Anomalous small-angle X-ray scattering on biological macromolecules at the P12 beamline of EMBL-Hamburg

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Anomalous small-angle X-ray scattering (ASAXS) utilizes the changes of the scattering patterns emerging due to the variation of the scattering amplitude of a particular atom type upon changing the X-ray wavelength in the vicinity of the absorption edge of the atom. ASAXS on biological macromolecules is challenging due to the weak anomalous scattering effect. Biological macromolecules are also prone to radiation damage and often only available in small quantities, which further complicates the ASAXS measurements. First biological ASAXS experiments were done in the early 80-s at the European Molecular Biology Laboratory (EMBL) beamlines of the synchrotron DESY in Hamburg on metallo-proteins [1] but overall, ASAXS was not widely used in biological studies.

Recent progress in synchrotron instrumentation and dramatic increase of the brilliance of modern synchrotron sources revitalized the interest to biological ASAXS. The biological SAXS beamline P12 operated by EMBL at PETRA III storage ring (DESY, Hamburg) is dedicated to study macromolecular solutions [2] and allows for ASAXS on macromolecular solutions. The beamline was adapted to accommodate the needs for ASAXS by implementing careful data collection and reduction procedures and we report the recent developments at P12 allowing to conduct ASAXS on different macromolecular systems. Examples of utilizing ASAXS on various systems including, in particular, surfactants, nanoparticles, polymers and metal-loaded proteins are presented. The beamline control, data acquisition and data reduction pipeline developed for ASAXS on P12 are now available as standard tools for the biological SAXS community.

[1] H. B. Stuhrmann, Q. Rev. Biophys. 14, 433 (1981).

[2] C. E. Blanchet et al., J. Appl. Crystallogr. 48, 431 (2015).

Keywords: ASAXS, SAXS, protein solution scattering, gold nanoparticles, synchrotron radiation