

Small-angle X-ray scattering (SAXS) is a fundamental method for structure analysis of condensed matter, and has emerged as an essential tool used to unravel structural details with characteristic dimensions at length scales of up to 100 nm and beyond. The applications cover various fields, from metallic alloys to synthetic polymers in solution and biological macromolecules, emulsions, porous materials and nano-particles. The method became increasingly important in the study of biological macromolecules in solution because it allowed for the first time to yield low-resolution structural information on the overall shape and size of the particle without the need to grow crystals. The random orientation of particles in solution leads to an averaged scattering pattern, so that only information about the global average three-dimensional structure can be obtained. Moreover, SAXS also makes it possible to investigate in real-time intermolecular interactions such as self-assembly and large-scale conformation changes, on which biological functionality often relies. In the offered module, we want to give an overview of the parameters obtained from SAXS measurements on biomolecules, such as proteins and lipid vesicles.