The X-ray beam size on VMXm will be less than 0.5 microns and with the use of novel X-ray optics and electron beam imaging methods we will be able to precisely align the tiniest protein crystals into this X-ray beam, *in vacuo*, and measure X-ray diffraction data from them. The ability to tune the X-ray energy will allow us to obtain additional information from heavy atoms with in the macromolecules to aid in structure determination by multicrystal SAD or MAD methods.

In many ways VMXm will be a hybrid X-ray/cryoEM instrument making use of methods for sample preparation from cryo-electron microscopy, imaging from scanning electron microscopy and diffraction data collection methods from X-ray crystallography.

VMXm is currently under construction and is scheduled for first user operations in the second half of 2018.

VMXi: Versatile MX *in-situ* beamline

The Versatile Macromolecular crystallography *in situ* (VMXi) beamline is an entirely automated facility for characterisation of, and data collection directly from, crystallisation experiments *in situ*.

4 key advantages of *in situ* diffraction:

- Experiments can be carried out without any manipulation of individual crystals, thus preserving the crystal integrity.
- It provides immediate feedback on the diffraction, crystal quality and, in many cases, unit-cell parameters, space group, even in the case of micro-crystals (2-5 μm).
- The method can be fully automated with high reliability.
- It provides a route for data collection from crystals that consistently lose all diffraction when conventionally harvested.