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Investigating the Structure of Proteins in Solution by Small-angle Scattering. Lise Arleth, The Royal Veterinary and Agricultural, Univ., Dept. of Natural Sciences, Thorvaldsensvej 40, DK-1871 Copenhagen, Denmark.

Small-angle scattering (SAS) of x-rays or neutrons is a well-established technique for investigating structures on the length scale of 1-100 nm. The technique is gaining increased importance in the determination of the structure of proteins and more general biomacromolecules in solution and is a strong complement to protein crystallography. In a SAS experiment, the Fourier transform of the 3-dimensional structure of the sample (in terms of the scattering length density fluctuations) is measured. After a simple data analysis, the radius of gyration, the maximum diameter and the molecular weight of the biomacromolecule or biomacromolecular complex is obtained. A more advanced analysis allows for determining the full 3-D structure of the biomacromolecule with a resolution down to 0.5-1.0 nm. One of the main advantages of SAS is that no special sample preparation is needed prior to analysis: The biomacromolecules can be studied in their native state in a physiologically relevant concentration and environment.