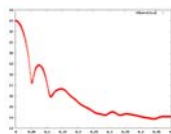




Fast SAXS Profile Computation with Debye Formula



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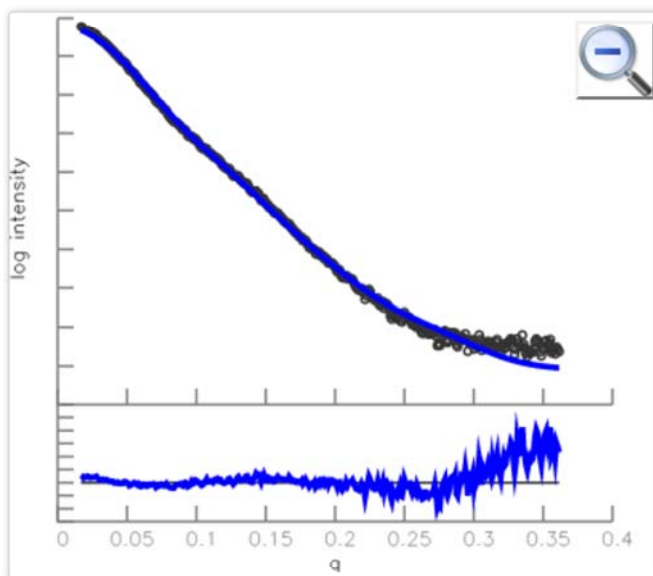
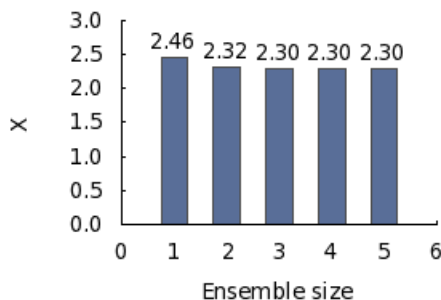
PDB files

26994.zip

Profile file

[SAXS_26994_merged.dat](#)

MES (Minimal Ensemble Search) Fit



Jmol_S

Ensemble size	<input type="checkbox"/> show all/hide all	X	models and weights		fit file
1	<input type="checkbox"/>	2.46	26994.B99990039.pdb	1.00	26994.B99990039_SAXS_26994_merged.dat
2	<input checked="" type="checkbox"/>	2.32	26994.B99990031.pdb	0.41	avg_2
			26994.B99990039.pdb	0.59	
3	<input type="checkbox"/>	2.30	26994.B99990088.pdb	0.22	avg_3
			26994.B99990034.pdb	0.22	
			26994.B99990039.pdb	0.56	
4	<input type="checkbox"/>	2.30	26994.B99990034.pdb	0.15	avg_4
			26994.B99990039.pdb	0.53	
			26994.B99990031.pdb	0.14	
			26994.B99990088.pdb	0.18	
5	<input type="checkbox"/>	2.30	26994.B99990088.pdb	0.18	avg_5
			26994.B99990031.pdb	0.14	

26994.B99990008.pdb	0.00
26994.B99990039.pdb	0.53
26994.B99990034.pdb	0.15

If you use [MES](#), please cite:

Pelikan M, Hura GL, Hammel M. Structure and Flexibility within proteins as identified through small angle X-ray scattering. General Physiology and Biophysics. 2009;28:174 - 89.