MS44 Crystallography in large scale facilities

MS44-02

From XFELs to synchrotrons and back: high-output serial crystallography to image the structure and dynamics of biological macromolecules

D. Oberthuer [1]

[1]*CFEL/DESY - Hamburg (Germany)*

Abstract

The establishment of serial methods in macromolecular crystallography since the seminal experiments by Chapman et al. at LCLS in 2008 led, together with the re-discovery of crystallography under ambient conditions to a re-emergence of time-resolved studies to track the dynamic properties of functioning proteins. It also enabled structure determination using sub-micron sized crystals and - using an XFEL - circumvents many challenges related to radiation damage. Initially many critics doubted that serial crystallography would work, but from experimental phasing to superior difference maps from time-resolved experiments, the critics could be proven wrong every single time. Today it is a robust method, thanks also to strong developments in sample delivery procedures and data processing algorithms. One challenge still remains, however: the availability of beamtime and access for novice user groups, even with five XFELs in operation. It is therefore necessary to strongly consider for which scientific question an XFEL is needed, what could be done by serial crystallography at synchrotron light sources (SSX), where experiments at both XFELs and Synchrotrons would complement each other and how such decisions can be made in a way that benefits science and at the same time lowers the access barriers for users. To address these issues, results from recent experiments at both the European XFEL and PETRAIII will be shown here, ranging from new protein structures using native nano-crystals and de novo structure determination through a combination of nanoSFX and Alphafold2, to approaches to data collection under (almost) physiological conditions.