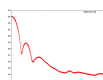




Fast SAXS Profile Computation with Debye Formula

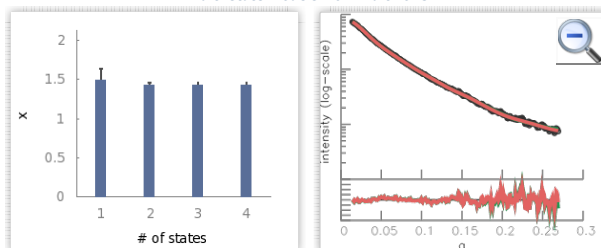


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PDB files  
26996.zip

Profile file  
SAXS\_26996\_merged\_q27.dat

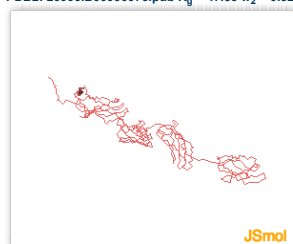
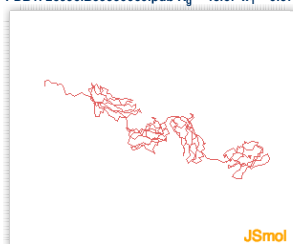
**NEW! MultiFoXS** Now with conformational sampling and multi-state modeling, try here  
Multi-state models from MultiFoXS



Best scoring 2-state model  $\chi = 1.42$   $c_1 = 1.05$   $c_2 = -0.28$  [show/hide weighted profile](#)

PDB1: 26996.B99990060.pdb  $R_g = 45.67$   $w_1 = 0.677$

PDB2: 26996.B99990075.pdb  $R_g = 47.85$   $w_2 = 0.323$

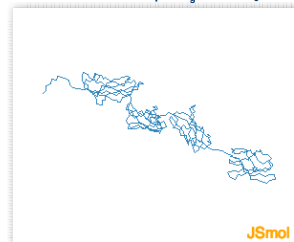
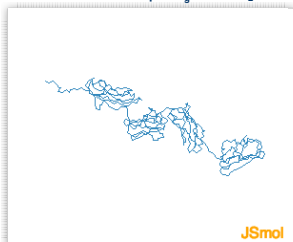
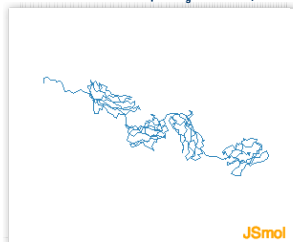


Best scoring 3-state model  $\chi = 1.41$   $c_1 = 1.05$   $c_2 = -0.18$  [show/hide weighted profile](#)

PDB1: 26996.B99990060.pdb  $R_g = 45.67$   $w_1 = 0.492$

PDB2: 26996.B99990066.pdb  $R_g = 45.91$   $w_2 = 0.273$

PDB3: 26996.B99990093.pdb  $R_g = 46.73$   $w_3 = 0.235$



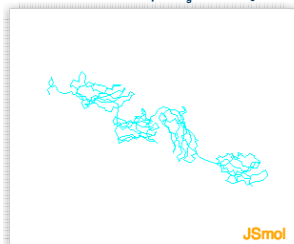
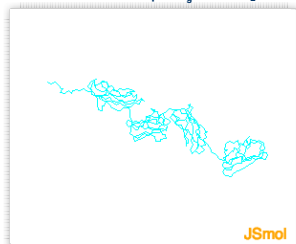
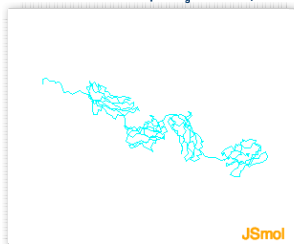
Best scoring 4-state model  $\chi = 1.41$   $c_1 = 1.05$   $c_2 = -0.25$  [show/hide weighted profile](#)

PDB1: 26996.B99990060.pdb  $R_g = 45.67$   $w_1 = 0.375$

PDB2: 26996.B99990066.pdb  $R_g = 45.91$   $w_2 = 0.210$

PDB3: 26996.B99990091.pdb  $R_g = 45.29$   $w_3 = 0.130$

PDB4: 26996.B99990075.pdb  $R_g = 47.85$   $w_4 = 0.284$



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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