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SMALL ANGLE X-RAY SCATTERING (SAXS) IN COMBINATION WITH OTHER TECHNIQUES, EXPERIMENTAL AND NON, TO DEAL WITH SOME TOUGH PROTEIN STRUCTURES

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Abstract

Small Angle X-ray Scattering (SAXS) is a powerful technique that is used to obtain structural information of both ordered and disordered biological molecules at low resolution. It provides information about the size and shape of proteins and complexes, as well as about structural changes that occur at different experimental conditions [1]. SAXS requires small (milligram) amounts of purified and monodisperse samples. The experiment can be performed rapidly using the dedicated beamlines at synchrotron light sources [2]. Even data analysis, when the quality of the sample is good enough, can be fast, thanks to powerful specialized software [3]. SAXS is a particularly useful technique for the characterization of multidomain proteins [4], which consist of two or more domains connected by linkers determining their flexibility. In a typical SAXS experiment, a collimated monochromatic X-ray beam illuminates a solution of particles, and the intensity of the scattered X-rays is registered by a detector. The recorded scattering pattern is reduced to a radially averaged one-dimensional scattering profile, which results in low structural resolution but can still provide important structural information. In contrast, Macromolecular Crystallography (MX) is an older and mature technique capable of revealing high-resolution details of biological macromolecules when good-sized and well-ordered crystals of such molecules are obtained. Information obtained from different biophysical experiments can be combined to obtain structural insights represented by molecular models. Combination of X-ray crystallography with SAXS data and other techniques including Molecular Dynamic simulations (DM), protein-protein docking, cryo-EM, NMR chemical shift perturbation or FRET and has proven very useful for obtaining detailed models of dynamic protein complexes. Some cases of proteins involved into the mechanism of ribosome biogenesis (Schwachman Diamond Syndrome) [5-6], endoplasmic reticulum quality control (ERQC) machinery [7] and human magnesium transport mediator [8] will be presented.

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About

Dr. Dritan Siliqi is senior scientist at Institute of Crystallography, Italian National Council of Research (IC-CNR and head of Bio-Crystallization Lab. Since 1994, Dr. Siliqi spent a part of his carrier on developing phasing techniques to solve protein structure from X-ray and neutron diffraction data. He is an expert on Small-Angle X-ray Scattering (SAXS) technique applied to biomolecules, and in combination with Wide-Angle Xray Scattering (WAXS) in scanning mode, for the study of biomaterials. He is author of more the 120 papers in international journal. He has been the as coordinator and participant of various and different scientific bilateral agreements with countries such as Mexico, Peru, Brazil, Argentina, UK, Albania, Morocco, and as well of European and National projects. He has also a long experience on experiments at various Xray (MX, SAXS) synchrotron beamlines (ESR, Diamond, DESY, SLS, LNLS) or neutron sources (LANSCE, ISIS). Dr. Siliqi was involved as well as lecturer/tutor at OPEN SESAME HERCULES School for the training of young researchers of the new SESAME synchrotron in Jordan.

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