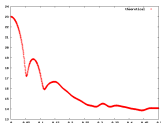




Fast SAXS Profile Computation with Debye Formula



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PDB files

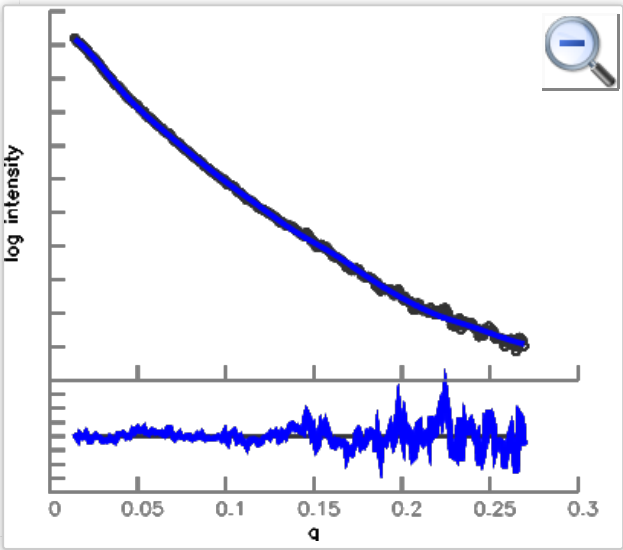
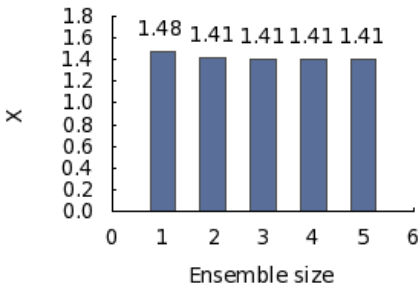
[26996.zip](#)

Profile file

[SAXS_26996_merged_q27.dat](#)

-

MES (Minimal Ensemble Search) Fit



Ensemble size	<input type="checkbox"/> show all/hide all	X	models and weights		fit file
1	<input type="checkbox"/>	1.48	26996.B99990086.pdb	1.00	26996.B99990086 SAXS 26996_merged_q27.dat
2	<input checked="" type="checkbox"/>	1.41	26996.B99990012.pdb	0.44	avg_2
			26996.B99990060.pdb	0.56	
3	<input type="checkbox"/>	1.41	26996.B99990093.pdb	0.14	avg_3
			26996.B99990060.pdb	0.63	
			26996.B99990012.pdb	0.23	
4	<input type="checkbox"/>	1.41	26996.B99990012.pdb	0.24	avg_4
			26996.B99990075.pdb	0.08	
			26996.B99990060.pdb	0.61	
			26996.B99990093.pdb	0.07	
5	<input type="checkbox"/>	1.41	26996.B99990093.pdb	0.07	avg_5
			26996.B99990060.pdb	0.61	

26996.B99990075.pdb	0.08
26996.B99990049.pdb	0.00
26996.B99990012.pdb	0.24

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.