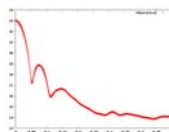




## Fast SAXS Profile Computation with Debye Formula



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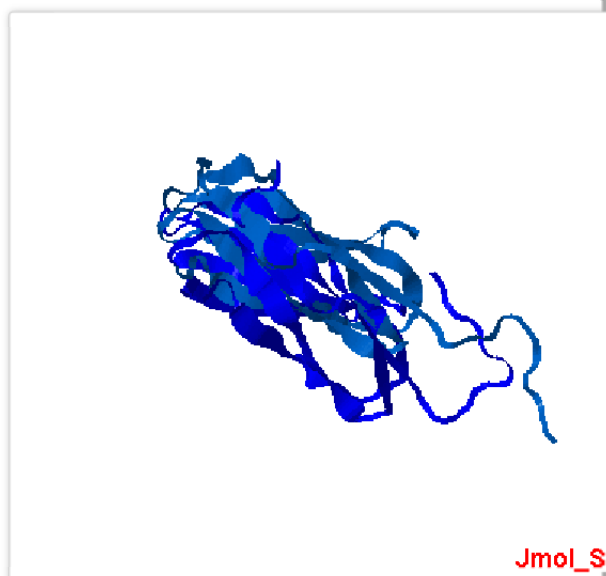
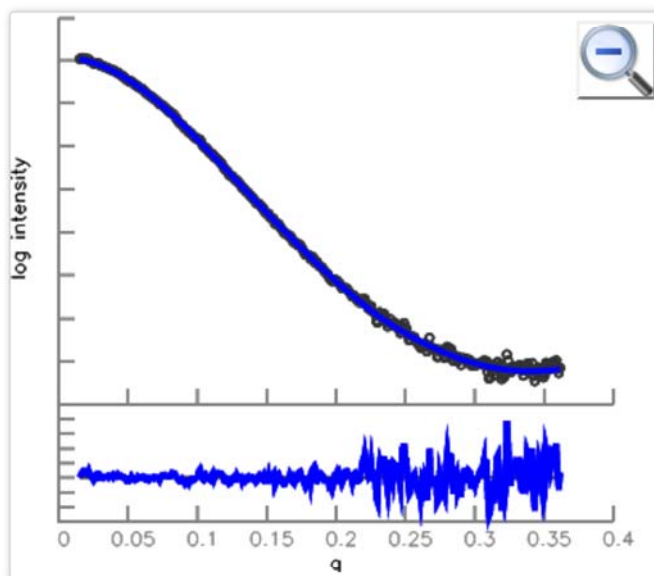
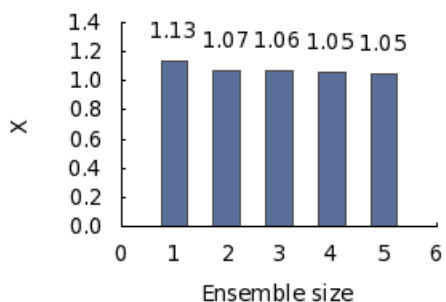
PDB files

aa.zip

Profile file

[SAXS\\_26993\\_merged.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"/>	1.13	26993.B99990021.pdb	1.00	<a href="#">26993.B99990021_SAXS_26993_merged.dat</a>
2	<input checked="" type="checkbox"/>	1.07	26993.B99990048.pdb	0.53	<a href="#">avg_2</a>
			26993.B99990091.pdb	0.47	
3	<input type="checkbox"/>	1.06	26993.B99990024.pdb	0.33	<a href="#">avg_3</a>
			26993.B99990021.pdb	0.43	
			26993.B99990091.pdb	0.24	
4	<input type="checkbox"/>	1.05	26993.B99990014.pdb	0.03	<a href="#">avg_4</a>
			26993.B99990091.pdb	0.49	
			26993.B99990085.pdb	0.13	
			26993.B99990008.pdb	0.34	
5	<input type="checkbox"/>	1.05	26993.B99990091.pdb	0.50	<a href="#">avg_5</a>
			26993.B99990023.pdb	0.18	

26993.B99990039.pdb	0.05
26993.B99990035.pdb	0.04
26993.B99990079.pdb	0.23

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**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.