Folder contents:

- Input data for ML-SAScombine

- Run scripts used with ML-SAScombine

- Output files for updated consensus files from ML-SAScombine with log and linear *q*-binning*.

- Output files for combined SEC-SAS data from ML-SAScombine with log *q*-binning

Individual scattering profiles in the folders are identified by their source, with the numerical designations given in the Table below. Data collection details are in **Table S2** of the Supporting Information from the round robin study (Trewhella et al. (2022) *Acta Cryst.* **D78**: 1315)

Naming convention for *.dat files is: instrument code and protein designation followed by SS for SEC-SAXS data or concentrations for batch data mg/mL expressed as XptY. A "-Gt" extension indicates the lowest-*q* data have been truncated to match the lowest-*q* data included by AutoGNOM.

Key for instruments designations:

SAXS Instruments	
Advanced Light Source - SIBYLS	X1
Advanced Photon Source – 12-ID-B	X2
Advanced Photon Source – BioCAT	X3
Australian synchrotron SAXSWAXS: AS	X4
Cornell High Energy Synchrotron Source (CHESS) – ID7a	X5
Diamond Light Source - B21	X6
NIST/IBBR, SAXSLab Ganesha Instrument	X7
Petra III, P12 BioSAXS (SAXS and WAXS configurations)	X8 (a and b)
Shanghai Synchrotron Radiation Facility – BL192U	X9
SOLEIL – SWING	X10
SPring-8 - BL40B2	X11
Stanford Synchrotron Radiation Laboratory (SSRL) – Beamline 4-2 BioSAXS	X12

 * We use "*q*" for the scattering vector amplitude as $4\pi(\sin\theta)/\lambda$, consistent with the convention used in the associated publication and note that SASBDB uses "*s*" in place of "*q*."