Full wwPDB Integrative Structure Validation Report

June 05, 2020 -- 07:20 PM

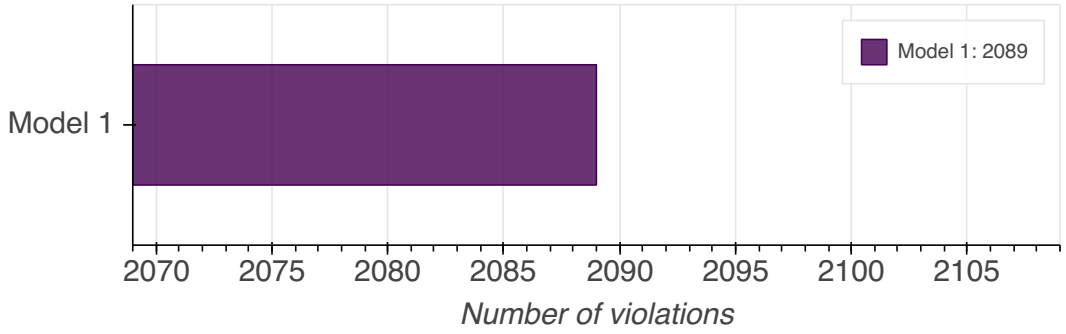
The following software were used in the production of this report:

Integrative Modeling Validation Package : Version 1.0

PDB ID	PDBDEV_00000017
Molecule Name	Molecular architecture of the major membrane ring component, Pom152, of the yeast nuclear pore complex
Title	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex.
Authors	Upla P;Kim SJ;Sampathkumar P;Dutta K;Cahill SM;Chemmama IE;Williams R;Bonanno JB;Rice WJ;Stokes DL;Cowburn D;Almo SC;Sali A;Rout MP;Fernandez-Martinez J

Overall quality

Model quality: Excluded Volume Analysis



Ensemble information

This entry consists of 1 distinct ensemble.

Entry composition

There is 1 unique type of model in this entry.This model is titled Cluster 0/None respectively.

Model ID	Subunit number	Subunit ID	Subunit name	Chain ID	Total residues
1	1	1	pom152	A	1337

Datasets used for modeling

There are 22 unique datasets used to build the models in this entry.

ID	Dataset type	Database name	Data access code
1	Experimental model	PDB	5TVZ
2	Comparative model	Not listed	None
3	Comparative model	Not listed	None
4	Comparative model	Not listed	None
5	Comparative model	Not listed	None

ID	Dataset type	Database name	Data access code
6	Comparative model	Not listed	None
7	Comparative model	Not listed	None
8	3DEM volume	EMDB	EMD-8543
9	3DEM volume	Not listed	None
10	2DEM class average	Not listed	None
11	2DEM class average	Not listed	None
12	2DEM class average	Not listed	None
13	2DEM class average	Not listed	None
14	2DEM class average	Not listed	None
15	2DEM class average	Not listed	None
16	2DEM class average	Not listed	None
17	2DEM class average	Not listed	None
18	SAS data	SASBDB	SASDBV9
19	SAS data	SASBDB	SASDBW9
20	SAS data	SASBDB	SASDBX9
21	SAS data	SASBDB	SASDBY9
22	SAS data	SASBDB	SASDBZ9

Representation

This entry has only one representation and includes 9 rigid bodies and 9 flexible units.

Chain ID	Rigid bodies	Non-rigid segments

Chain ID	Rigid bodies	Non-rigid segments
A	379-472:Comparative model/None, 520-611:Comparative model/None, 616-714:Comparative model/None, 722-818:Comparative model/None, 824-918:Comparative model/None, 931-1026:Comparative model/None, 1036-1141:Comparative model/None, 1150-1229:Comparative model/None, 1244-1337:Comparative model/None.	1-378, 473-519, 612-615, 715-721, 819-823, 919-930, 1027-1035, 1142-1149, 1230-1243.

Methodology and software

Step number	Protocol ID	Method name	Method type	Number of computed models	Multi state modeling	Multi scale modeling
1	1	Replica exchange monte carlo	Sampling	100000	False	True

There are 3 software packages reported in this entry.

ID	Software name	Software version	Software classification	Software location
1	Integrative Modeling Platform (IMP)	develop-0a5706e202	integrative model building	https://integrativemodeling.org
2	IMP PMI module	67456c0	integrative model building	https://integrativemodeling.org
3	MODELLER	9.13	comparative modeling	https://salilab.org/modeller/

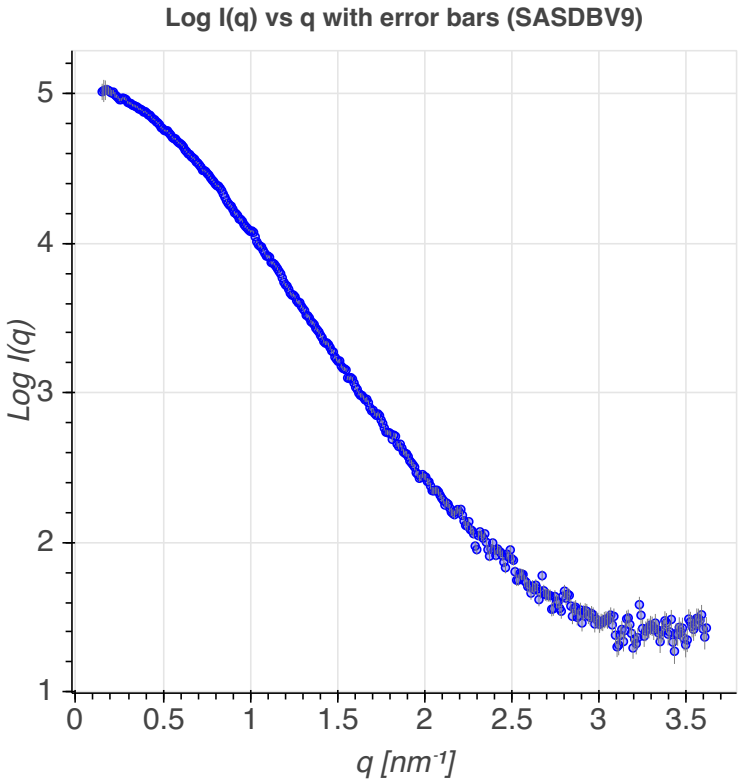
Data quality

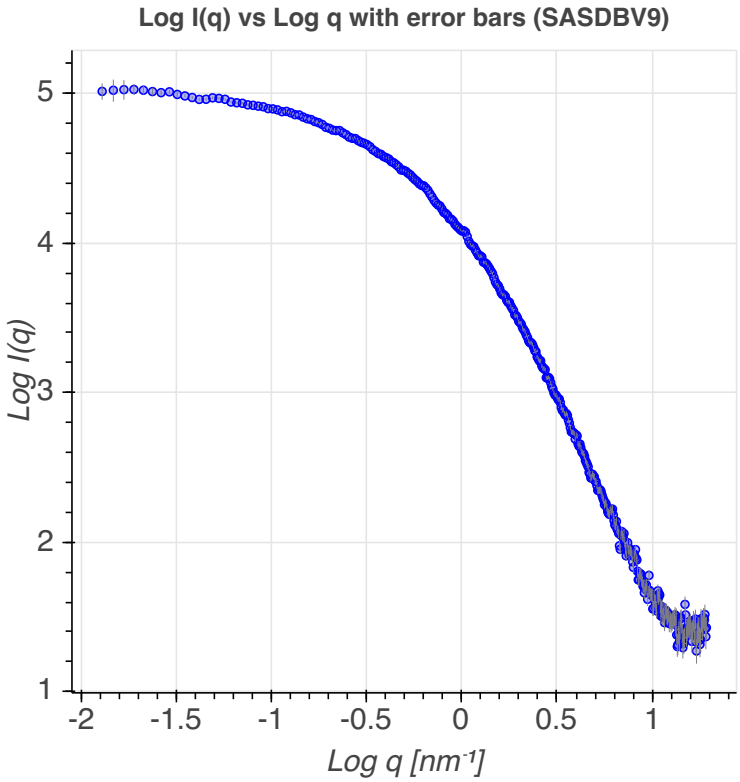
Scattering profile

SAS data used in this integrative model was obtained from 5 deposited SASBDB entry (entries).

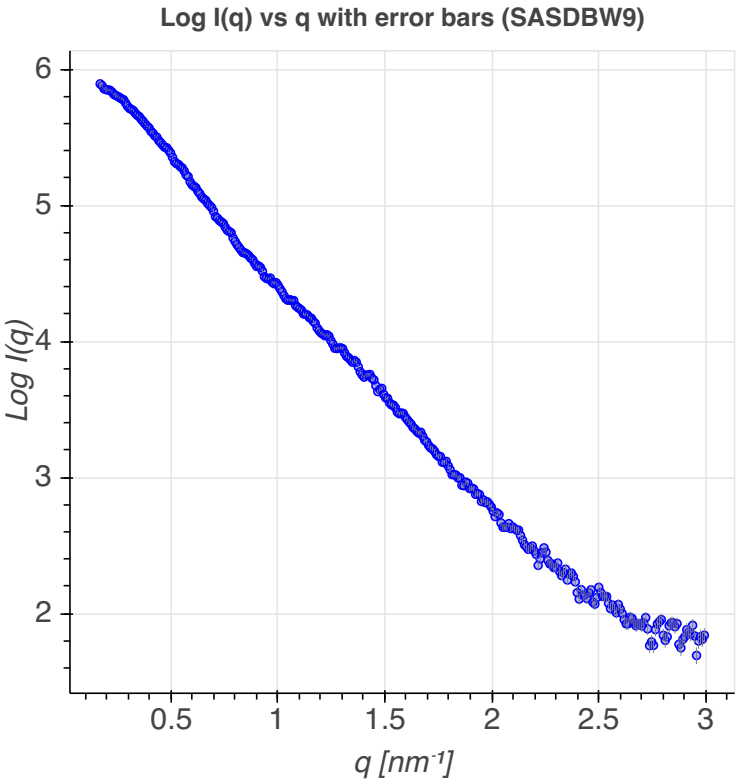
Scattering profile for SASDBV9: data from solutions of biological macromolecules are presented as both log I(q) vs q and log I(q) vs log (q) based on SAS validation task force (SASvtf) recommendations. I(q) is the

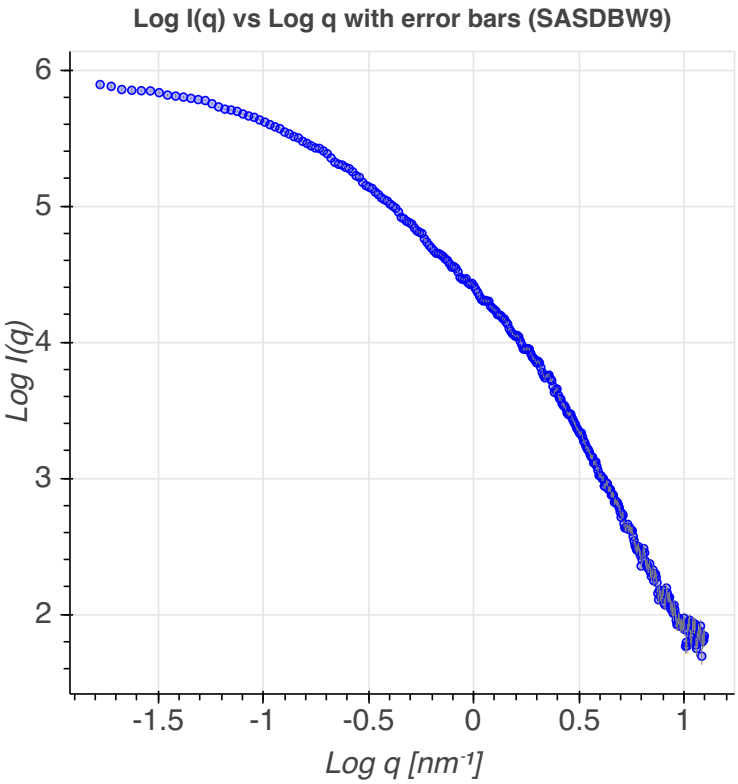
intensity (in arbitrary units) and q is the modulus of the scattering vector.



