Example Table (*update grayed-out sections to reflect your actual running conditions*).

(b) SAS data collection parameters	
Instrument	BioSAXS facility at the Cornell High Energy Synchrotron Source beamline G1 with dual Pilatus 100k (Dectris) detector
Wavelength, energy	1.249 Å , 9.924 keV
Flux	7.7×10^{11} ph/s
Beam size	250 μm × 250 μm
q-measurement range	0.008-0.28 $Å^{-1}$ (SAXS) 0.26-0.7 $Å^{-1}$ (WAXS)
Absolute scaling method	water standard
Basis for normalization	transmitted intensity via beamstop photodiode
Method of monitoring radiation damage	comparison of sequential exposures via CORMAP statistic
Exposure time, number of exposures	1 s × 10 exposures
Sample configuration	1.5 mm OD quartzglass capillary with 10 μm thick walls *in vacuuo*; Robot: oscillating 30 μl sample SEC: Atka Pure system; superdex 200 increase 5/150, 10/300 columns
Sample temperature	4°C
(c) Software employed	
SAXS data reduction	Radial averaging, frame comparison, and subtraction using BioXTAS RAW 1.5.0 (Hopkins et al., 2017)
Basic analysis	Guinier fit, molecular weight using BioXTAS RAW, P(r) using GNOM (Svergun, 1992)

Methods Section (*For use as an example only. Do not copy!)*

All samples were centrifuged at 14,000 RPM for 20 minutes prior to data collection. Each sample was prepared at four concentrations (1, 1/2, 1/4,1/8 dilution of maximum) to assess concentration dependence. SAXS data were collected on CHESS beamline G1 at 9.924 keV (1.249 Å) at 7.7×10^{11} photons/s. The X-ray beam was collimated to 250 × 250 μm^2 diameter and centered on a capillary sample cell with 1.5 mm path length and 25 μm thick quartzglass walls (Charles Supper Company, Natik, MA). The sample cell and full X-ray flight path, including beamstop, were kept *in vacuo (< 1×10^{-3} torr)* to eliminate air scatter. Temperature was maintained at 4°C. Images were collected on a dual Pilatus 100K-S detector system (Dectris, Baden, Switzerland). Sample-to-detector distance was calibrated using silver behenate powder (The Gem Dugout, State College, PA). The useful q-space range ($4\pi Sin\theta/\lambda$ with 2θ being the scattering angle) was generally from q_{min}= 0.008 $Å^{-1}$ to q_{max}= 0.27 $Å^{-1}$ (0.8 $Å^{-1}$ when using WAXS data). Image integration, normalization, and subtraction was carried out using the BioXTAS RAW program (1). Radiation damage was assessed using the CORMAP criterion as implemented in RAW's built-in averaging function (2). Sample and buffer solutions were normalized to equivalent exposure before subtraction using beamstop photodiode counts.

Standard high-throughput SAXS

Sample plugs of approximately 20-30 μl were delivered from a 96-well plate to the capillary using a Hudson SOLO single-channel pipetting robot (Hudson Robotics Inc.

Springfield, New Jersey). To reduce radiation damage, sample plugs were oscillated in the X-ray beam using a computer-controlled syringe pump. Typically 10-20 undamaged 1s exposures were averaged to produce buffer and sample profiles. Scattering intensities were placed on an absolute scale using water as a standard. Lysozyme at 3 mg/ml in 100 mM NaCl at pH 4.5 in Acetate buffer was used as a molecular weight standard.

Inline chromatography (SEC-SAXS)
Chromatographic separation of samples was conducted at 4°C using Superdex 200 5/150 and 10/300 columns on an AKTA Pure system (GE Healthcare Life Sciences, Marlborough, MA). Sequential 1s (5/150) or 2s (10/300) exposures with flow rates of 0.15 (5/150) to 0.5 (10/300) ml/min were used.

The complete automated BioSAXS system and protocols are described elsewhere (3,4).

1. Hopkins, J.B., Gillilan, R.E. and Skou, S. (2017) BioXTAS RAW: improvements to a free open-source program for small-angle X-ray scattering data reduction and analysis. *J. Appl. Cryst.*, **50**, 1545-1553.
2. Franke, D., Jeffries, C.M. and Svergun, D.I. (2015) Correlation Map, a goodness-of-fit test for one-dimensional X-ray scattering spectra. *Nat. Methods*, **12**, 419.
3. Acerbo, A.S., Cook, M.J. and Gillilan, R.E. (2015) Upgrade of MacCHESS facility for X-ray scattering of biological macromolecules in solution. *J. Synchrotron Rad.*, **22**, 180-186.
4. Skou, S., Gillilan, R.E. and Ando, N. (2014) Synchrotron-based small-angle X-ray scattering of proteins in solution. *Nat. Protoc.*, **9**, 1727-1739.