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SAXS of Biological Macromolecules and the Canadian Light Source. Brian H. Shilton, Dept. of Biochemistry, The Univ. of Western Ontario, London, ONT., Canada.

Small Angle X-ray Scattering (SAXS) is used to determine the size and shape of macromolecules in solution. The data from SAXS experiments are complementary to structural information obtained from high resolution X-ray crystallography or NMR spectroscopy. For example, in the case of multi-domain proteins, individual domain structures determined at high resolution can be used with SAXS data to model the structure of the complete protein in solution. SAXS is useful for detecting conformational changes attendant upon ligand binding, and it can detect crystal packing effects in high resolution structures. The basic principles of a SAXS experiment will be outlined along with examples of SAXS experiments that have been used for structural studies of biological macromolecules. The possibilities for incorporation of a biological SAXS beamline at the CLS will be discussed. Because the user community is relatively small, such a beamline would likely have to be multifunctional.