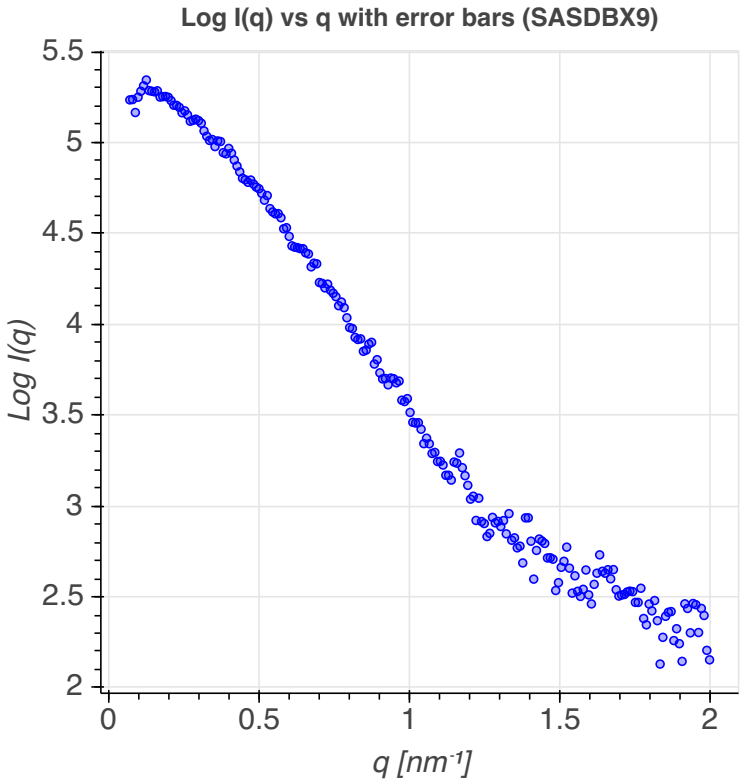


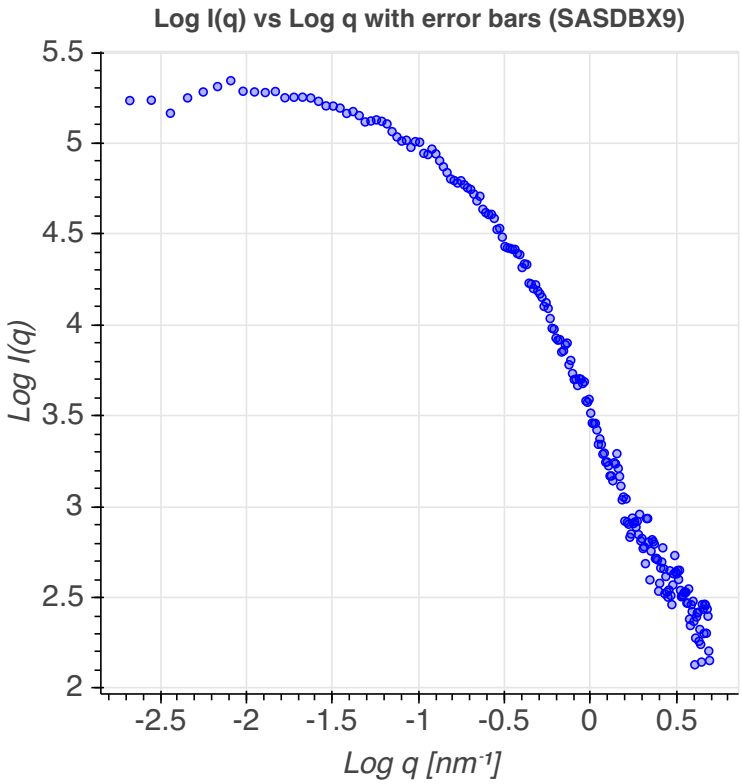
Scattering profile for SASDBW9: data from solutions of biological macromolecules are presented as both log I(q) vs q and log I(q) vs log (q) based on SAS validation task force (SASvtf) recommendations. I(q) is the intensity (in arbitrary units) and q is the modulus of the scattering vector.



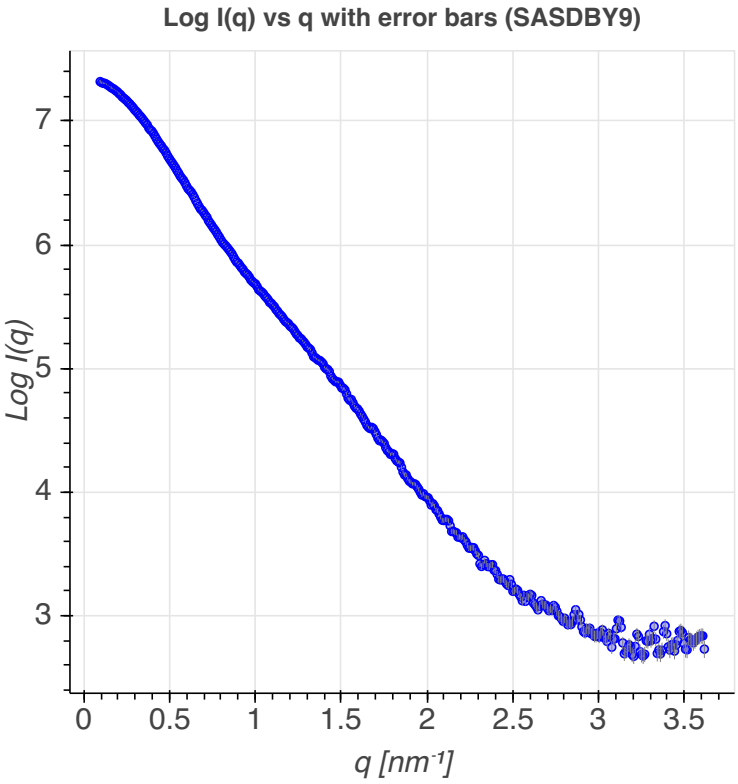


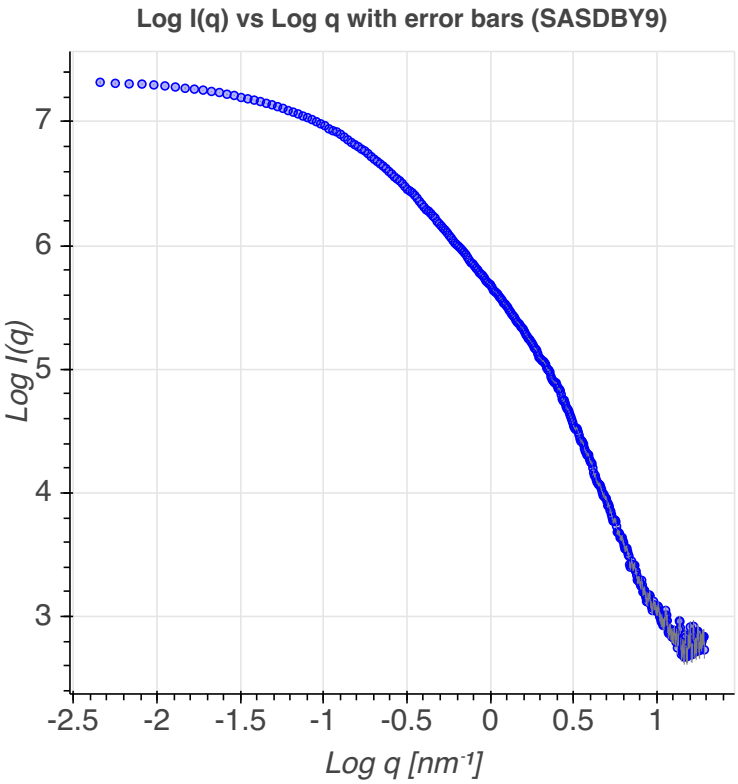
Scattering profile for SASDBX9: data from solutions of biological macromolecules are presented as both log I(q) vs q and log I(q) vs log (q) based on SAS validation task force (SASvtf) recommendations. I(q) is the intensity (in arbitrary units) and q is the modulus of the scattering vector.



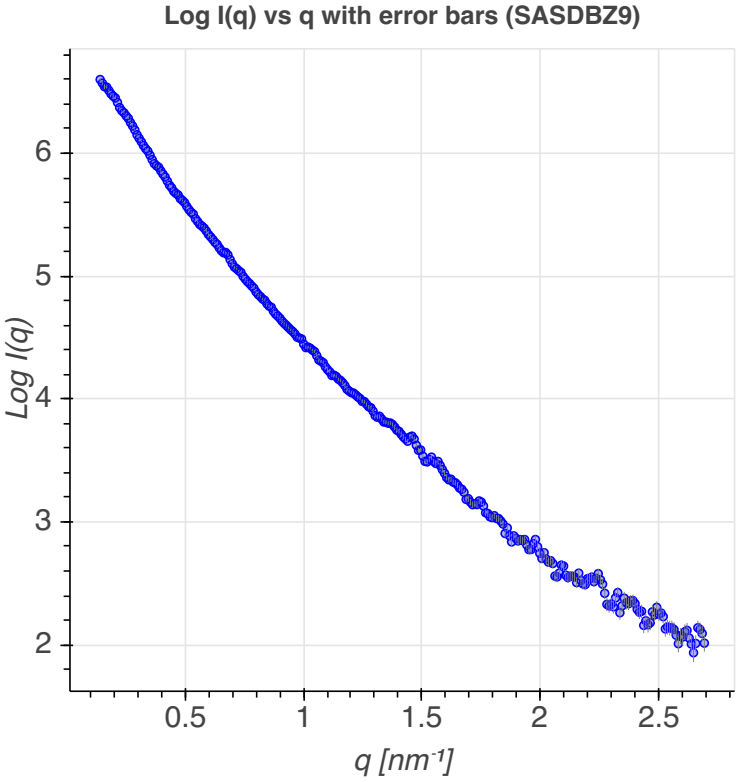


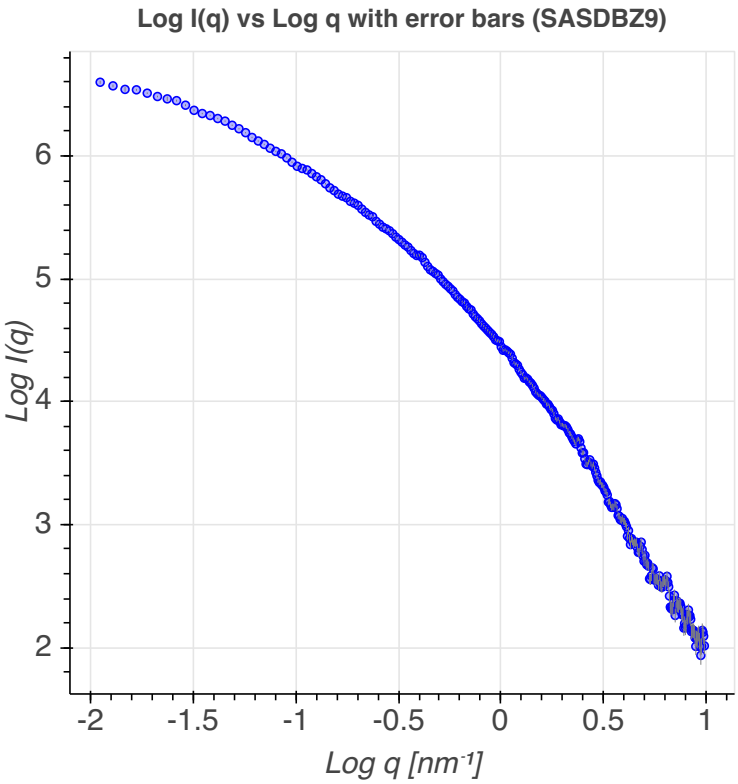
Scattering profile for SASDBY9: data from solutions of biological macromolecules are presented as both log I(q) vs q and log I(q) vs log (q) based on SAS validation task force (SASvtf) recommendations. I(q) is the intensity (in arbitrary units) and q is the modulus of the scattering vector.





Scattering profile for SASDBZ9: data from solutions of biological macromolecules are presented as both log I(q) vs q and log I(q) vs log (q) based on SAS validation task force (SASvtf) recommendations. I(q) is the intensity (in arbitrary units) and q is the modulus of the scattering vector.





Key experimental estimates

Molecular weight (MW) estimates from experiments and analysis true molecular weight can be compared to the Porod estimate from scattering profiles.

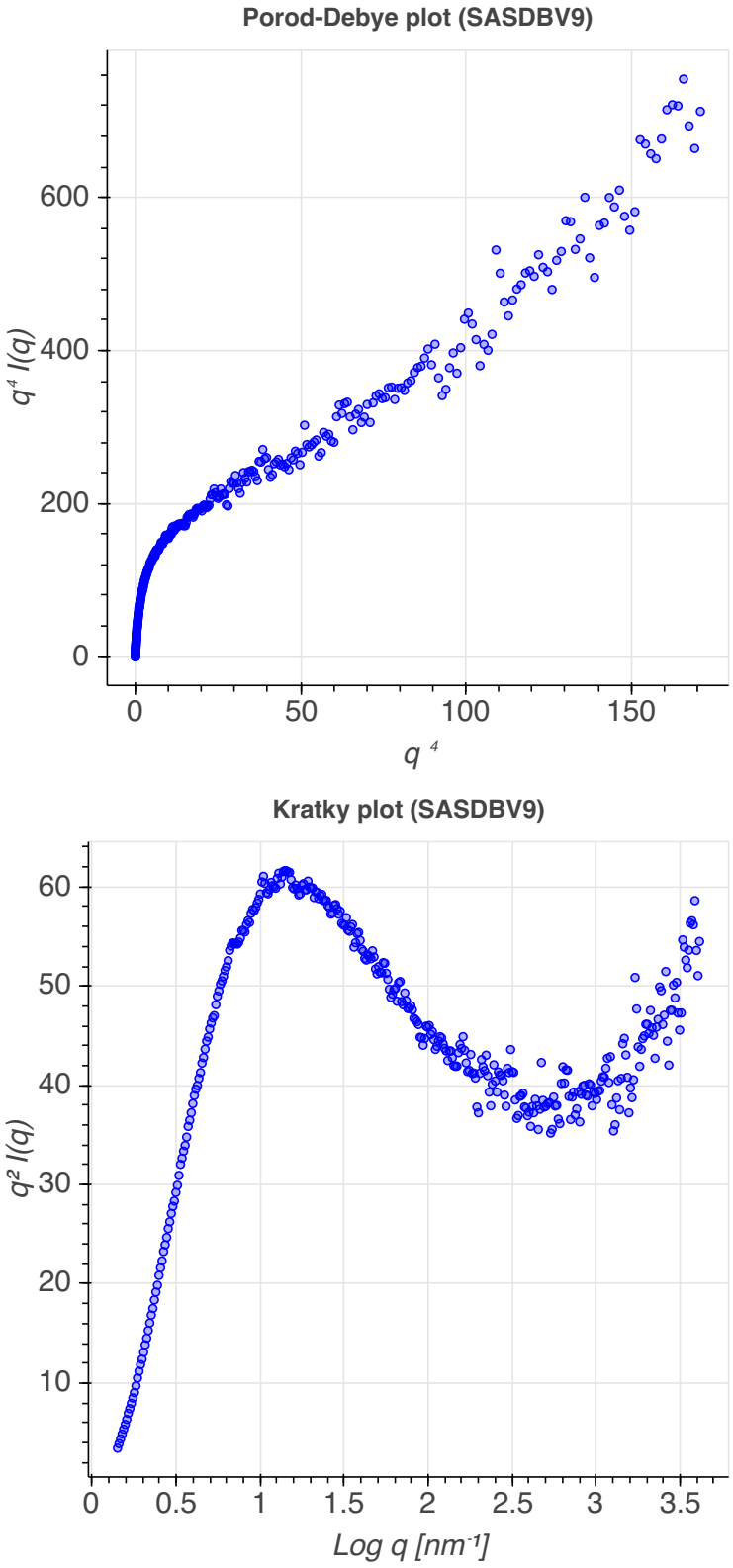
SASDB ID	Sequence MW	Experimental MW	Porod MW
SASDBV9	12.386 kDa	12.600 kDa	N/A
SASDBW9	12.386 kDa	12.600 kDa	N/A
SASDBX9	12.386 kDa	12.600 kDa	N/A
SASDBY9	12.386 kDa	12.600 kDa	N/A
SASDBZ9	12.386 kDa	12.600 kDa	N/A

Volume estimates from experiments and analysis: estimated volume can be compared to Porod volume obtained from scattering profiles.

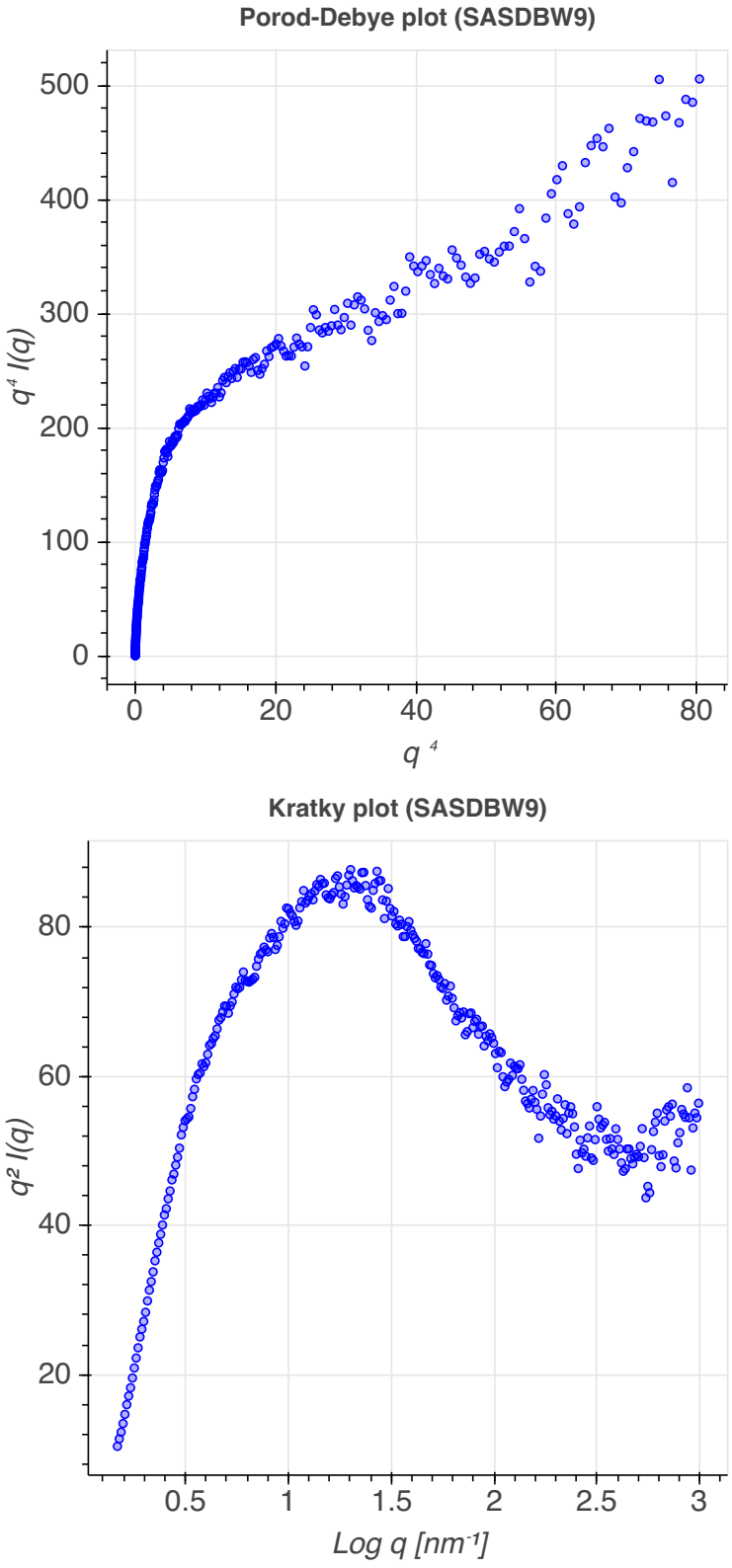
SASDB ID	Estimated volume	Estimated volume method	Porod volume
SASDBV9	None	None	17.94 nm^3
SASDBW9	None	None	22.50 nm^3
SASDBX9	None	None	56.68 nm^3
SASDBY9	None	None	27.97 nm^3
SASDBZ9	None	None	66.59 nm^3

Flexibility analysis

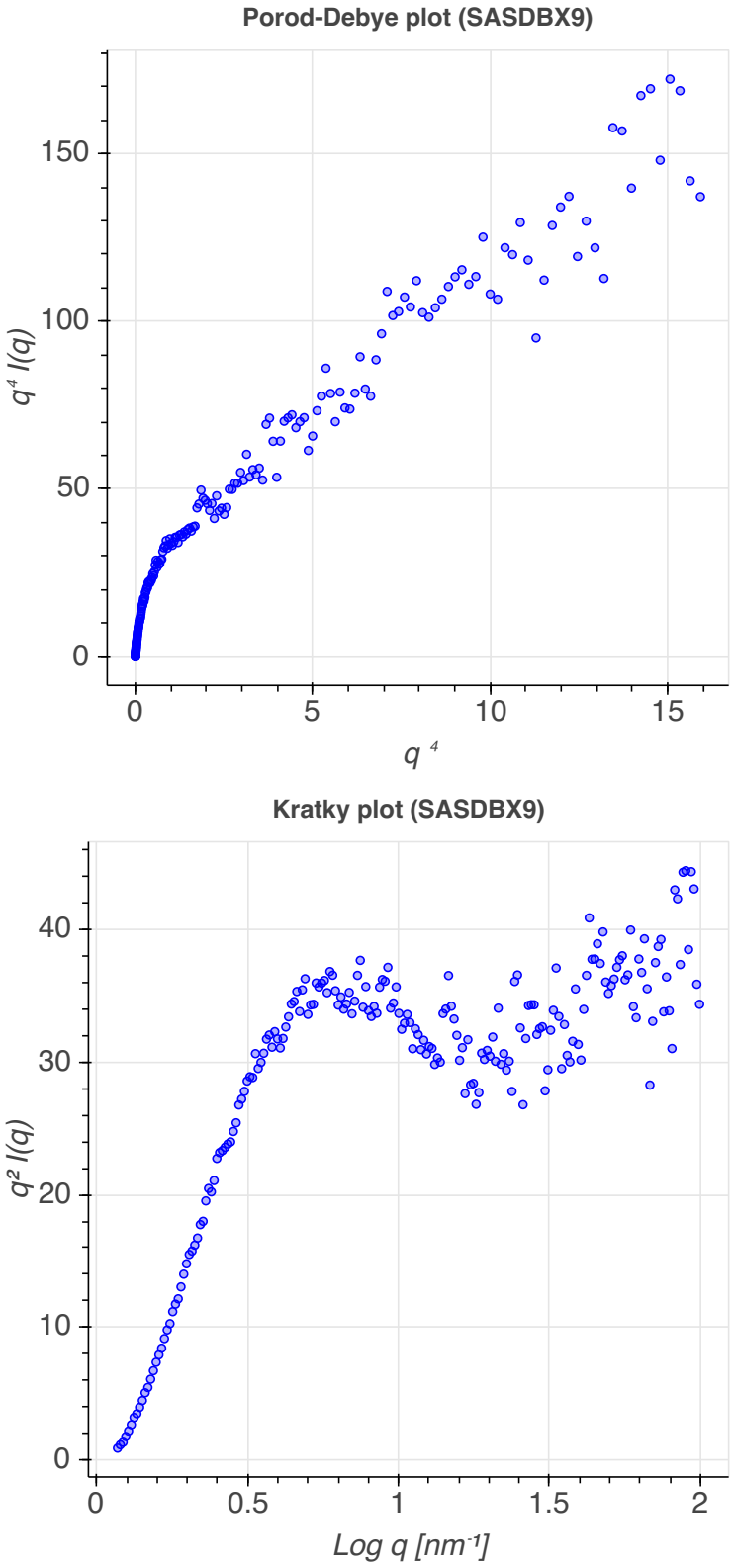
Flexibility analysis for SASDBV9: In a Porod-Debye plot, a clear plateau is observed for globular (partial or fully folded) domains, whereas, fully unfolded domains are devoid of any discernable plateau. For details, refer to Figure 5 in Rambo and Tainer, 2011 . In a Kratky plot, a parabolic shape is observed for globular (partial or fully folded) domains and a hyperbolic shape is observed for fully unfolded domains.



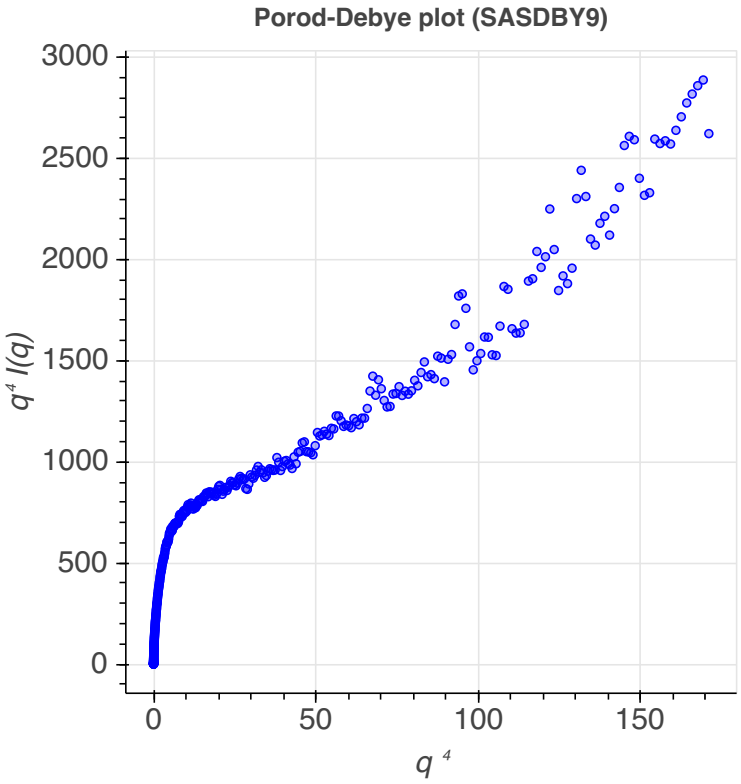
Flexibility analysis for SASDBW9: In a Porod-Debye plot, a clear plateau is observed for globular (partial or fully folded) domains, whereas, fully unfolded domains are devoid of any discernable plateau. For details, refer to Figure 5 in Rambo and Tainer, 2011 . In a Kratky plot, a parabolic shape is observed for globular (partial or fully folded) domains and a hyperbolic shape is observed for fully unfolded domains.

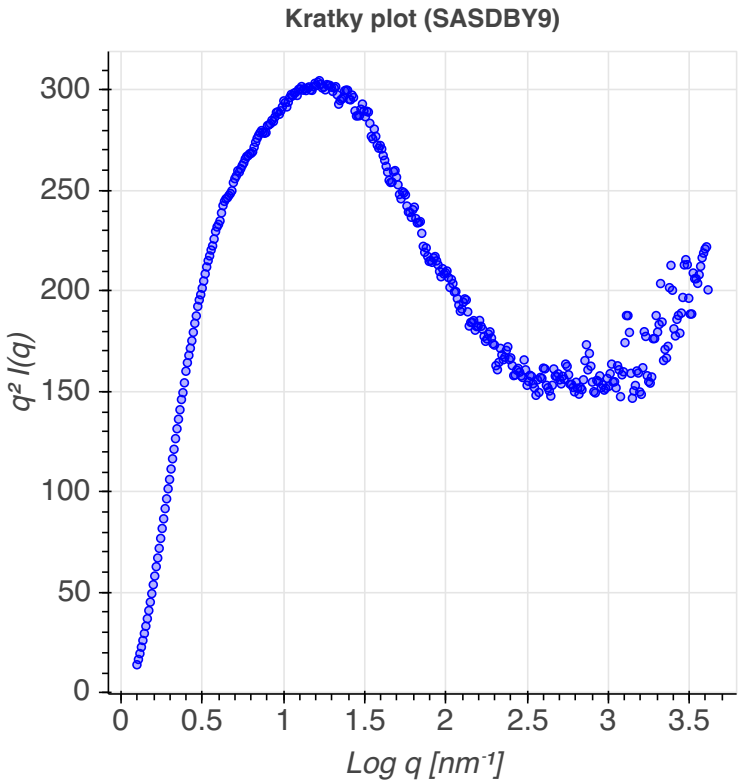


Flexibility analysis for SASDBX9: In a Porod-Debye plot, a clear plateau is observed for globular (partial or fully folded) domains, whereas, fully unfolded domains are devoid of any discernable plateau. For details, refer to Figure 5 in Rambo and Tainer, 2011 . In a Kratky plot, a parabolic shape is observed for globular (partial or fully folded) domains and a hyperbolic shape is observed for fully unfolded domains.

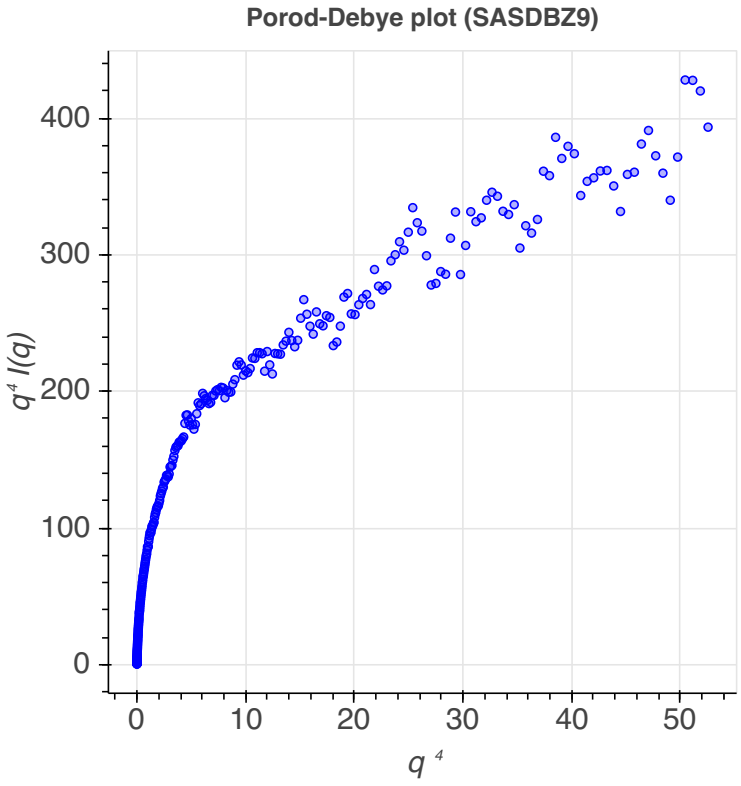


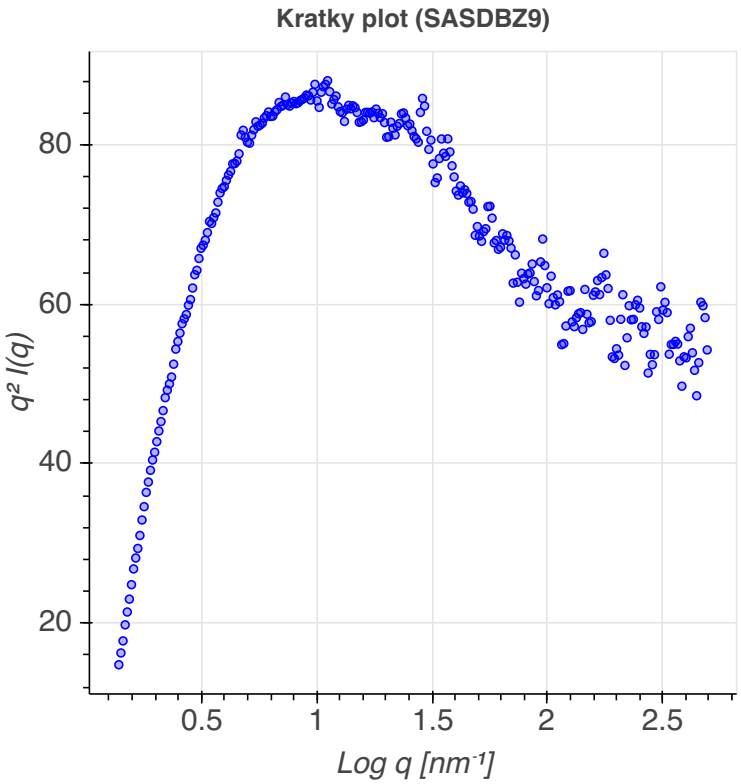
Flexibility analysis for SASDBY9: In a Porod-Debye plot, a clear plateau is observed for globular (partial or fully folded) domains, whereas, fully unfolded domains are devoid of any discernable plateau. For details, refer to Figure 5 in Rambo and Tainer, 2011 . In a Kratky plot, a parabolic shape is observed for globular (partial or fully folded) domains and a hyperbolic shape is observed for fully unfolded domains.





Flexibility analysis for SASDBZ9: In a Porod-Debye plot, a clear plateau is observed for globular (partial or fully folded) domains, whereas, fully unfolded domains are devoid of any discernable plateau. For details, refer to Figure 5 in Rambo and Tainer, 2011 . In a Kratky plot, a parabolic shape is observed for globular (partial or fully folded) domains and a hyperbolic shape is observed for fully unfolded domains.





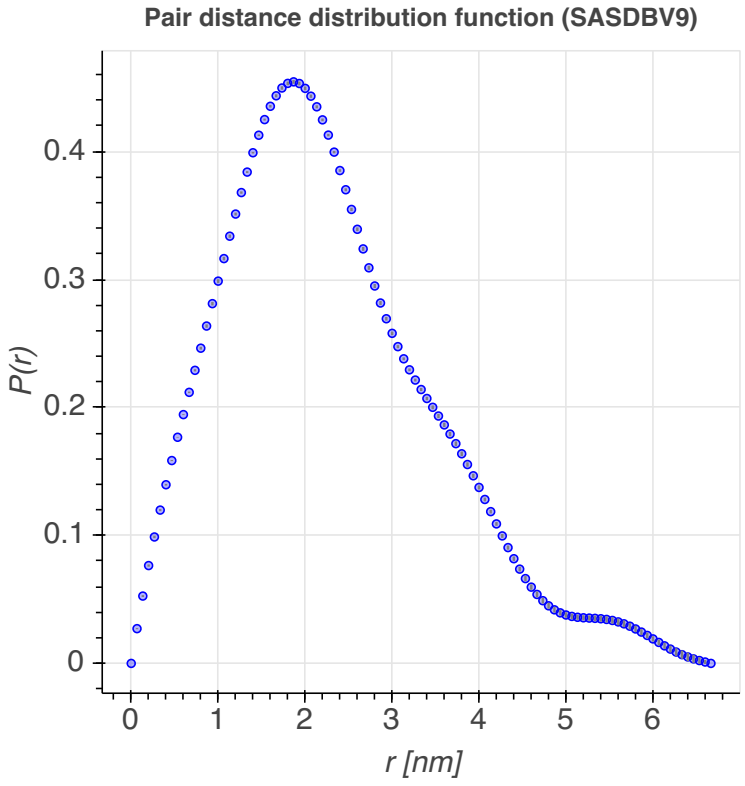
Pair-distance distribution analysis

P(r) analysis: p(r) represents the distribution of distances between all pairs of atoms within the particle weighted by the respective electron densities. p(r) is the Fourier transform of I(s) (and vice versa). Rg can be estimated from integrating the p(r) function. Agreement between the p(r)

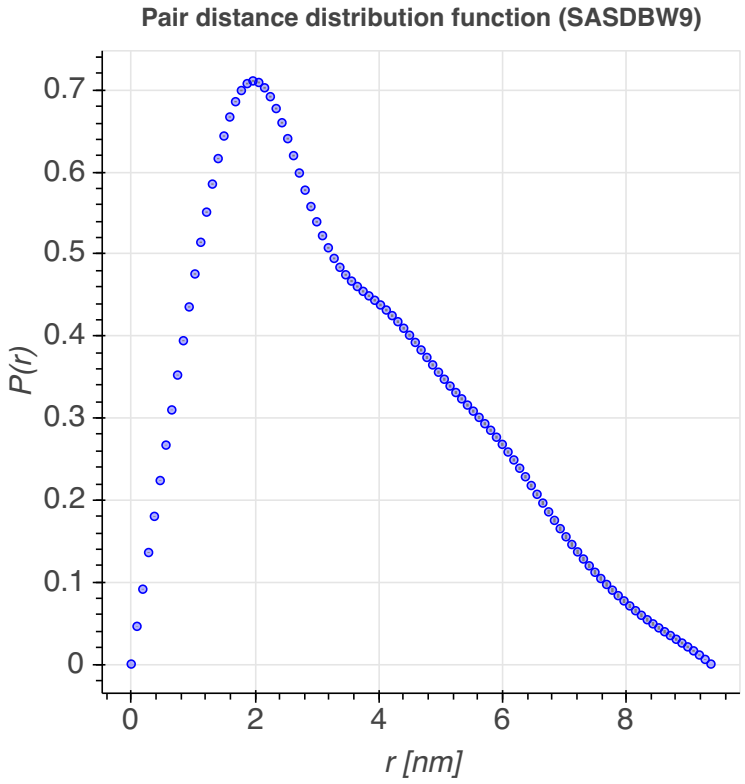
and Guinier-determined Rg (table below) is a good measure of the self-consistency of the SAS profile. Rg is a measure for the overall size of a macromolecule; e.g. a protein with a smaller Rg is more compact than a protein with a larger Rg, provided both have the same molecular weight (MW). The point where p(r) is decaying to zero is called Dmax and represents the maximum size of the particle.

SASDB ID	Software used	Dmax	Dmax error	Rg	Rg error
SASDBV9	ATSAS GNOM	6.66 nm	N/A	1.824 nm	0.006 nm
SASDBW9	ATSAS GNOM	9.37 nm	N/A	2.787 nm	0.007 nm
SASDBX9	ATSAS GNOM	7.93 nm	N/A	2.636 nm	0.008 nm
SASDBY9	ATSAS GNOM	10.45 nm	N/A	2.976 nm	0.005 nm
SASDBZ9	ATSAS GNOM	15.43 nm	N/A	4.629 nm	0.011 nm

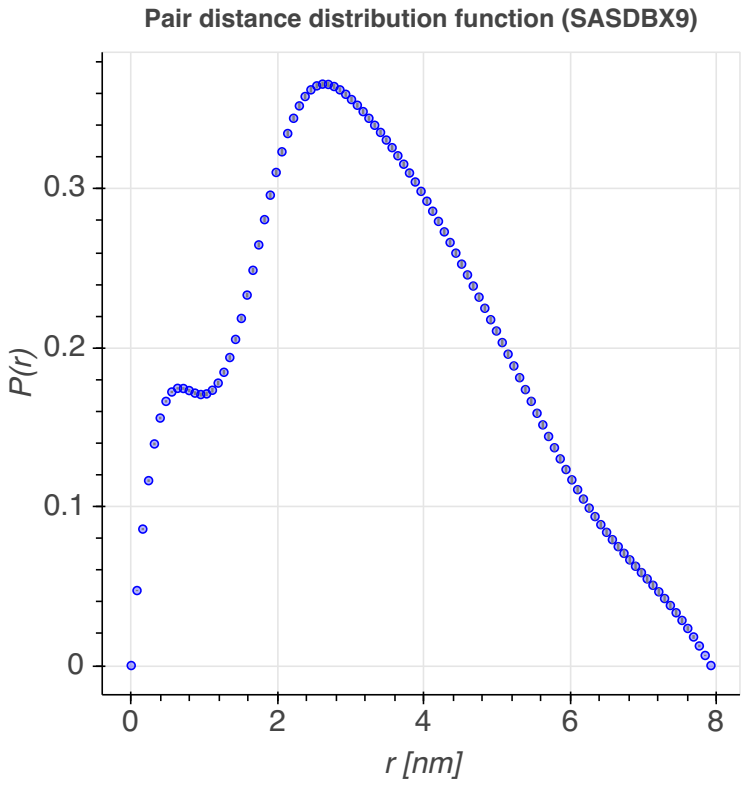
P(r) for SASDBV9: The value of P(r) should be zero beyond r=Dmax.



