

Integrating SAXS and Complementary Techniques for Structure Determination of Biomolecules

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Structural analysis of biomolecules is a key challenge in current biology and a prerequisite for understanding the molecular basis of essential cellular processes. The use of solution techniques is important for characterizing structure, complex formation and dynamics of biomolecules and biomolecular complexes.

As experimental data for large biomolecules and biomolecular complexes are often sparse, it is advantageous to combine these data with additional information from other solution techniques. In this contribution we will show highlights of recent achievements in integrating Small-Angle X-ray Scattering (SAXS) data with complementary data from e. g., Nuclear Magnetic Resonance Spectroscopy and X-ray crystallography to study structure and dynamics of large disease-related proteins and protein complexes [1-9]. By using our integrated approach we were able to provide a comprehensive and accurate description of protein complex structure and dynamics in a native-like environment. This underscores the central role of SAXS for structure determination of protein complexes and ensures its unique role and contributions in integrated structural biology approaches in the future.

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