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Colloque III : Structure et désordre

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Everything you always wanted to know about SAXS and were afraid to ask Or tracking the order in structural disorder

Small Angle X-ray scattering approaches (SAXS) are very useful for the study of macromolecules in solution. This low resolution technique (10-15Å resolution) provides information on the tertiary and quaternary structures of proteins and of macromolecular assemblies through their dimensions, their overall shape and/or the conformational properties of the polypeptide chain. It is a very valuable technique for structural studies when crystallography cannot be applied, as it is the case for Intrinsically Disordered Proteins (IDPs), whose flexibility and the large distribution of conformation prevents from obtaining any crystal.

A part from the dimensions of the protein (radius of gyration, maximum diameter, ...) assessing its compacity, it is now possible to retrieve many structural information from the scattering curve. Recent advances in computational approaches allow now to reveal the envelop of the protein using SAXS, and to build the average structure adopted by the disordered regions in a complex or in plurimodular proteins. The spatial arrangement of the different ordered and disordered domains can thus be revealed. In some cases, one can also determine the distribution of conformations attained by the IDP in solution. Combing SAXS with other complementary biophysical techniques (X-ray diffraction, NMR, Molecular Dynamics, etc...can then lead to a complete description of the structural properties of IDPs and their mode of action both at the residue and the molecular level.