



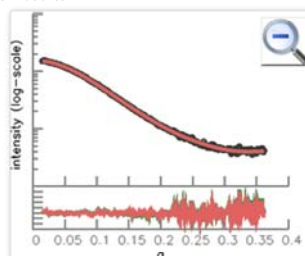
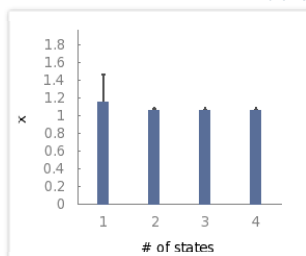
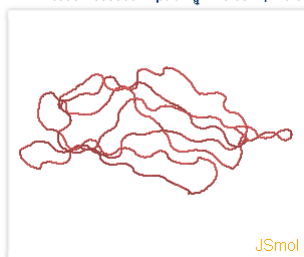
Fast SAXS Profile Computation with Debye Formula


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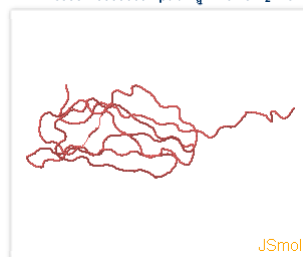
 PDB files
aa.zip

 Profile file
SAXS_26993_merged.dat

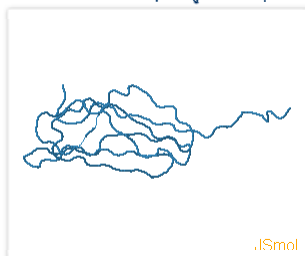
MultiFoXS Results


 Best scoring 2-state model $\chi = 1.05$ $c_1 = 1.05$ $c_2 = -0.22$ ☒ show/hide weighted profile
PDB1: 26993.B99990022.pdb $R_q = 15.08$ $w_1 = 0.529$ PDB2: 26993.B99990091.pdb $R_q = 16.75$ $w_2 = 0.471$ 

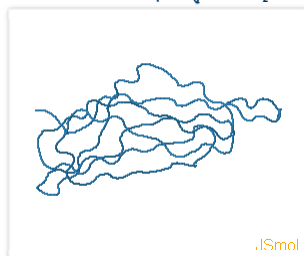
JSmol



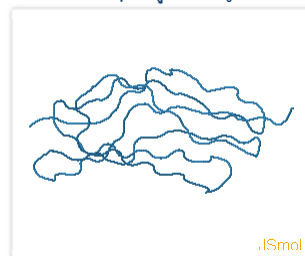
JSmol

 Best scoring 3-state model $\chi = 1.05$ $c_1 = 1.05$ $c_2 = -0.17$ ☐ show/hide weighted profile
PDB1: 26993.B99990091.pdb $R_q = 16.75$ $w_1 = 0.441$ PDB2: 26993.B99990038.pdb $R_q = 15.25$ $w_2 = 0.304$ PDB3: NMR.pdb $R_q = 14.12$ $w_3 = 0.255$ 

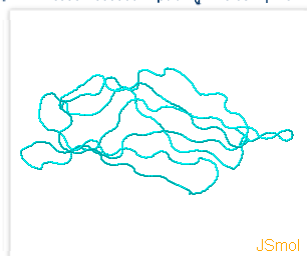
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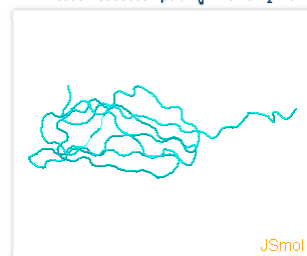
JSmol



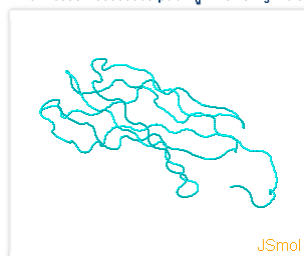
JSmol

 Best scoring 4-state model $\chi = 1.05$ $c_1 = 1.05$ $c_2 = -0.49$ ☐ show/hide weighted profile
PDB1: 26993.B99990022.pdb $R_q = 15.08$ $w_1 = 0.119$ PDB2: 26993.B99990091.pdb $R_q = 16.75$ $w_2 = 0.475$ PDB3: 26993.B99990008.pdb $R_q = 15.49$ $w_3 = 0.333$ PDB4: 26993.B99990035.pdb $R_q = 14.39$ $w_4 = 0.07$ 

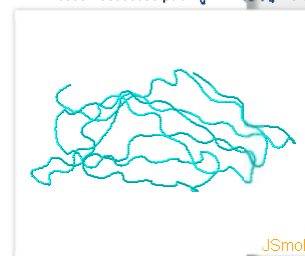
JSmol



JSmol



JSmol



JSmol

If you use FoXS, please cite:

D. Schneidman-Duhovny, M. Hammel, J.A. 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

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