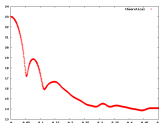




Fast SAXS Profile Computation with Debye Formula



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PDB files

[26996.zip](#)

Profile file

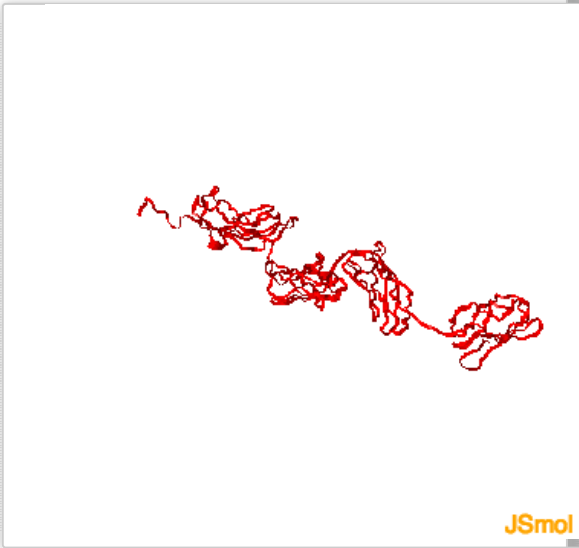
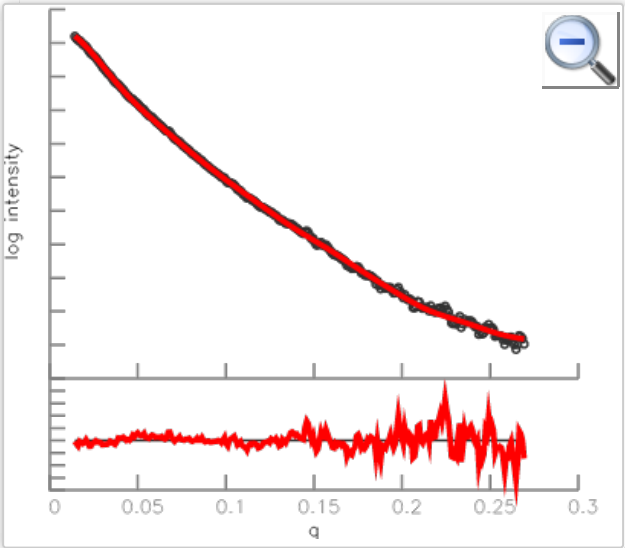
[SAXS_26996_merged_q27.dat](#)

-

[Multi-state models by MultiFoXS](#) [Minimal Ensemble Search \(MES\) \(about MES\)](#)

NEW! [MultiFoXS](#) Now with conformational sampling and multi-state modeling

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



JSmol

PDB file	show all/hide all	X	c ₁	c ₂	R _g	# atoms	fit file
26996.B99990086	<input checked="" type="checkbox"/>	1.48	1.05	-0.30	46.57	3461	26996.B99990086 SAXS 26996_merged_q27.dat
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26996.B99990020	2.44	1.05	0.06	47.72	3461	26996.B99990020 SAXS 26996 merged q27.dat
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26996.B99990088	3.25	1.05	0.22	48.11	3461	26996.B99990088 SAXS 26996 merged q27.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: