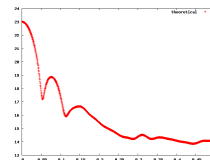




## Fast SAXS Profile Computation with Debye Formula



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PDB files

[27005.zip](#)

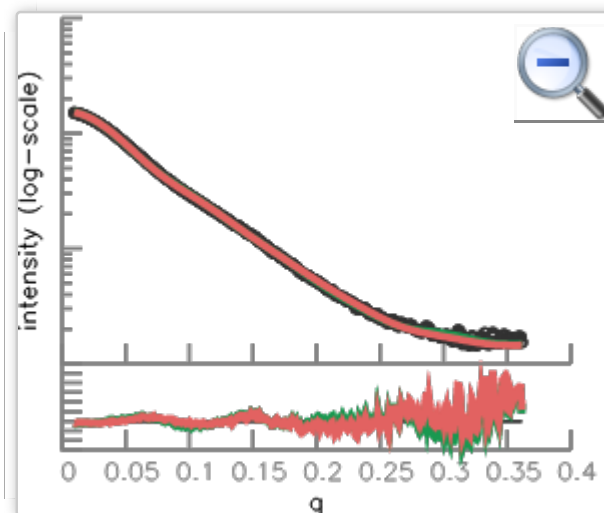
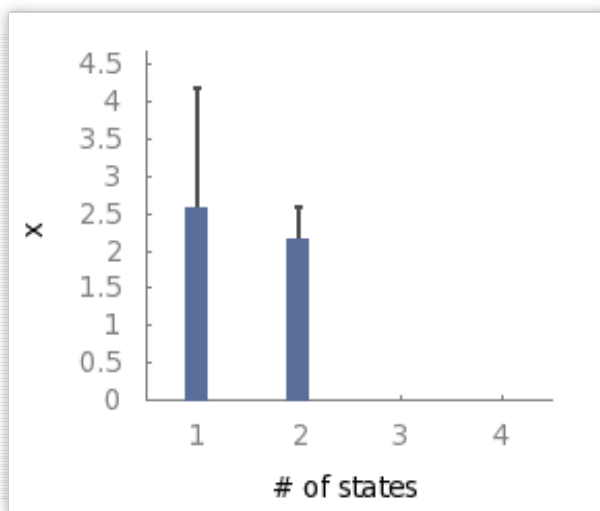
Profile file

[27005\\_merged.dat](#)

-

**NEW! MultiFoXS** [Now with conformational sampling and multi-state modeling, try here](#)

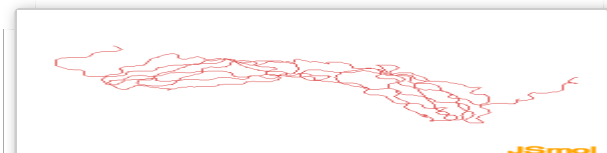
### Multi-state models from MultiFoXS

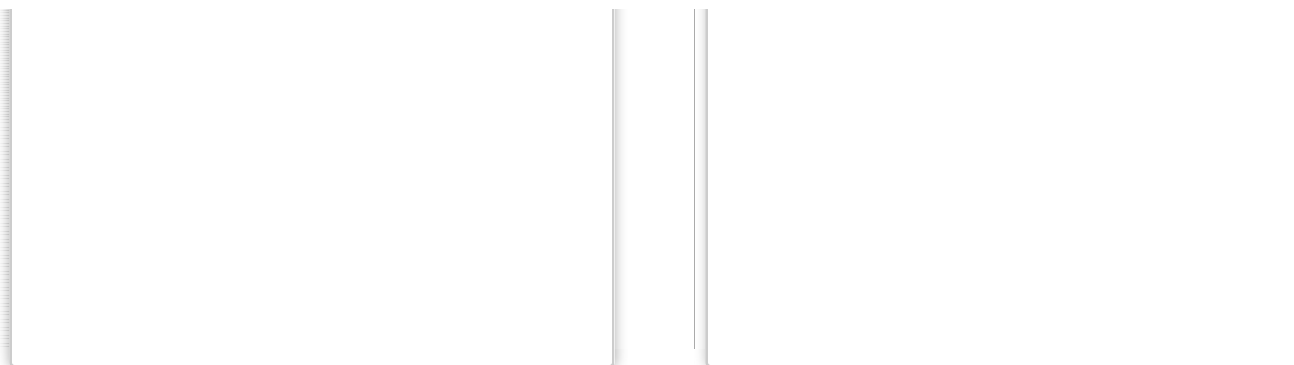


Best scoring 2-state model  $\chi = 2.14$   $c_1 = 1.04$   $c_2 = 0.51$  ☒ [show/hide weighted profile](#)

PDB1: 27005.B99990059.pdb  $R_g = 28.92$   $w_1 = 0.584$

PDB2: 27005.B99990060.pdb  $R_g = 27.91$   $w_2 = 0.416$





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**If you use FoXS, please cite:**

D. Schneidman-Duhovny, M. Hammel, JA. 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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