

# **Small angle X-ray scattering in structural biology**

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Recently, the progress in the molecular and structural biology as well as growing access to synchrotron radiation has resulted in a significant increase of the number of the structures of proteins and other biomacromolecules deposited at the Protein Data Bank ([www.pdb.org](http://www.pdb.org)). In the middle of June 2009 the number of structures deposited at the Protein Data Bank has reached over 58000 structures of proteins, nucleic acids and their complexes. About 50000 structures have been solved by the methods of X-ray crystallography.

Such progress in the structural biology has produced also the need for development of the independent methods allowing a comparison of the protein structure in crystal and in physiological conditions (in solution). The small angle X-ray scattering (SAXS) is one of the most effective methods permitting of comparison of the crystal structure of biomacromolecules with structure in solution and therefore is an excellent tool supplementing crystallography and NMR in structural biology. The SAXS method can be applied in study of biological systems ranging from peptides or small proteins to such huge objects like ribosomes or viruses. It provides the low-resolution structural information on the overall shape, internal structure and conformational changes also for the macromolecules whose crystals could not have been grown.

The performance of selected and the most popular applications of the SAXS method in structural biology will be illustrated on the some practical examples.