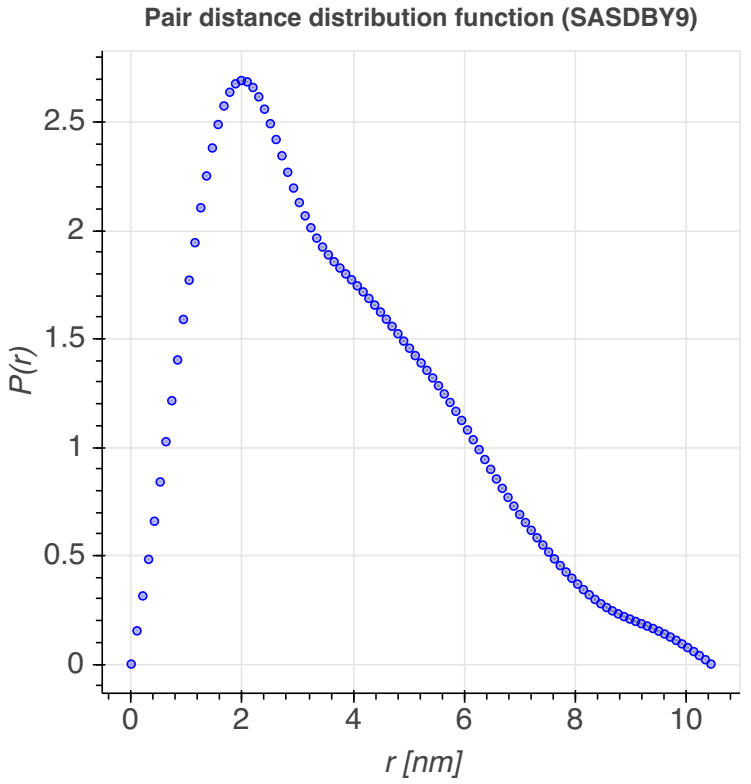
P(r) for SASDBW9: The value of P(r) should be zero beyond r=Dmax.



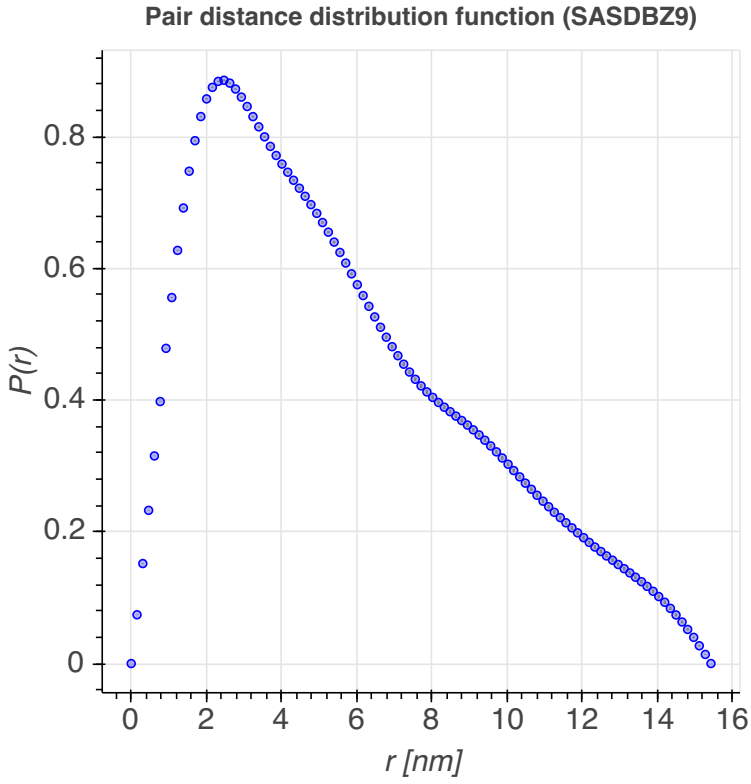
P(r) for SASDBX9: The value of P(r) should be zero beyond r=Dmax.



P(r) for SASDBY9: The value of P(r) should be zero beyond r=Dmax.



P(r) for SASDBZ9: The value of P(r) should be zero beyond r=Dmax.

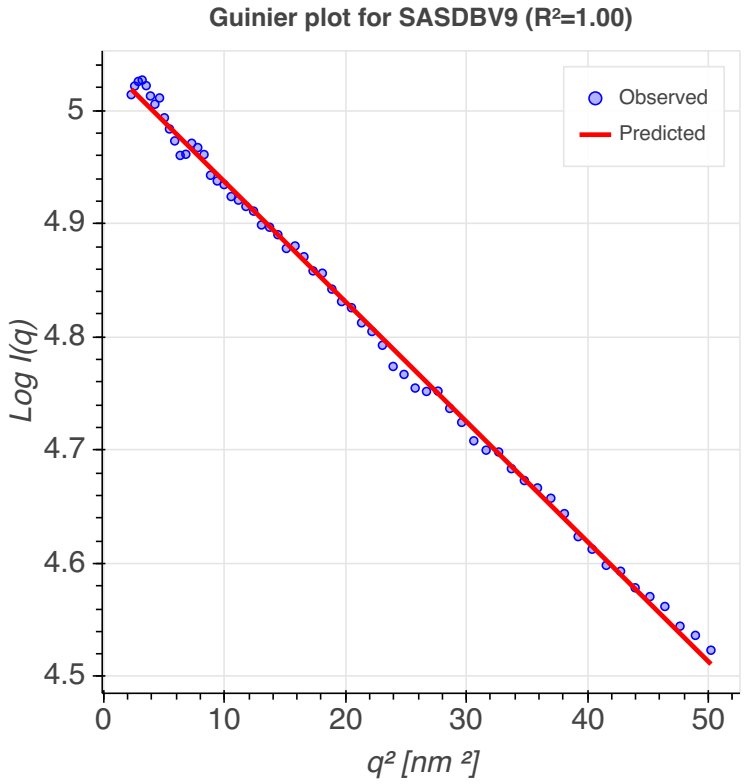


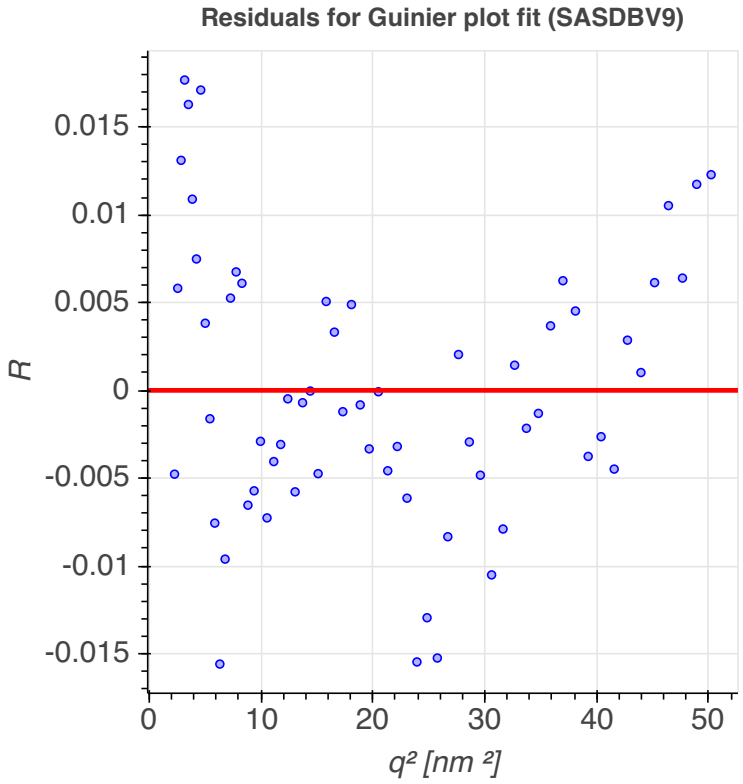
Guinier analysis

Guinier analysis: agreement between the p(r) and Guinier-determined Rg (table below) is a good measure of the self-consistency of the SAS profile. Molecular weight estimates can also be compared to Porod and sample molecular weights for consistency.

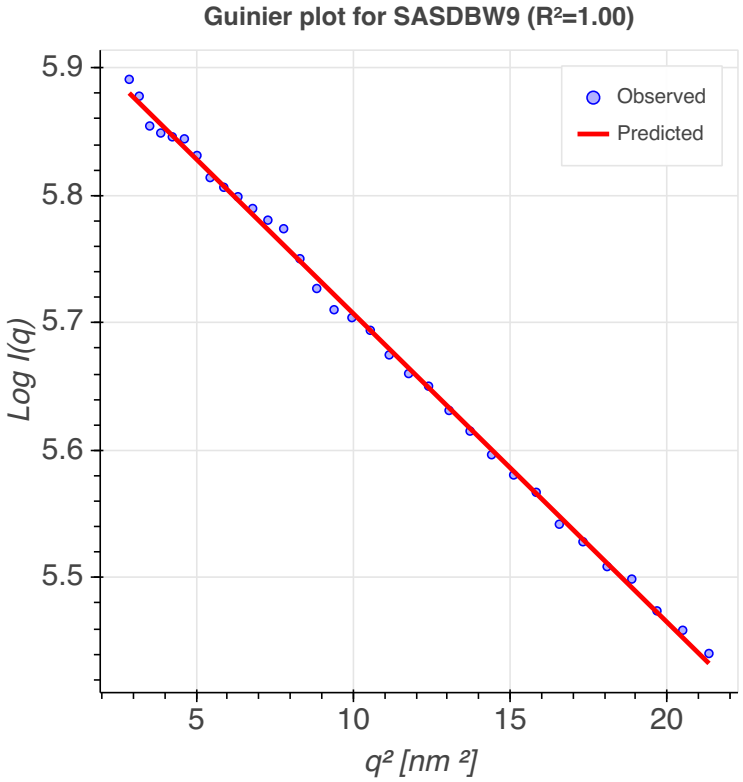
SASDB ID	Rg	Rg error	MW	MW error
SASDBV9	1.77 nm	0.048 nm	12.200 nm	N/A
SASDBW9	2.71 nm	0.063 nm	25.200 nm	N/A
SASDBX9	2.78 nm	0.180 nm	14.700 nm	N/A
SASDBY9	2.95 nm	0.110 nm	25.200 nm	N/A
SASDBZ9	4.34 nm	0.170 nm	48.300 nm	N/A

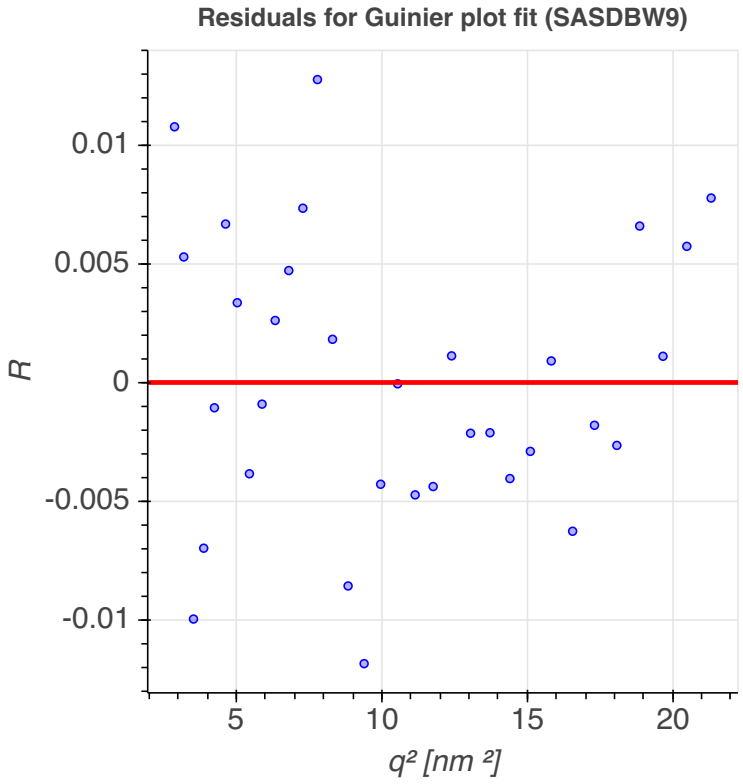
Guinier analysis for SASDBV9: the linearity of the Guinier plot is a sensitive indicator of the quality of the experimental SAS data; a linear Guinier plot is a necessary but not sufficient demonstration that a solution contains monodisperse particles of the samesize. Deviations from linearity usually point to strong interference effects, polydispersity of the samples or improper background subtraction. Residual value plot and coefficient of determination (R^2) are measures to assess linear fit to the data. A perfect fit has an R^2 value of 1. Residual values should be equally and randomly spaced around the horizontal axis.



