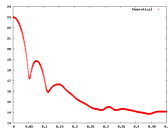




Fast SAXS Profile Computation with Debye Formula



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PDB files

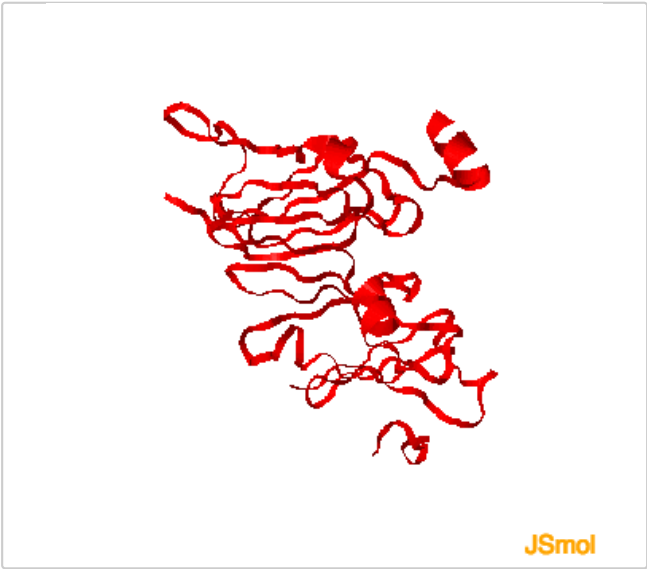
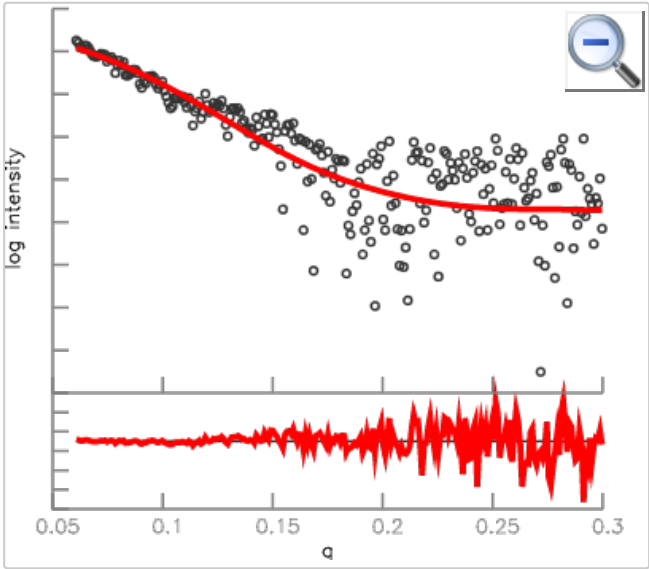
[Nup82_4_229_C.pdb](#)

Profile file

[24367_01B_S008_0_01.sub](#)

-

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



PDB file	show/hide	χ	c_1	c_2	R_g	# atoms	fit file	png file
Nup82_4_229_C	<input checked="" type="checkbox"/>	1.49	1.03	0.16	19.18	1743	Nup82_4_229_C_24367_01B_S008_0_01.dat	Nup82_4_229_C_24367_01B_S008_0_01.png

If you use FoXS, please cite:

Schneidman-Duhovny D, Hammel M, Tainer JA, and Sali A. Accurate SAXS profile computation and its assessment by contrast variation experiments. Biophysical Journal 2013. 105 (4), 962-974

Schneidman-Duhovny D, Hammel M, Tainer JA, and Sali A. FoXS, FoXSDock and MultiFoXS: Single-state and multi-state structural modeling of proteins and their complexes based on SAXS profiles NAR 2016 [[FREE Full Text](#)]

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