

Biocrystallography at the high brilliance beamline (ID2) of the ESRF

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The high brilliance beamline at the ESRF is one of the most intense sources of low divergence x-rays for protein crystallography. The beamline has been designed with studies on both large sized cells and small crystals in mind.

Until recently a complete 30 cm MAR Research system was used. Now a five-circle Huber diffractometer, retaining only the MAR scanner itself, has been installed, with a maximum crystal-to-detector distance of 1 meter. There are two detector arms. The MAR scanner is mounted on one arm, which allows an angular rotation of plus/degrees. The second is used for an alignment apparatus, and it is envisaged that this arm could also be used to mount a small fast-scan CCD camera for the purpose of screening crystals.

The improvements to the protein crystallography station of ID2 makes routine data collection from crystals with very large unit cells (for example viruses and ribosomes) possible. Notably, data has been successfully collected from crystals of Blue Tongue Virus (largest unit cell dimension 1550Å; Stuart et al, Oxford, UK).

New software for rational data collection using the goniometer is being developed. The aim is to use the Eulerian geometry to maximize data collection efficiency. The software uses a graphical user interface (written in TclTk) to allow smooth use of the beamline.