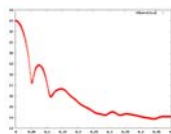




Fast SAXS Profile Computation with Debye Formula



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PDB files

aa.zip

Profile file

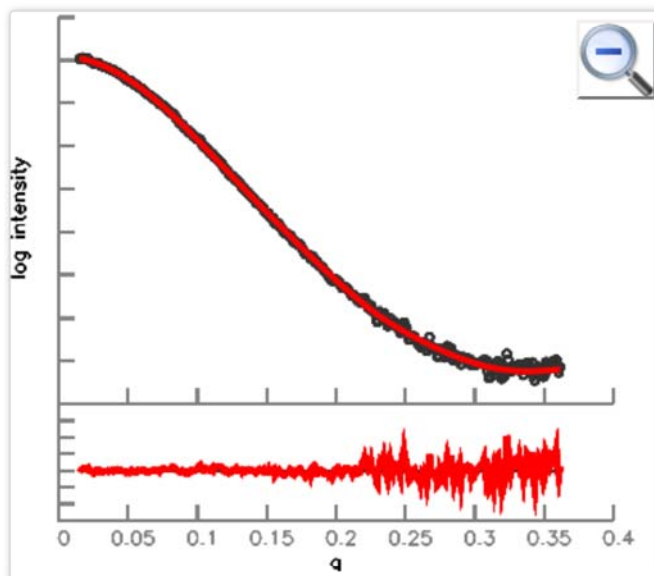
SAXS_26993_merged.dat

-

[Multi-state models by MultiFoXS](#)

[Minimal Ensemble Search \(MES\) \(about MES\)](#)

Can't see interactive display? Use [old interface](#)



JSmol

PDB file	<input type="checkbox"/> show all/hide all	X	C ₁	C ₂	R _g	# atoms	fit file
26993.B99990021	<input checked="" type="checkbox"/>	1.13	1.05	-0.37	16.17	874	26993.B99990021_SAXS_26993_merged.dat
26993.B99990050	<input type="checkbox"/>	1.25	1.04	-0.75	16.17	874	26993.B99990050_SAXS_26993_merged.dat
26993.B99990018	<input type="checkbox"/>	1.28	1.05	-0.16	15.67	874	26993.B99990018_SAXS_26993_merged.dat
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26993.B99990013	<input type="checkbox"/>	1.42	1.04	-0.44	15.67	874	26993.B99990013_SAXS_26993_merged.dat
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26993.B99990076	<input type="checkbox"/>	1.51	1.05	-0.29	15.33	874	26993.B99990076_SAXS_26993_merged.dat

26993.B99990087	<input type="checkbox"/>	1.52	1.05	-0.15	15.50	874	26993.B99990087 SAXS 26993_merged.dat
26993.B99990048	<input type="checkbox"/>	1.57	1.05	-0.45	15.19	874	26993.B99990048 SAXS 26993_merged.dat
26993.B99990079	<input type="checkbox"/>	1.59	1.05	-0.56	15.45	874	26993.B99990079 SAXS 26993_merged.dat
26993.B99990056	<input type="checkbox"/>	1.61	1.05	0.10	15.69	874	26993.B99990056 SAXS 26993_merged.dat
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26993.B99990098	<input type="checkbox"/>	1.62	1.05	-0.18	15.61	874	26993.B99990098 SAXS 26993_merged.dat
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26993.B99990064		1.63	1.05	0.18	15.54	874	26993.B99990064 SAXS 26993_merged.dat
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26993.B99990083		1.76	1.05	-0.03	15.64	874	26993.B99990083 SAXS 26993_merged.dat
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26993.B99990052		1.98	1.05	0.40	15.29	874	26993.B99990052 SAXS 26993_merged.dat
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26993.B99990047	3.07	1.04	-0.44	14.86	874	26993.B99990047_SAXS_26993_merged.dat
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26993.B99990035	3.55	1.05	-0.11	14.39	874	26993.B99990035_SAXS_26993_merged.dat
26993.B99990014	4.83	1.05	-0.56	14.21	874	26993.B99990014_SAXS_26993_merged.dat

If you use FoXS, please cite:

D. Schneidman-Duhovny, M. Hammel, JA. Tainer, and A. Sali. Accurate SAXS profile computation and its assessment by contrast variation experiments. Biophysical Journal 2013.

D. Schneidman-Duhovny, M. Hammel, and A. Sali. FoXS: A Web server for Rapid Computation and Fitting of SAXS Profiles. NAR 2010.38 Suppl:W540-4

Contact: