

THE APPLICATIONS OF SMALL ANGLE SCATTERING OF SYNCHROTRON RADIATION IN STRUCTURAL BIOLOGY

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Profound progress in molecular biology observed over the last two decades produced a demand for effective tools for structural analysis of proteins. An excellent tool supplementing crystallography and NMR for this purpose is the small angle X-ray scattering (SAXS) [1]. The SAXS method can be applied to biological systems ranging from small proteins or lipids to large multimeric proteins and even such huge systems like ribosomes or viruses [2]. It allows determination of the structural parameters of the molecules studied such as the radius of gyration, the maximum size of particle, and provides information on the conformational changes taking place in solution [3]. The use of small angle X-ray scattering in structural analysis enables a verification of the crystal structure of biomolecules with the data collected in solution. The SAXS data and the *ab initio* calculations provide also the information on the shape of the protein molecules in solution [4]. The measurements with the use of synchrotron radiation allow collection of the scattering data for protein solutions in the wide angle range (WAXS). The WAXS data provide valuable information on the low-resolution structure of proteins [5]. The above-mentioned possibilities of SAXS application in investigation of biological systems should be taken into regard in designing the SAXS measuring line within the project on the polish national source of synchrotron radiation.

The presentation gives analysis of performance of selected and the most popular applications of the SAXS method in investigation of biological systems. The possibilities of the SAXS method with the use of synchrotron radiation are illustrated on the four examples: small protein xylanase XYNII from *Trichoderma longibrachiatum* [6,7], human

ketoheksokinase, human protein HC [8] and glucose isomerase from *Streptomyces rubiginosus*.

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