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Protein Characterization in Solution by Small-Angle X-Ray Scattering

H. Santner

Anton Paar GmbH, Graz, Austria
E-mail: heiner.Santner@anton-paar.com


For many biomedical applications of proteins the knowledge of the three-dimensional structure of proteins is of great importance. It is the key to understand their function in biological processes. Small-Angle X-ray Scattering (SAXS), in contrast to other methods e.g. Protein Crystallography and Cryo-TEM, allows investigating proteins in solution, i.e. in their native state and under biological conditions. Furthermore SAXS does not need any specific sample preparation which might change the protein sample. SAXS enables to study structural changes upon changing the external conditions and is a valuable tool for determining several important parameters: (1) protein size and shape, (2) aggregated structures, (3) folding state, (4) subunit structures.

By knowing these parameters of the proteins in native, valuable conclusions can be derived in order to explain the proteins’ functionalities. In this contribution the application of laboratory-based small-angle x-ray scattering studies performed with the SAXSess mc² system in the field of biomedical applications is presented and discussed.