Macromolecular Crystallography at EMBL Hamburg

Isabel Bento, Saravanan Panneerselvam, Thomas R. Schneider, *EMBL Hamburg, Germany*

Abstract

EMBL in Hamburg operates two beamlines dedicated to Macromolecular Crystallography (P13 and P14) at PETRA III (DESY, Hamburg). P13 delivers high photon fluxes at energies down to 4 keV and S-SAD phasing is achieved routinely for single[1] and multiple crystals[2].
P14 provides two beam modes, a collimated rectangular homogeneous beam that can be shaped to any size between 10 and 200 µm (crystal life-time ~2 minutes at 100 K) or a micro-double-focus beam that can reach 5 µm size (crystal life-time ~500 ms at 100 K). The collimated beam can be used to illuminate large (50-200 µm) and small crystals homogeneously and/or to resolve diffraction from large (>1000 Å) unit cells. Prominent recent applications: the determination of a set of structures of the human 20S proteasome[3], the crystal structure of the mediator complex[4], structural enzymology at atomic resolution[5], serial data collections both on cryogenically cooled crystalline suspensions[6] and in situ on crystals as grown in CrystalDirect crystallization plates. In situ structure determinations have been successfully performed from crystals in crystallization drops, in lipidic cubic phase, or as grown in living cells[7]. P14 is equipped with a second end-station, 'T-REXX', which provides an open environment for the implementation of custom pump-probe time-resolved experiments [8-10]. Furthermore, in both beamlines, special beamline configurations are available that allow 2min per data collection.
Both beamlines are equipped with automated sample changers and can be operated from remote via the MXCuBE user interface and are connected to the ISPyB data base. Commercial access is facilitated by EMBLEM.The beamlines are embedded in the Integrated Facility for Structural Biology that offers access to up-stream service such as characterization of samples prior to crystallization, high throughput crystallization, and automatic crystal harvesting with a CrystalDirect Harvester.
More information including access routes can be found at:
www.embl-hamburg.de/services/mx/Industry .

References:

1) Freire DM et al., An NAD(+) Phosphorylase Toxin Triggers Mycobacterium tuberculosis Cell Death. Mol Cell. 2019 Mar 21;73(6):1282-1291.
2) Cianci M et al., Long-wavelength Mesh&Collect native SAD phasing from microcrystals. Acta Crystallogr D Struct Biol. 2019 Feb 1;75(Pt2):192-199.
3) Schrader J et al.,The inhibition mechanism of human 20S proteasomes enables next-generation inhibitor design. Science 2016 Aug 5;353(594-8).
4) Nozawa K et al., Core Mediator structure at 3.4 Å extends model of transcription initiation complex. Nature 2017 May 11;545:248-251.
5) Dai S et al., Low-barrier hydrogen bonds in enzyme cooperativity. Nature. 2019 Sep;573:609-613.
6) Gati C et al., Serial crystallography on in vivo grown microcrystals using synchrotron radiation. IUCrJ. 2014 Feb 10;1(Pt 2):87-94
7) Collaborative Projects, Manuscripts in preparation
8) Mehrabi P et al., Liquid application method for time-resolved analyses by serial synchrotron crystallography. Nat Methods. 2019 Oct;16(10):979-982.
9) Pearson AR, Mehrabi P., Serial synchrotron crystallography for time-resolved structural biology. Curr Opin Struct Biol. 2020 Dec;65:168-174. doi: 10.1016/j.sbi.2020.06.019. Epub 2020 Aug 23.

10) Mehrabi P, et al, The HARE chip for efficient time-resolved serial synchrotron crystallography, J Synchrotron Radiat. 2020 Mar 1;27(Pt 2):360-370. doi: 10.1107/S1600577520000685.