

Small Angle X-ray Scattering (SAXS) in combination with other complementary techniques to tackle challenging protein structures

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Small Angle X-ray Scattering (SAXS) is widely used in the study of biomolecules, providing valuable insights into their structural properties and behavior in solution. SAXS is particularly suitable for investigating biomolecules' overall shape, size, conformation, and flexibility, including proteins, nucleic acids, and complexes. In the case of proteins, SAXS can provide information about their tertiary and quaternary structure, domain organization, and overall shape. SAXS is also useful for studying protein-protein interactions and the assembly of biomolecular complexes. One of the advantages of SAXS in studying biomolecules is its ability to analyze molecules in solution under near-physiological conditions. This allows for the investigation of biomolecular behavior in their native state, providing insights into their dynamics and conformational changes. Small Angle X-ray Scattering (SAXS) is often combined with other complementary techniques, such as X-ray Crystallography, Nuclear Magnetic Resonance (NMR) Spectroscopy, Electron Microscopy (EM), Mass Spectroscopy, Molecular Dynamic simulations (DM) and protein-protein docking, to tackle challenging protein structures and obtain a more comprehensive understanding of their properties. Results obtained from the study of proteins and their complexes involved in the mechanism of diseases such as Shwachman Diamond [1-2] and Jalili [3] syndromes, and tuberculosis [4], will be shown.

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