

Macromolecular X-Ray Diffraction

Atomic-resolution images of macromolecules



The [School of Biosciences \(/schools/biosciences/index.aspx\)](/schools/biosciences/index.aspx) features a new, state-of-the-art X-ray diffraction facility for proteins. The facility includes a new-generation microfocus rotating anode generator and a CCD chip-based area detector for rapid data acquisition. Protein crystallisation, largely a trial-and-error process, is often hampered by the scarcity of pure protein. With the aid of a liquid handling robot, capable of dispensing nano-litre volumes, the number of potential growth conditions can be vastly extended, enhancing the chance of success and rendering possible the crystallisation of difficult proteins or protein complexes.

“Unsurpassed in its ability to provide atomic-resolution images”

X-ray diffraction is unsurpassed in its ability to provide atomic-resolution images of macromolecules of virtually any size, furnishing us with detailed insights into proteins and their complexes with other biomolecules.

X-ray crystallography began in 1912 with the pioneering work of Max von Laue and coworkers, but it took several decades until this method matured and became applicable to proteins and their complexes. Provided that the protein of interest can be crystallised, structures of almost any size can be determined to atomic or near-atomic resolution.