

Supporting Information

Homogeneous and Heterogeneous Dynamics in Native and Denatured Bovine Serum Albumin

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Table S1: Dynamic parameters of native BSA obtained from fits based on stretched exponential functions for the description of internal dynamics. The values of R correspond to the measured Guinier radius by SAXS*, the effective hydrodynamic radius determined from SAXS#, and the hydrodynamic radius determined by DLS\$ given in the literature¹. $R = 39 \text{ \AA}$ is the average value as determined from fits to the QENS data sets.

	R	30.2 \AA^*	$36.2 \text{ \AA}^{\#}$	$36.6 \text{ \AA}^{\$}$	$39 \text{ \AA}^{\$}$
TOFTOF	β	$0.41 +/- 0.03$	0.46 ± 0.03	0.42 ± 0.03	$0.45 +/- 0.03$
	$D_{\text{int}}(\text{\AA}^2/\text{ns})$	$13.9 +/- 2.5$	33.7 ± 3.8	30.4 ± 4.5	$47.7 +/- 6.1$
	χ	1.78	1.78	1.80	1.73
SPHERES	β	1	1	1	1
	$D_{\text{int}}(\text{\AA}^2/\text{ns})$	$19.9 +/- 1.0$	$23.6 +/- 1.3$	$23.9 +/- 1.4$	$26.1 +/- 1.6$
	χ	1.61	1.63	1.63	1.65

Table S2: Dynamic parameters of native BSA obtained from fits based on the Brownian oscillator for the description of internal dynamics. Dependence of effective protein radius is reported. The values of R correspond to the measured Guinier radius by SAXS*, the effective hydrodynamic radius determined from SAXS#, and the hydrodynamic radius determined by DLS\$. The R values in the last column are fitted to the QENS data sets. The average value $\langle R \rangle$ determined from the fits equals 39 \AA .

	R	30.2 \AA^*	$36.2 \text{ \AA}^{\#}$	$36.6 \text{ \AA}^{\$}$	39 \AA	$R_{\text{TOFTOF}} = 49.1 +/- 0.4 \text{ \AA}$
TOFTOF	$D_{\text{int}}(\text{\AA}^2/\text{ns})$	$68.5 +/- 1.2$	$83.8 +/- 1.5$	$86.0 +/- 1.6$	$95.8 +/- 1.8$	$140.9 +/- 3.9$
	RMSD (\AA)	$3.04 +/- 0.21$	$3.96 +/- 0.44$	$3.55 +/- 0.32$	$3.86 +/- 0.40$	$16.6 +/- 37.4$
	p	$0.77 +/- 0.01$	$0.80 +/- 0.01$	$0.80 +/- 0.01$	$0.81 +/- 0.01$	$0.85 +/- 0.01$
	χ	1.89	1.89	1.86	1.85	1.84
SPHERES	$D_{\text{int}}(\text{\AA}^2/\text{ns})$	$16.9 +/- 0.8$	$21.3 +/- 1.2$	$21.6 +/- 1.2$	$24.5 +/- 1.5$	$16.50 +/- 1.08$
	RMSD	$3.25 +/-$	$3.22 +/- 0.50$	$3.22 +/- 0.50$	$3.23 +/- 0.53$	$3.26 +/- 0.47$
	p	$0.56 +/- 0.01$	$0.61 +/- 0.01$	$0.62 +/- 0.01$	$0.64 +/- 0.01$	$0.55 +/- 0.02$
	χ	1.64	1.64	1.64	1.65	1.64

1 F. Roosen-Runge, M. Hennig, F. Zhang, R. M. J. Jacobs, M. Sztucki, H. Schober, T. Seydel and F. Schreiber, Protein self-diffusion in crowded solutions., *Proc. Natl. Acad. Sci. U. S. A.*, 2011, **108**, 11815–20.