MS07-02 | Crystallographic Enzymology: Using Synchrotroton Radiation for High Resolution in Space and Time

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With the advent of highly brilliant synchrotron sources such as PETRA III, MAX IV (and a number ongoing or planned upgrades of other synchrotrons), it has become possible to produce X-ray beams optimally tailored to applications in structural enzymology. While highly homogenous and stable X-rays can be used to extract the best possible data from large (> 20 µm) crystals, micro-focus beams can be used to obtain data from small (< 20 µm) crystals. Being able to exploit small crystals is of particular value in the context of time-resolved crystallography as – in a pump-probe scenario - a homogeneous and synchronized triggering of a chemical reaction is often only possible for limited sample volumes. The routine availability of micro-focus X-ray beams on synchrotrons in combination with novel 'serial' sample presentation technologies (in many cases originating from experiments designed for XFELs) is now paving the way to a renaissance of pump-probe time-resolved macromolecular crystallography.

The EMBL beamline P14 on PETRA III (DESY, Hamburg) offers a wide range of beam properties and sample presentation modalities. We will discuss how high-resolution structural data can be obtained on large molecular machineries such as the 20S proteasome, how serial approaches can be used to extract structural data from micro-crystals, and how pump-probe time-resolved diffraction data can be collected on the new T-REXX endstation.