Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.

Hydration dynamics of proteins in reverse micelles probed by ^{1}H-NOESY/^{1}H-ROESY NMR and ^{17}O-Nuclear Quadrupole Resonance (NQR)

Supplementary Information

Philipp Honegger and Othmar Steinhauser

1 Detailed NQR relaxation times

Table S1: Relaxation times of water rotational dynamics derived from the second Legendre polynomial time correlation function. This relaxation times are resolved with respect to the dual shell membership - surfactant and protein - as well as the three different rotational axes displayed in Fig. 2 in the main article.

system	**shell$_{RM}$**	**shell$_{UBQ}$**	τ_{ortho} /ps	τ_{HH} /ps	τ_{dipole} /ps
unscaled	1	1	202	226	247
		2	11.7	12.6	14.7
		3	5.1	6.8	7.1
		4	3.6	4.7	4.8
	2	1	37.4	43.4	41.7
		2	1.9	2.8	2.5
		3	1.6	2.4	2.2
		4	1.7	2.4	2.2
	3	1	20.8	26.3	22.2
		2	1.6	2.5	2.1
		3	1.4	2.2	1.9
		4	1.4	2.2	1.8
	4	1	8.3	9.8	8.5
		2	1.6	2.5	2.0
		3	1.4	2.2	1.8
		4	1.4	2.2	1.8
half-scaled	1	1	194	200	219
		2	12.2	14.3	15.7
		3	5.1	6.9	7.1
		4	3.4	4.6	4.6
	2	1	51	59	62
		2	1.9	2.7	2.5
		3	1.6	2.4	2.2
		4	1.7	2.4	2.2
	3	1	15.9	18.6	16.4
		2	1.6	2.5	2.1
		3	1.4	2.2	1.8
		4	1.4	2.2	1.8
	4	1	9.2	10.4	9.8
		2	1.6	2.5	2.0
		3	1.4	2.2	1.8
		4	1.4	2.2	1.8
fully scaled	1	1	146	151	171
		2	10.4	12.5	14.2
		3	5.1	6.8	7.0
		4	3.6	4.8	4.8
	2	1	41	45	46
		2	1.9	2.7	2.4
		3	1.6	2.4	2.1
		4	1.7	2.4	2.2
	3	1	17.1	20.6	18.1
		2	1.6	2.5	2.1
		3	1.4	2.2	1.9
		4	1.4	2.3	1.9
	4	1	11	12.7	11.4
		2	1.6	2.5	2.1
		3	1.4	2.2	1.8
		4	1.3	2.2	1.8

2 Correlation of NOE/ROE and residence times

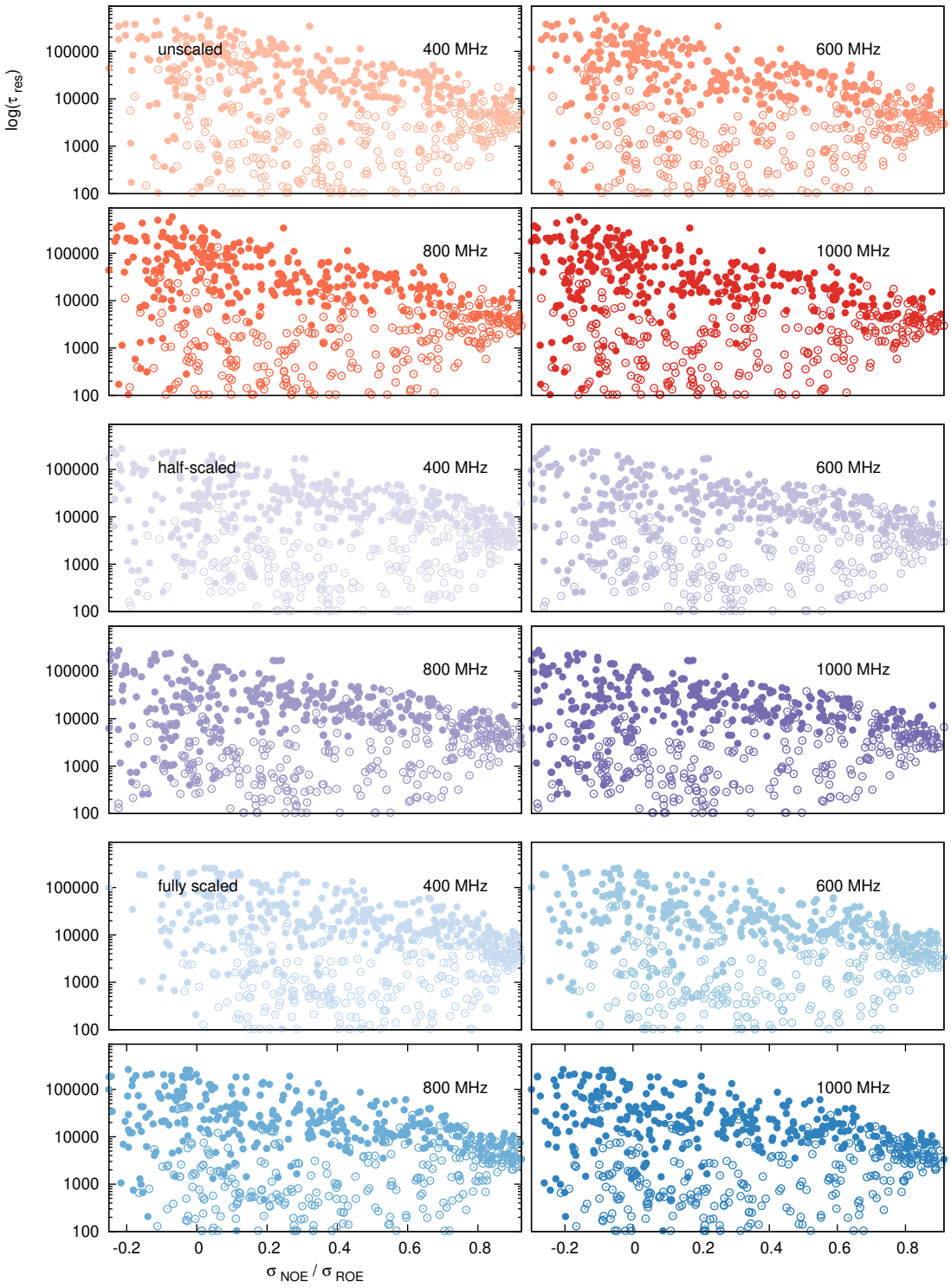

Figure S1: Correlation plots of the NOE to ROE ratio at four typical spectrometer frequencies for all protein hydrogen atoms versus the logarithmic residence time of each atom. While the surface protons are marked as full circles, the non-surface ones are marked as open circles. Note that correlation is only found for surface protons interacting with water directly. Furthermore, this correlation holds true both for the unscaled system (top four panels, red), the half-scaled system (middle four panels, purple) and the fully scaled system (bottom four panels, blue).

3 λ-scaling

In the frame of this project, λ-scaling was performed on protein-water non-binding, non-electrostatic potentials as described originally by Best, Mittal *et al.* [1]:

$$U_{\text{Lennard-Jones}}(r_{ij}) = 4\epsilon_{ij}\left\{\left(\frac{\sigma_{ij}}{r_{ij}}\right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}}\right)^{6}\right\} \quad (1)$$

$$U^{\text{scaled}}_{\text{Lennard-Jones}}(r_{ij}) = \lambda\, U_{\text{Lennard-Jones}}(r_{ij}) \quad (2)$$

with i and j as the water and protein atom types in question, σ_{ij} determining the distance of repulsion and ϵ_{ij} determining the potential well depth. Technically, CHARMM does not store pair-wise parameters σ_{ij} and ϵ_{ij} persistently, but creates them on-the-fly upon force field construction during simulation initialization from atom type parameters σ_i, σ_j and ϵ_i, ϵ_j using the Lorentz-Berthelot relations

$$\sigma_{ij} = (\sigma_i + \sigma_j)\frac{1}{2} \quad (3)$$

$$\epsilon_{ij} = (\epsilon_i \cdot \epsilon_j)^{\frac{1}{2}} \quad (4)$$

These pair-wise parameters were then changed to previously calculated, scaled values using NBFIX commands summarized in the tables below.

