Time-resolved crystallography

Lecturer: Prof. Henry Chapman

Center for Free Electron Laser Science, DESY, and University of Hamburg

X-ray free-electron lasers have opened up a method of serial crystallography, based upon the principle of “diffraction before destruction” to overcome previous limits due to radiation damage. The method is used to measure diffraction from macro-molecular crystals without having to cryogenically cool the sample. This then gives us the means to measure protein structures under physiological conditions, without biases due to cooling. It allows us to follow reactions in time by initiating a reaction in a crystal at a prescribed time before its measurement (and subsequent destruction) by the femtosecond-duration X-ray pulse. Irreversible reactions can be studied this way since each measurement is made on a fresh crystal that is scanned or flowed across the beam.

The method has benefitted from inventive ways to stream crystals across the beam, and relies upon advanced detectors. It has required a new paradigm for analysis of diffraction data. The extreme intensities of X-ray FEL pulses also enable measurements from tiny samples that were not previously amenable to such investigation. Indeed, we can now think about time-resolved diffractive imaging of 2D crystals of membrane proteins, single fibres, virus particles, and even single molecules.

In this lecture I will introduce the methodology for time-resolved crystallography and diffractive imaging used at X-ray FELs, explain crystallographic analysis, and present case studies of time-resolved structures of photoactive proteins as well as systems triggered by reaction with a ligand. The use of other radiation sources and facilities will also be discussed.