Supporting information

DMSO-induced denaturation of hen egg white lysozyme

1 Small angle neutron scattering

We demonstrate the effect of subtracting different values for the incoherent background on small angle neutron scattering profiles and the corresponding Kratky representations and pair-distance-distribution functions, $p(r)$ of two samples containing lysozyme in a folded state (30 g l^{-1} at $\varphi_{DMSO} = 0$) and unfolded state (10 g l^{-1} at $\varphi_{DMSO} = 0.8$) in Figures S1, S2, and S3. As 0.011 and 0.0012 cm^{-1} correspond to the incoherent background to be subtracted from the profiles in Figures S1-S3a and S1-S3b, all other values correspond to incorrect background corrections, namely too little (0 cm^{-1}) or too much (0.024, 0.049, 0.0022, and 0.0029 cm^{-1}). It is clear that the Kratky representations are particularly sensitive to the background subtraction and that the $p(r)$ only starts in the origin (0,0) when too much background is subtracted. The latter is due to the fact that lysozyme is not a homogeneous particle at length scales corresponding to the highest q values probed; i.e., the Porod regime (q^{-4} decay) lies outside of the accessible q-range. This leads to a lack of information at very small values of r in the p(r) function. However, the values for R_g and $I(0)$ tabulated in in the main document (Table 1) are only marginally affected. By contrast, it is clear from Figure S1 that the effect of background subtraction on S_0 is more pronounced. In Table 1 we have listed the mean values and corresponding standard deviations as determined for three different background subtractions (no subtraction, correct subtraction, and slight over subtraction, see for example the 0, 0.011, and 0.024

scattering profiles in Figure S1a).

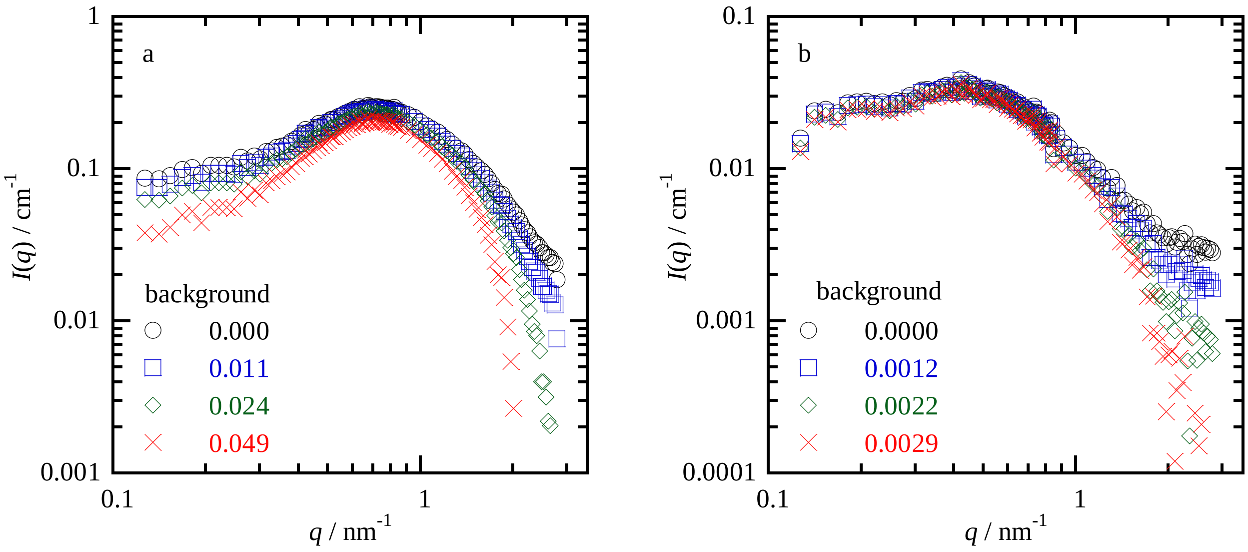

Figure S1. Small angle neutron scattering profiles, $I(q)$ versus q, for a (a) 30 g l^{-1} lysozyme solution at φ_{DMSO} = 0 and a (b) 10 g l^{-1} lysozyme solution at φ_{DMSO} = 0.8 after subtraction of incoherent background as indicated.

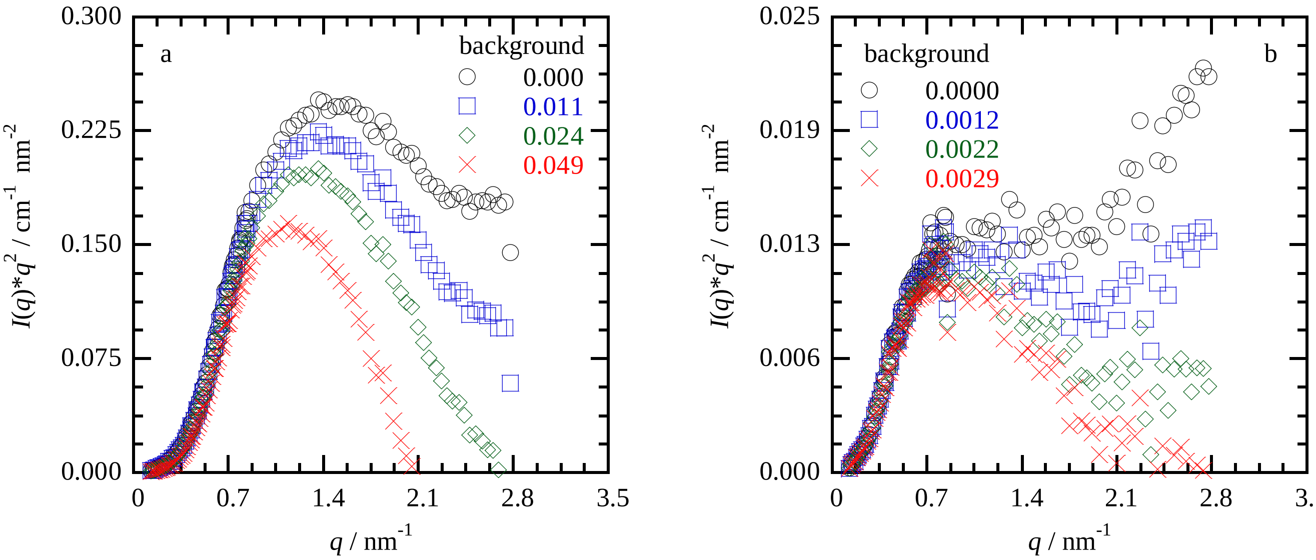

Figure S2. Kratky representations ($I(q)\cdot q^2$ versus q) for a (a) 30 g l^{-1} lysozyme solution at φ_{DMSO} = 0 and a (b) 10 g l^{-1} lysozyme solution at φ_{DMSO} = 0.8 after subtraction of incoherent background as indicated.

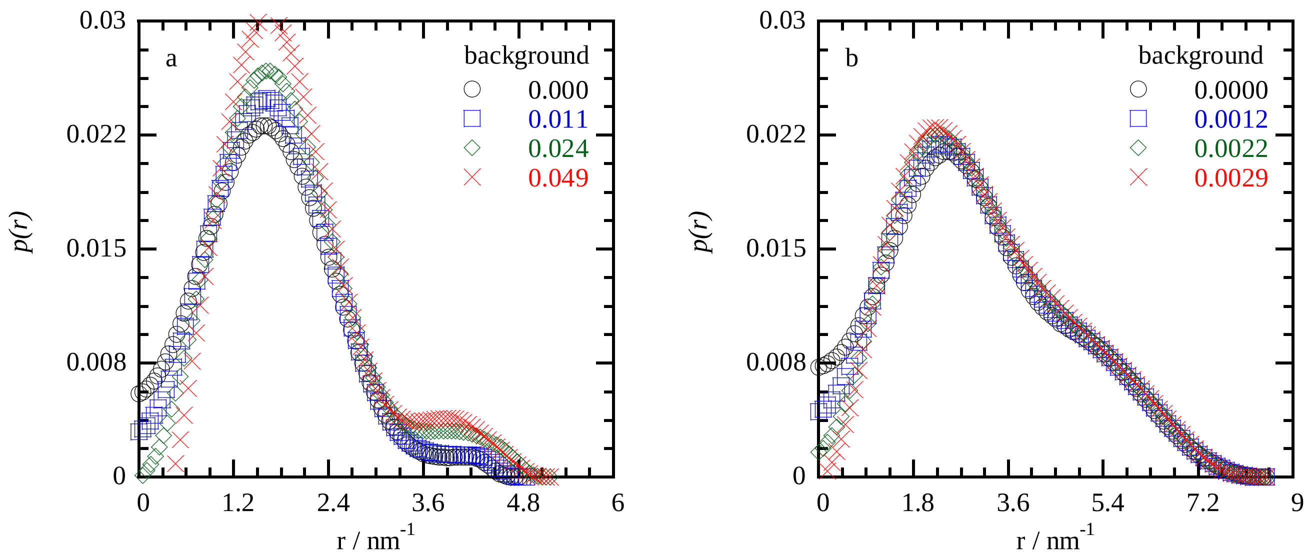

Figure S3. Pair distance distribution functions, $p(r)$ for a (a) 30 g l^{-1} lysozyme solution at φ_{DMSO} = 0 and a (b) 10 g l^{-1} lysozyme solution at φ_{DMSO} = 0.8 after subtraction of incoherent background as indicated. The curves have been normalised to a total area of 1.

2 Input values for light and neutron scattering

Table S1: Refractive indices of the sample, n_{sample}, and the specific refractive index increment of the sample, $\frac{dn}{dC}$ as a function of the DMSO volume fraction, φ_{DMSO}, for lysozyme concentrations, C_{LYS} = 9.1 – 9.5 g l^{-1} used to calculate the values for S_{90} as depicted in Figures 2 and 7 in the main text. The scattering length density of lysozyme, $\rho_{lysozyme}$, and solvent, $\rho_{solvent}$ as a function of φ_{DMSO} used to determine the measured molecular weight of lysozyme in Table 1 in the main text.

φ_{DMSO}	n_{sample}	$\frac{dn}{dC}$	$\rho_{lysozyme}$ / 10^{10} cm^{-2}	$\rho_{solvent}$ / 10^{10} cm^{-2}
0	1.3319	0.0001535	3.08	6.37

0.1	1.3490	0.0001465	3.08	6.26
0.2	1.3656	0.0001388	3.08	6.15
0.3	1.3816	0.0001307	3.08	6.04
0.4	1.3969	0.0001221	3.08	5.92
0.5	1.4099	0.0001129	3.08	5.81
0.6	1.4255	0.0001037	3.08	5.70
0.7	1.4396	0.0000965	3.49	5.59
0.8	1.4523	0.0000812	3.49	5.48
0.9	1.4635	0.0000648	3.49	5.37
1.0	1.4732	0.0000644	1.93	5.26