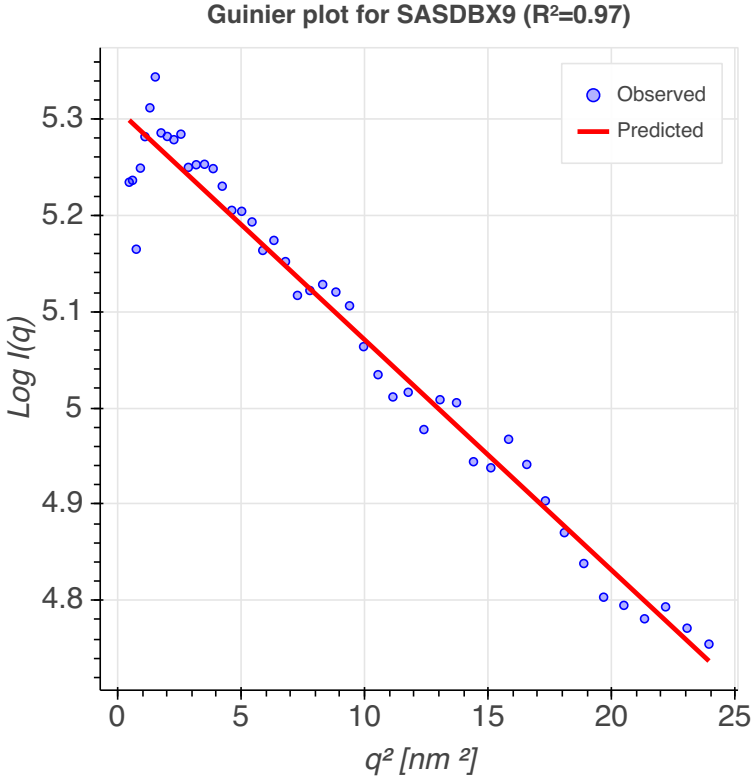


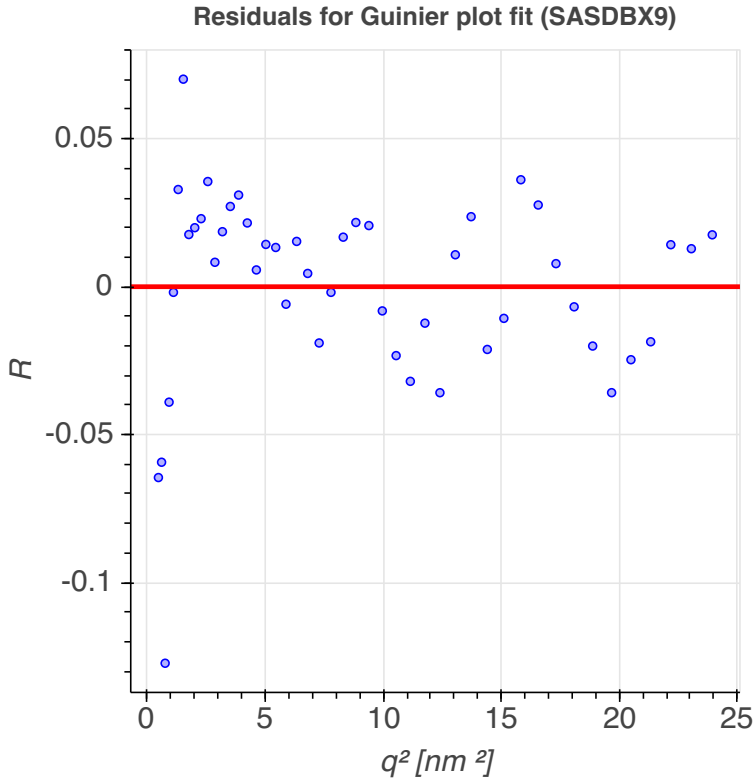
Guinier analysis for SASDBW9: the linearity of the Guinier plot is a sensitive indicator of the quality of the experimental SAS data; a linear Guinier plot is a necessary but not sufficient demonstration that a solution contains monodisperse particles of the samesize. Deviations from linearity usually point to strong interference effects, polydispersity of the samples or improper background subtraction. Residual value plot and coefficient of determination (R^2) are measures to assess linear fit to the data. A perfect fit has an R^2 value of 1. Residual values should be equally and randomly spaced around the horizontal axis.



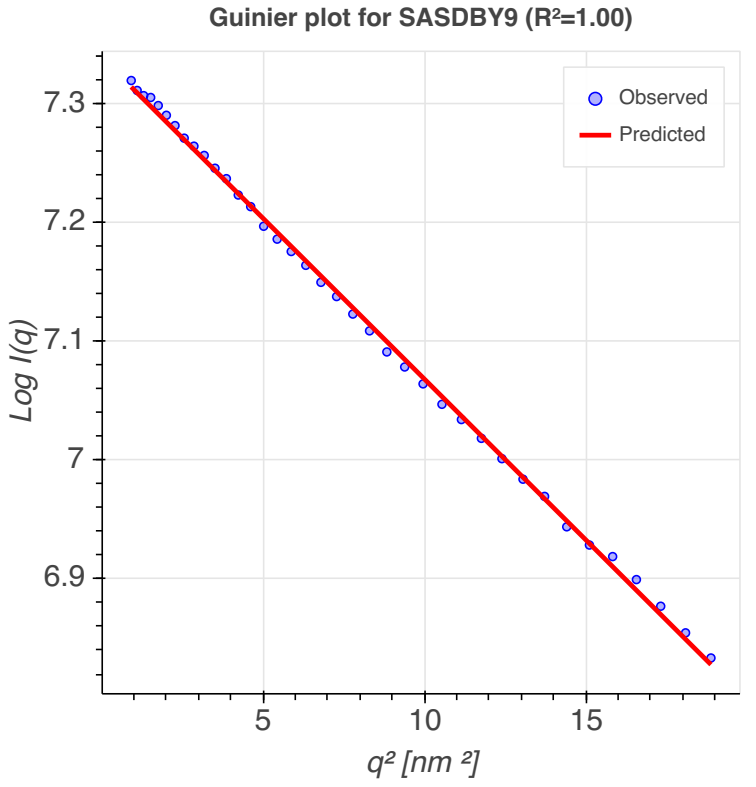


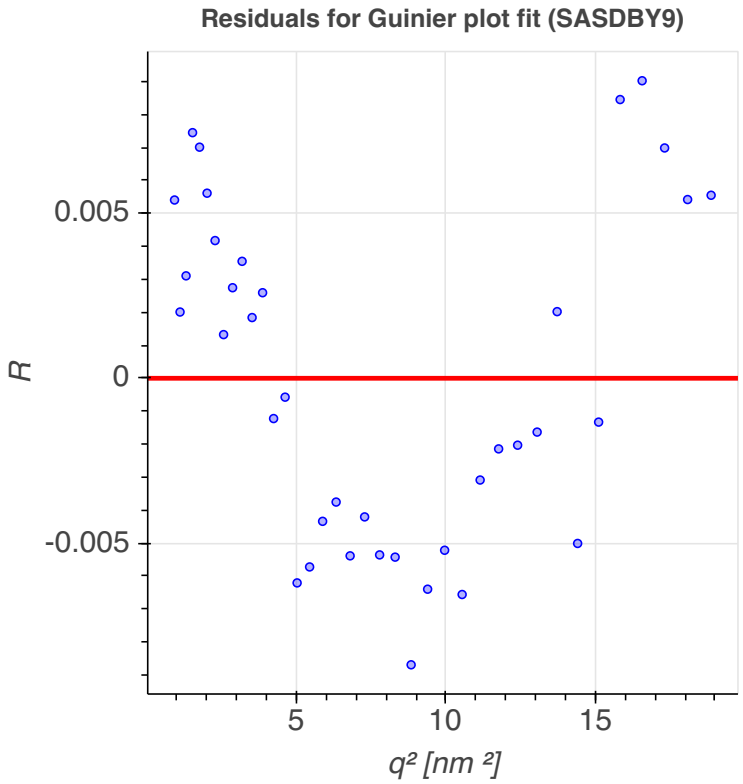
Guinier analysis for SASDBX9: the linearity of the Guinier plot is a sensitive indicator of the quality of the experimental SAS data; a linear Guinier plot is a necessary but not sufficient demonstration that a solution contains monodisperse particles of the samesize. Deviations from linearity usually point to strong interference effects, polydispersity of the samples or improper background subtraction. Residual value plot and coefficient of determination (R^2) are measures to assess linear fit to the data. A perfect fit has an R^2 value of 1. Residual values should be equally and randomly spaced around the horizontal axis.



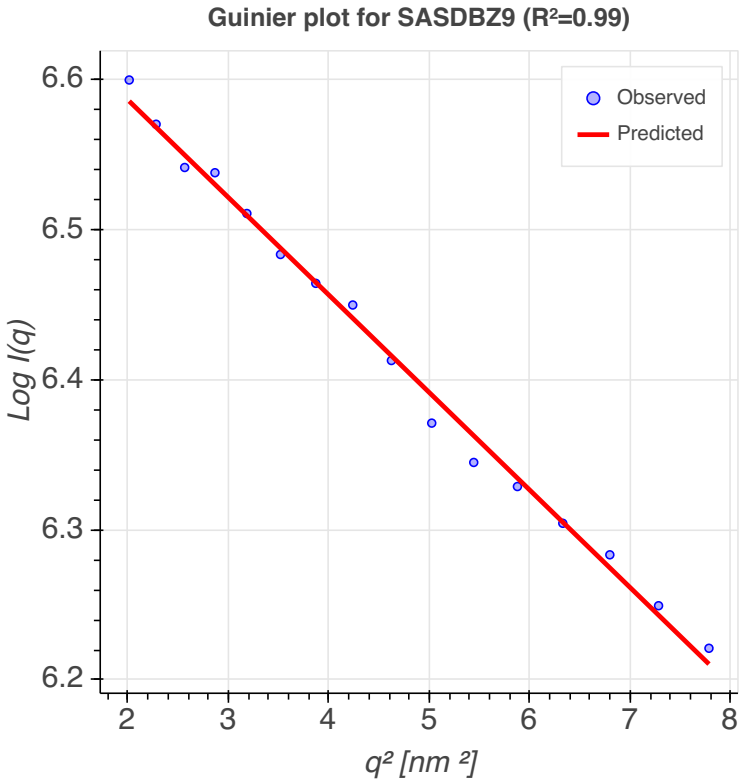


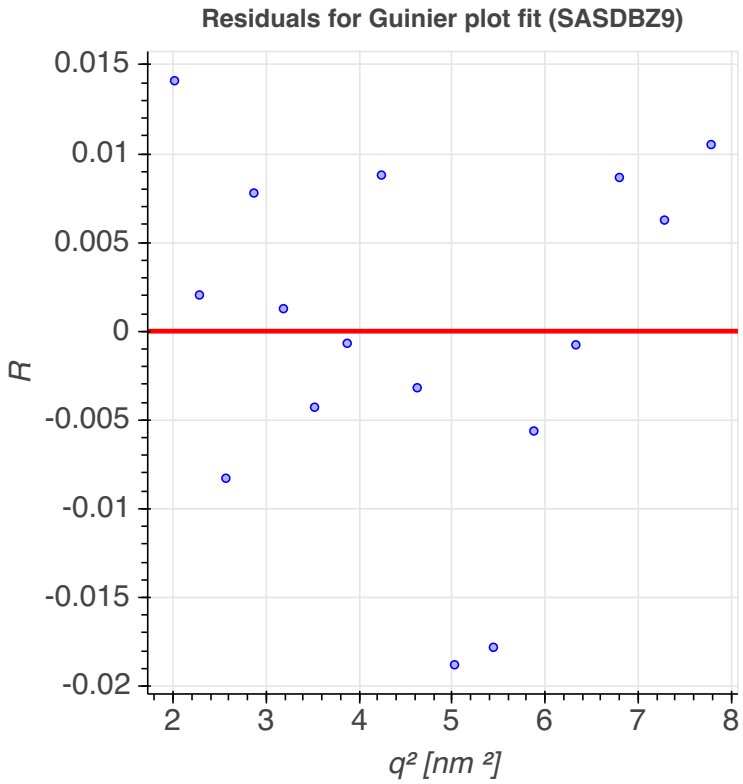
Guinier analysis for SASDBY9: the linearity of the Guinier plot is a sensitive indicator of the quality of the experimental SAS data; a linear Guinier plot is a necessary but not sufficient demonstration that a solution contains monodisperse particles of the samesize. Deviations from linearity usually point to strong interference effects, polydispersity of the samples or improper background subtraction. Residual value plot and coefficient of determination (R^2) are measures to assess linear fit to the data. A perfect fit has an R^2 value of 1. Residual values should be equally and randomly spaced around the horizontal axis.





