

Static and time-resolved SAXS in structural biology

Thomas M. Weiss

*Stanford Synchrotron Radiation Lightsource, SLAC National Accelerator Laboratory,
2575 Sand Hill Road, Menlo Park, CA 94025, USA*

The application of small angle x-ray scattering techniques (SAXS) to problems in structural biology has experienced a tremendous growth within the last decade. This development has been the result of a confluence of several factors: the changed needs of the biological research community for experimental methods able to provide structural and dynamic information on large, multi-domain proteins and complex biological assemblies; the development and widespread accessibility of new powerful computational tools for SAXS data analysis; and an increased availability of SAXS beamlines at high brightness synchrotron sources with advanced instrumentation that are able to provide high quality data even under dilute conditions. The beamline BL4-2 at the Stanford Synchrotron Radiation Lightsource (SSRL) is a state-of-the-art SAXS station dedicated to research in the field of structural biology and biophysics. It provides experimental facilities for a wide variety of SAXS applications ranging from static and time-resolved solution scattering on proteins, protein assemblies and multicomponent complexes, to lipid membrane and fiber diffraction. Using recent examples of static and time-resolved SAXS applications the presentation will illustrate the unique information that SAXS data can contribute helping to solve complex problems in structural biology.