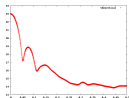




Fast SAXS Profile Computation with Debye Formula



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PDB files

Profile file

[Nup82_7_452.zip](#)

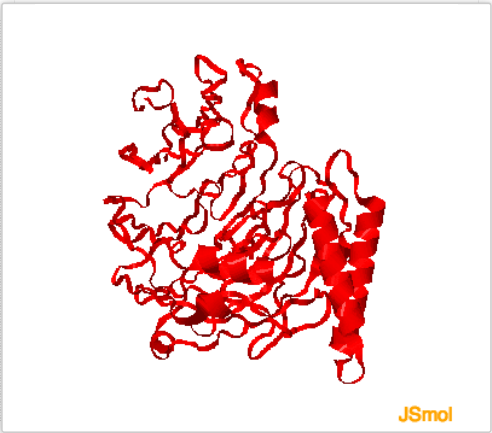
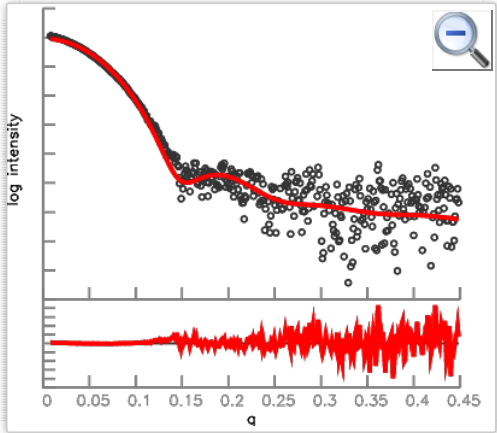
[25005_02D_S022_0_01.sub](#)

-

[Multi-state models by MultiFoXS](#) [Minimal Ensemble Search \(MES\) \(about MES\)](#)

NEW! **MultiFoXS** Now with conformational sampling and multi-state modeling

Can't see interactive display? Use [old interface](#)



PDB file	<input type="checkbox"/> show all / hide all	X	c ₁	c ₂	R _g	# atoms	fit file	png file
Nup82_7_452_D	<input checked="" type="checkbox"/>	2.55	1.00	4.00	22.31	3538	Nup82_7_452_D_25005_02D_S022_0_01.dat	Nup82_7_452_D_25005_02D_S022_0_01.png
Nup82_7_452_C	<input type="checkbox"/>	2.56	1.00	4.00	22.31	3538	Nup82_7_452_C_25005_02D_S022_0_01.dat	Nup82_7_452_C_25005_02D_S022_0_01.png

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
Contact: dina@salilab.org