Guinier analysis for SASDBZ9: the linearity of the Guinier plot is a sensitive indicator of the quality of the experimental SAS data; a linear Guinier plot is a necessary but not sufficient demonstration that a solution contains monodisperse particles of the samesize. Deviations from linearity usually point to strong interference effects, polydispersity of the samples or improper background subtraction. Residual value plot and coefficient of determination (R^2) are measures to assess linear fit to the data. A perfect fit has an R^2 value of 1. Residual values should be equally and randomly spaced around the horizontal axis.





Model quality

Excluded volume satisfaction

Excluded volume satisfaction for the models in the entry are listed below.

Models	Excluded Volume Satisfaction	Number of violations
1	99.46	2089.0

Fit of model to data used for modeling

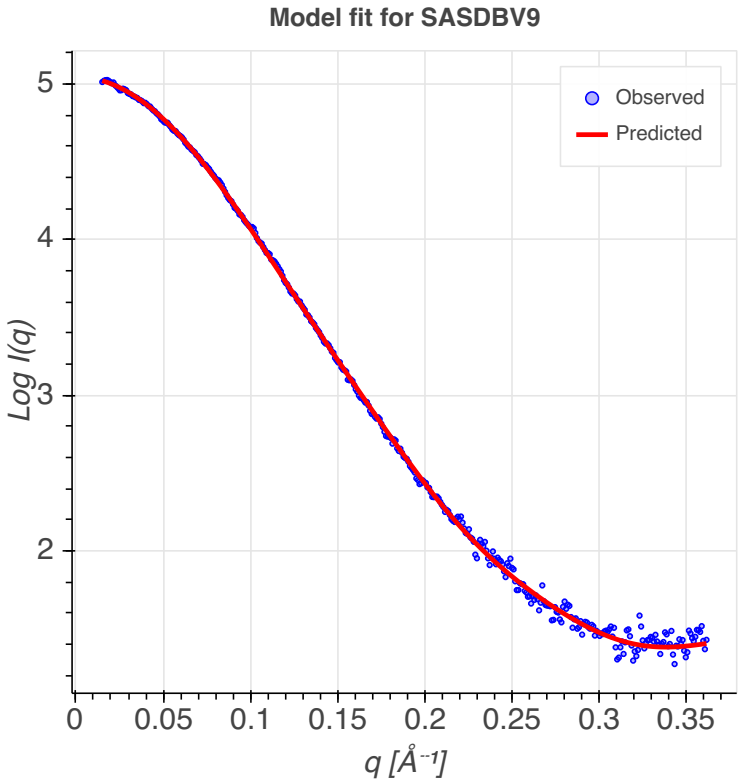
Fit of model(s) to SAS data

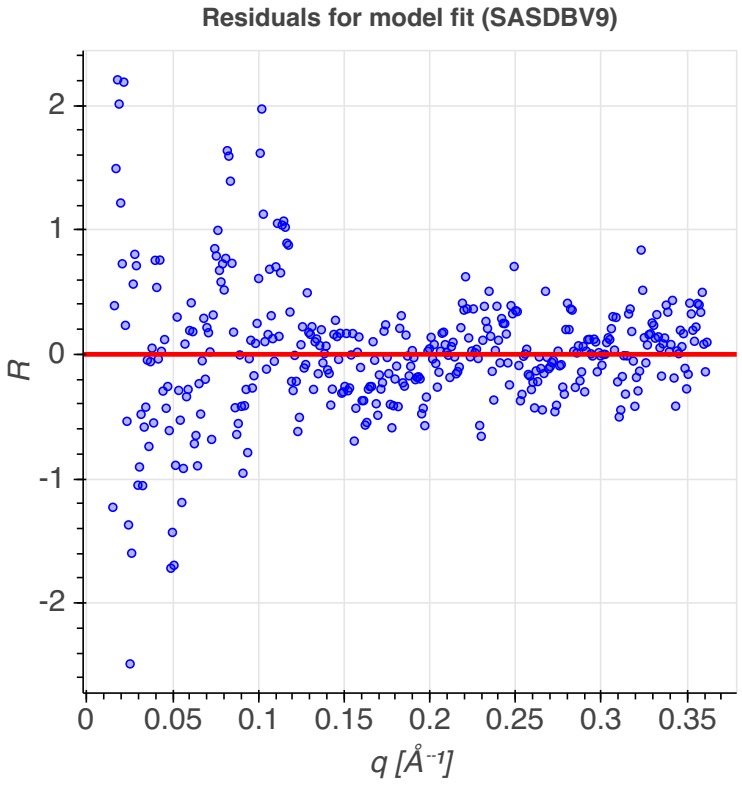
χ^2 goodness of fit analysis

Model and fits displayed below were obtained from SASBDB. χ^2 values are a measure of fit of the model to data. A perfect fit has a χ^2 value of zero.

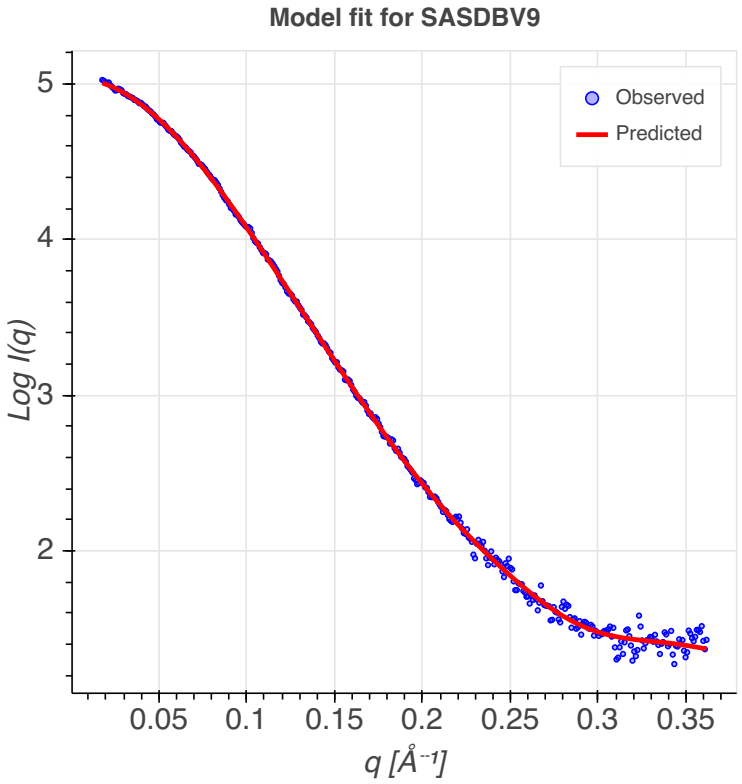
SASDB ID	Model	χ^2
SASDBV9	1	1.13
SASDBV9	2	1.1
SASDBW9	1	1.97
SASDBX9	1	2.86
SASDBY9	1	2.02
SASDBZ9	1	1.94

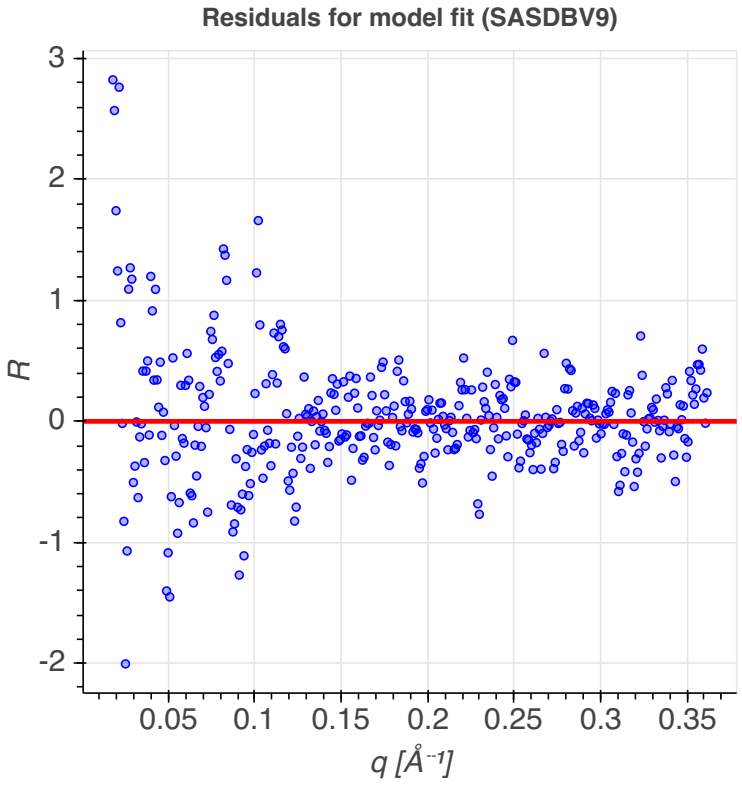
Model fit for SASDBV9 (fit/model number 1): Residual value plot is a measure to assess fit to the data. sResidual values should be equally and randomly spaced around the horizontal axis.



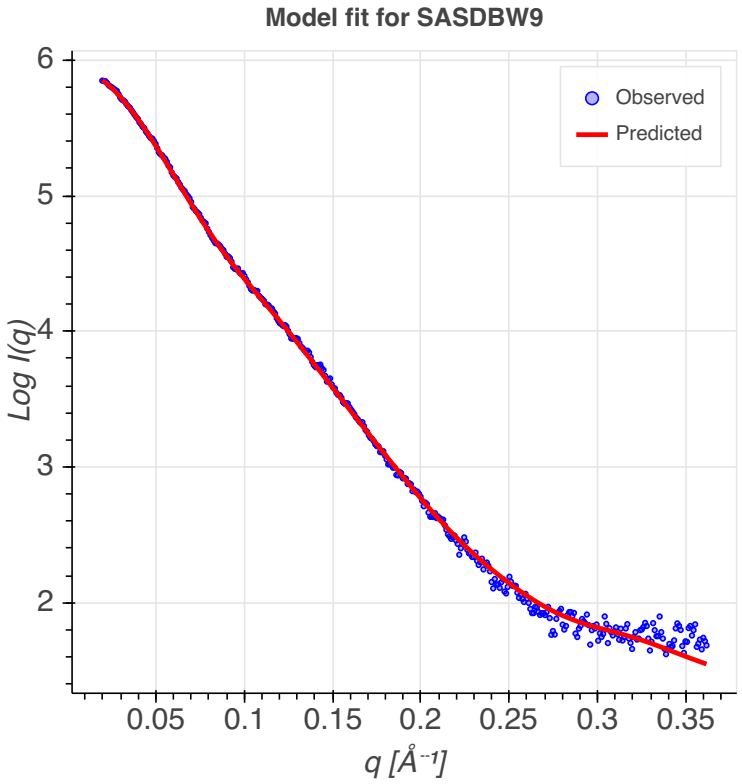


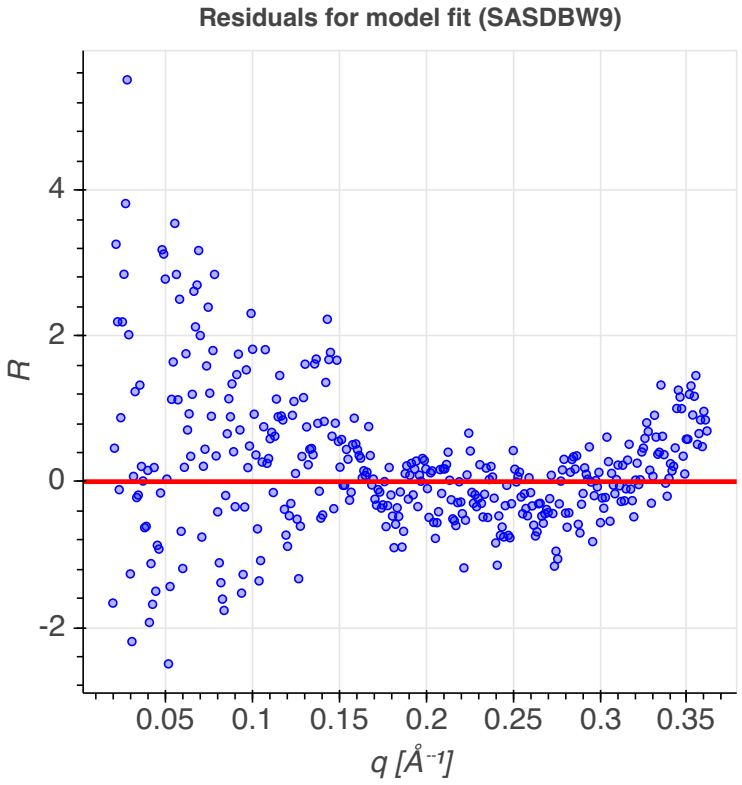
Model fit for SASDBV9 (fit/model number 2): Residual value plot is a measure to assess fit to the data. sResidual values should be equally and randomly spaced around the horizontal axis.



