MS06-1-2 Structural enzymology on EMBL beamlines at PETRA III #MS06-1-2

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Abstract

EMBL is operating three endstations – P13, P14, T-REXX - for macromolecular crystallography on the PETRA III synchrotron in Hamburg. T-REXX is operated in collaboration with HARBOR (https://www.cui.uni-hamburg.de/en/harbor.html). Instrumentation for sample characterization and crystallization are available in the adjacent Sample Preparation and Characterization Facility. We will present an overview of recent applications of the facilities in structural enzymology including:

- Atomic resolution: Rindfleisch .. Tittmann (2022): Ground-state destabilization by electrostatic repulsion is not a driving force in orotidine-5'-monophosphate decarboxylase catalysis. Nature Catalysis 5: 332.

- Time-resolved: Mehrabi .. Pai (2019): Time-resolved crystallography reveals allosteric communication aligned with molecular breathing. Science 365:1167

- Micro-crystals: Shahsavar ... Nissen (2021): Structural insights into the inhibition of glycine reuptake. Nature 591:677

- Large complexes: Singh ... Chari (2020): Discovery of a Regulatory Subunit of the Yeast Fatty Acid Synthase. Cell. 180:1130.

- S-SAD phasing: Loch ... Jaskolski (2021): Crystal structures of the elusive Rhizobium etli L-asparaginase reveal a peculiar active site. Nat Commun. 12:6717.

New opportunities arising with the recently installed EIGER2 16M CdTe detector and the planned fourth generation synchrotron PETRA IV will be discussed.

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