Accurately characterizing protein assembly states in solution with a combination of size exclusion chromatography (SEC), multi-angle light scattering (MALS) and small angle X-ray scattering (SAXS)

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Protein conformations and assemblies determine their fundamental biological functions in cells. X-ray crystallography and cryo-electron microscopy are preferred high resolution methods to obtain detailed structural information and provide insights into function. Nevertheless, with advances in liquid handling, integrated workflows and software, solution methods such as small-angle X-ray scattering (SAXS) coupled with other methods rapidly provide accurate characterization of shapes, conformations, and assembly states of proteins. We now routinely use an approach that benefits from improved sample preparation by size exclusion chromatography (SEC) and in-line collection of multi-angle light scattering (MALS) and small angle X-ray scattering (SAXS) data at the Advanced Photon Source's 18-ID-D Bio-CAT beamline (Argonne National Lab). We will illustrate how this integrative approach has been critical in furthering research in a number of projects.