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In addition to the classic methods of structural biology--X-ray crystallography and NMR--solution X-ray scattering (SAXS) is a technique for determining the three-dimensional structure of macromolecules. In this chapter, we describe the basics of SAXS, including sample preparation, data collection, and preliminary data analysis. We also discuss common pitfalls that can go wrong with SAXS data measurement so the user can have confidence in the data before undertaking structural modeling.

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