SAXS IN THE ERA OF FOURTH-GENERATION LIGHT SOURCES

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The advent of third-generation synchrotron sources in the mid-nineties led to significant broadening of the scope of small-angle X-ray scattering (SAXS) methods in the investigation of soft matter and biophysical systems. The high brilliance of these sources enabled time-resolved experiments in the millisecond range even with low contrast samples, and high angular resolution and spatially resolved measurements [1]. Indeed, parallel developments of advanced detectors, sample environments and most importantly new data analysis methods were pivotal in exploiting the source properties [2]. As a result, SAXS methods now allow simultaneous access to a broad range of size and time scales deciphering the structural information from sub-nm to micron size scales and kinetics down to the sub-millisecond time range in hierarchically organized systems [1]. This talk will present some representative applications ranging from soft matter self-assembly [1] to cellular processes under thermodynamically or physiologically pertinent states [3].

The fourth-generation sources such as the ESRF-Extremely Brilliant Source, Sirius, APS-U, etc. offer even more exciting opportunities for SAXS and related methods [4]. The order of magnitude increases in the brightness and degree of coherence open new avenues for the investigation of soft matter and biological systems by scattering methods. In particular, the X-ray photon correlation spectroscopy (XPCS) has received a major boost. As a result, the equilibrium dynamics over a broader time and length scales has become accessible by this method. The improved beam properties together with the advanced pixel array detectors readily enhance the q-resolution of SAXS and ultra SAXS in the pinhole collimation. These new features will be illustrated by means of several examples such as the hierarchical self-assembly of amphiphilic systems, the emergence of active dynamics upon self-propulsion of colloids, etc. Indeed, the rapid onset of radiation damage is a significant challenge with vast majority of samples and appropriate protocols need to be adopted for circumventing this problem.

References

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