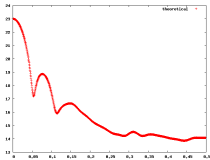




Fast SAXS Profile Computation with Debye Formula



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PDB files

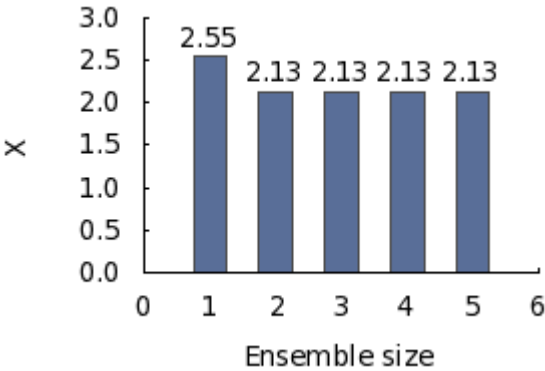
[27005.zip](#)

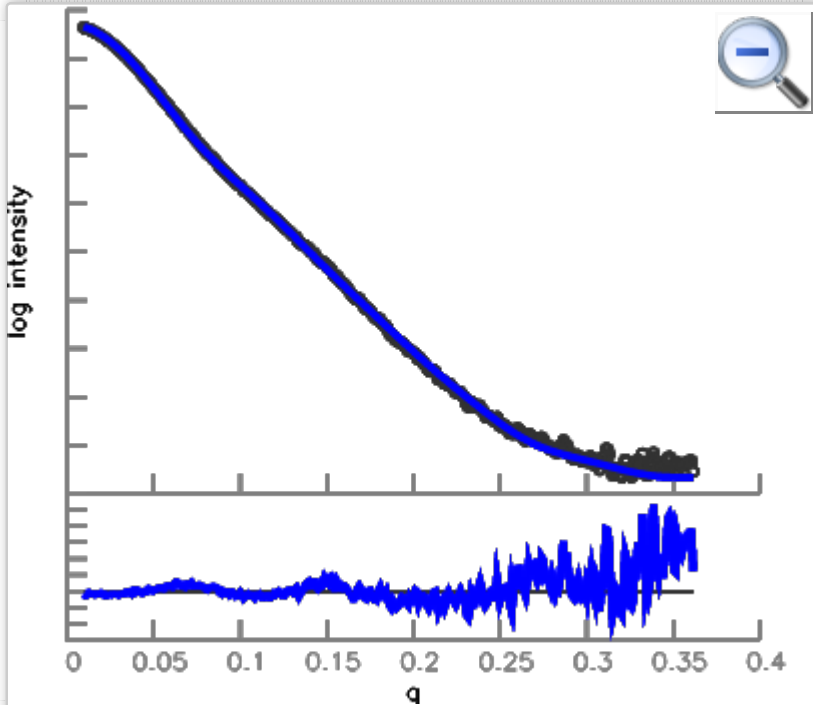
Profile file

[27005_merged.dat](#)

-

MES (Minimal Ensemble Search) Fit





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Ensemble size	<input type="checkbox"/> show all/hide all	X	models and weights		fit file
1	<input type="checkbox"/>	2.55	27005.B99990059.pdb	1.00	27005.B99990059 27005_merged.dat
2	<input checked="" type="checkbox"/>	2.13	27005.B99990060.pdb	0.42	avg_2
			27005.B99990059.pdb	0.58	
3	<input type="checkbox"/>	2.13	27005.B99990060.pdb	0.40	avg_3
			27005.B99990059.pdb	0.59	
			27005.B99990032.pdb	0.01	
4	<input type="checkbox"/>	2.13	27005.B99990059.pdb	0.59	avg_4
			27005.B99990017.pdb	0.00	
			27005.B99990032.pdb	0.01	
			27005.B99990060.pdb	0.40	
5	<input type="checkbox"/>	2.13	27005.B99990060.pdb	0.40	avg_5

27005.B99990017.pdb	0.00
27005.B99990021.pdb	0.00
27005.B99990032.pdb	0.01
27005.B99990059.pdb	0.59

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.