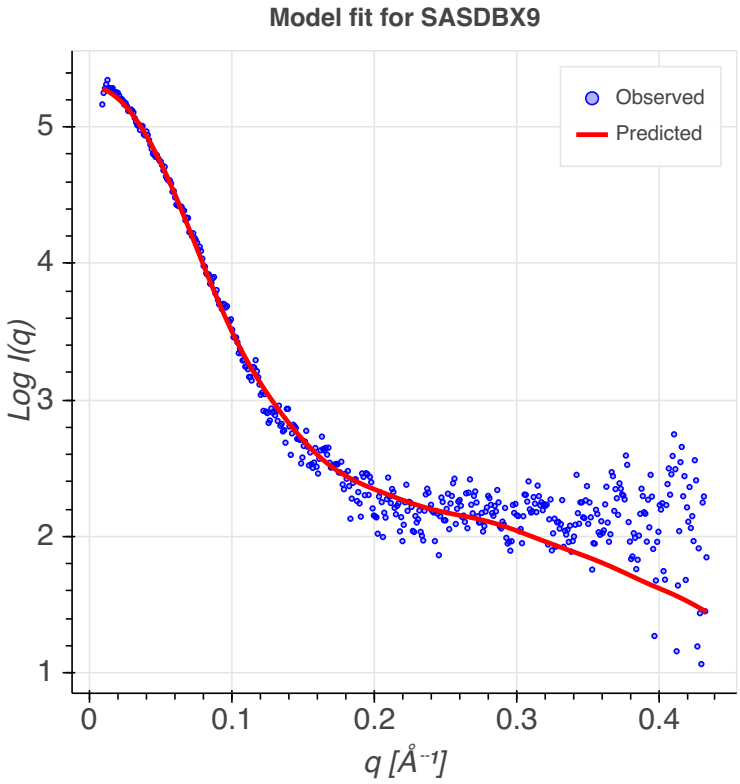


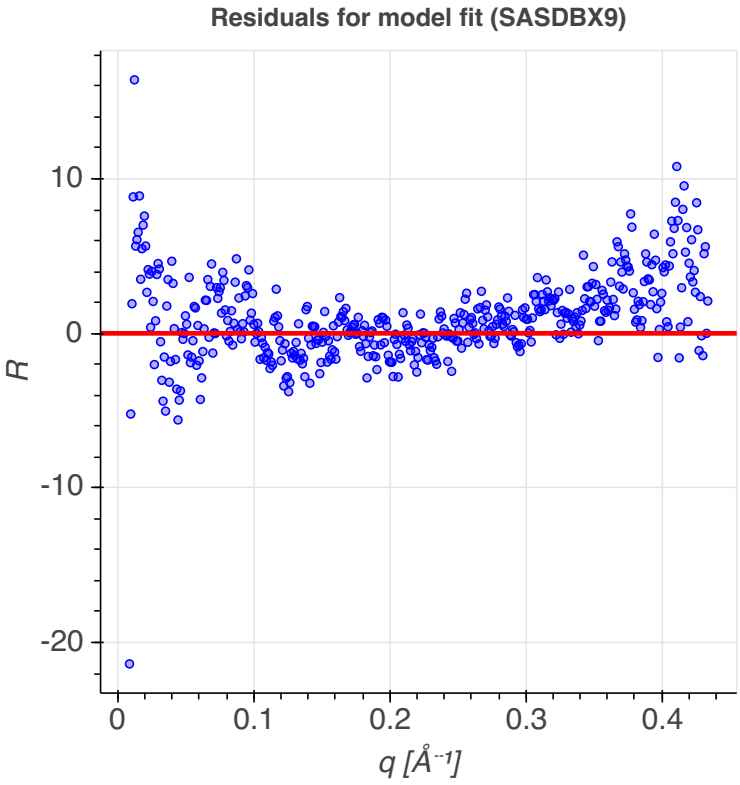
Model fit for SASDBW9 (fit/model number 1): Residual value plot is a measure to assess fit to the data. sResidual values should be equally and randomly spaced around the horizontal axis.



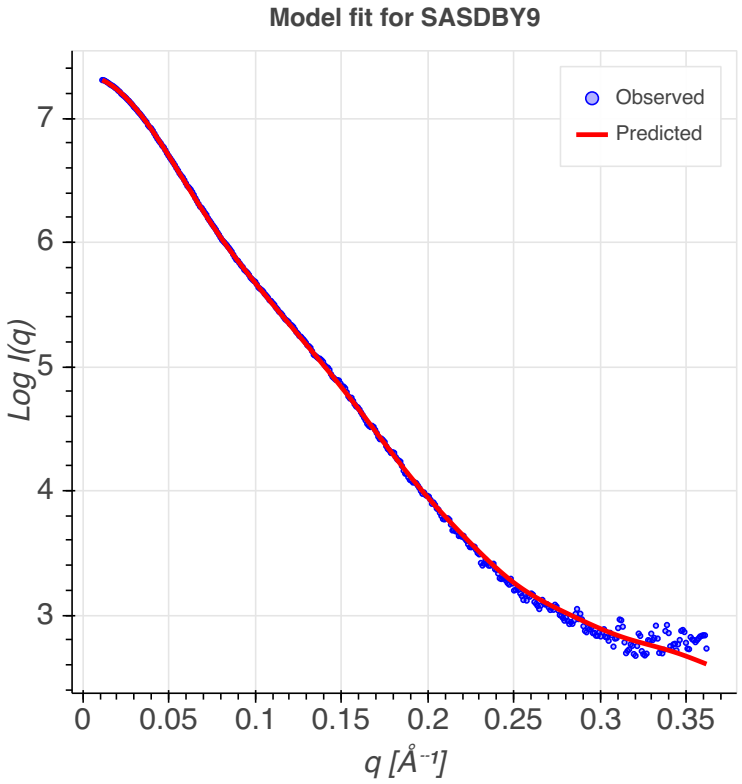


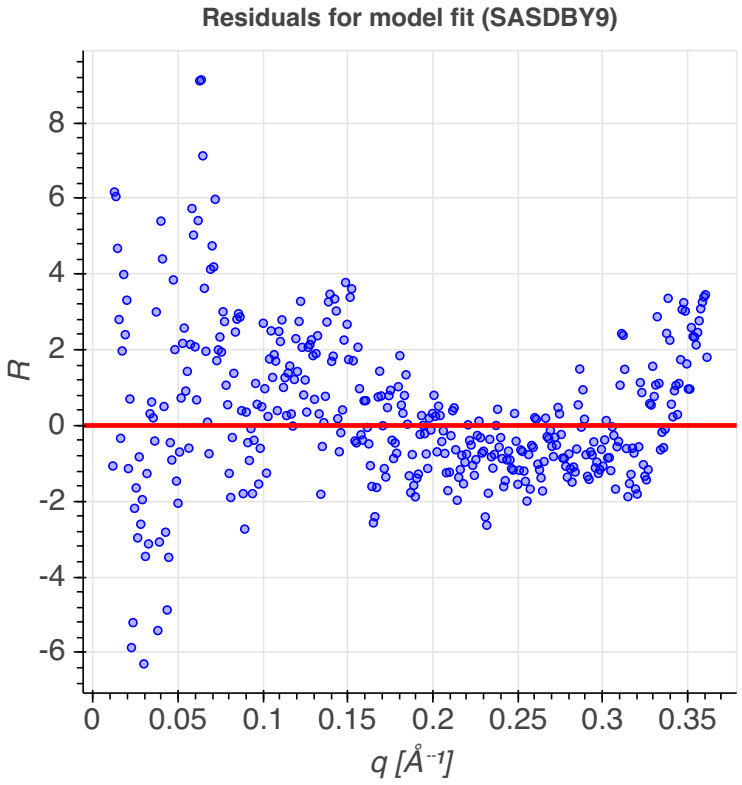
Model fit for SASDBX9 (fit/model number 1): Residual value plot is a measure to assess fit to the data. sResidual values should be equally and randomly spaced around the horizontal axis.



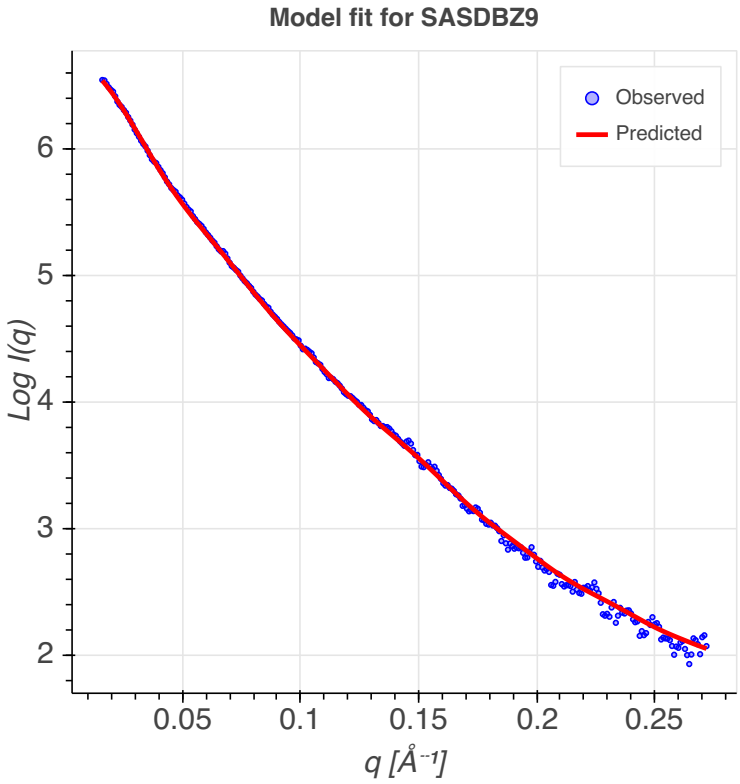


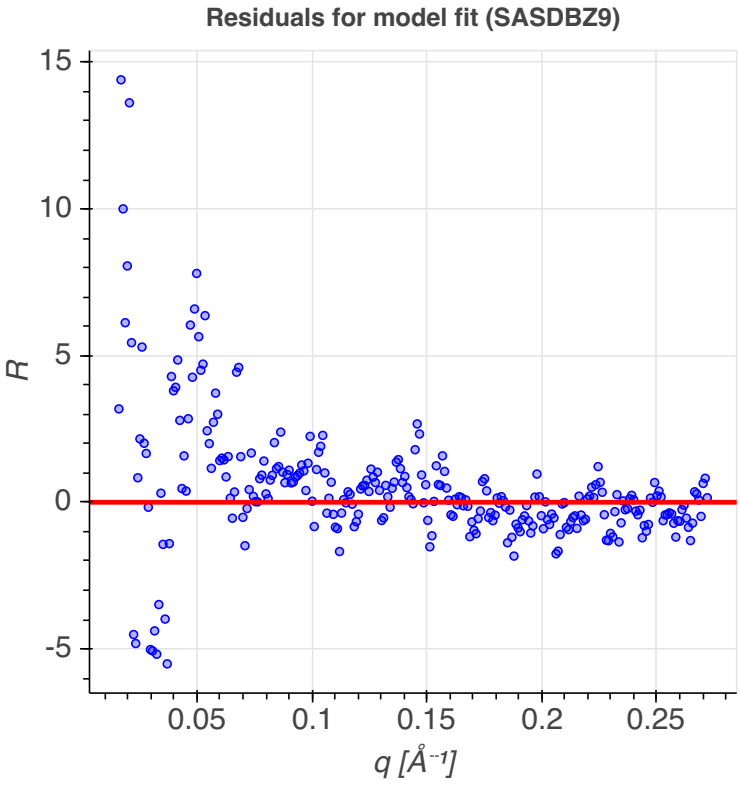
Model fit for SASDBY9 (fit/model number 1): Residual value plot is a measure to assess fit to the data. sResidual values should be equally and randomly spaced around the horizontal axis.





Model fit for SASDBZ9 (fit/model number 1): Residual value plot is a measure to assess fit to the data. sResidual values should be equally and randomly spaced around the horizontal axis.


Model fit for SASDBZ9
Observed
Predicted
Log I(q)
q [Å⁻¹]


Residuals for model fit (SASDBZ9)
R
q [Å⁻¹]

Fit of model to data not used for modeling

Uncertainty of data and model