Table S2: NBFIX commands for the half-scaled system (λ_{protein} = 1.1, $\lambda_{\text{surfactant}}$ = 1)

atom type 1	**atom type 2**	ϵ	σ
OT	C	-0.142283	3.777
OT	CA	-0.113503	3.7694
OT	CC	-0.113503	3.777
OT	CD	-0.113503	3.777
OT	CE1	-0.11187	3.867
OT	CE2	-0.108529	3.857
OT	CP1	-0.06067	4.052
OT	CP2	-0.100609	3.952
OT	CP3	-0.100609	3.952
OT	CPH1	-0.095927	3.577
OT	CPH2	-0.095927	3.577
OT	CS	-0.142283	3.977
OT	CPT	-0.134982	3.637
OT	CY	-0.115909	3.767
OT	CAI	-0.115909	3.767
OT	CT	-0.06067	4.052
OT	CT1	-0.076742	3.777
OT	CT2	-0.10152	3.787
OT	CT2A	-0.10152	3.787
OT	CT3	-0.119813	3.817
OT	H	-0.09201	2.0015
OT	HA	-0.063631	3.097
OT	HB1	-0.063631	3.097
OT	HB2	-0.071785	3.117
OT	HE1	-0.075533	3.027
OT	HE2	-0.069174	3.037
OT	HB	-0.063631	3.097
OT	HC	-0.09201	2.0015
OT	HP	-0.074305	3.1352
OT	HR1	-0.09201	2.677
OT	HR2	-0.09201	2.477
OT	HR3	-0.037888	3.245

OT	HS	-0.135662	2.227
OT	HA1	-0.091005	3.117
OT	HA2	-0.079104	3.117
OT	HA3	-0.06646	3.117
OT	N	-0.191855	3.627
OT	NC2	-0.191855	3.627
OT	NH1	-0.191855	3.627
OT	NH2	-0.191855	3.627
OT	NH3	-0.191855	3.627
OT	NP	-0.191855	3.627
OT	NR1	-0.191855	3.627
OT	NR2	-0.191855	3.627
OT	NR3	-0.191855	3.627
OT	NY	-0.191855	3.627
OT	O	-0.14861	3.477
OT	OB	-0.14861	3.477
OT	OC	-0.14861	3.477
OT	OH1	-0.16731	3.547
OT	OS	-0.16731	3.547
OT	S	-0.287782	3.777
OT	SM	-0.264453	3.752
OT	SS	-0.294108	3.97

Table S3: NBFIX commands for the fully scaled system ($\lambda_{\text{protein}} = 1.1$, $\lambda_{\text{surfactant}} = 1.1$)

atom type 1	**atom type 2**	ϵ	σ
OT	C	-0.142283	3.777
OT	CA	-0.113503	3.7694
OT	CC	-0.113503	3.777
OT	CD	-0.113503	3.777
OT	CE1	-0.11187	3.867
OT	CE2	-0.108529	3.857
OT	CP1	-0.06067	4.052
OT	CP2	-0.100609	3.952
OT	CP3	-0.100609	3.952
OT	CPH1	-0.095927	3.577
OT	CPH2	-0.095927	3.577
OT	CS	-0.142283	3.977
OT	CPT	-0.134982	3.637
OT	CY	-0.115909	3.767
OT	CAI	-0.115909	3.767
OT	CT	-0.06067	4.052
OT	CT1	-0.076742	3.777
OT	CT2	-0.10152	3.787
OT	CT2A	-0.10152	3.787
OT	CT3	-0.119813	3.817
OT	H	-0.09201	2.0015
OT	HA	-0.063631	3.097
OT	HB1	-0.063631	3.097
OT	HB2	-0.071785	3.117
OT	HE1	-0.075533	3.027
OT	HE2	-0.069174	3.037
OT	HB	-0.063631	3.097
OT	HC	-0.09201	2.0015
OT	HP	-0.074305	3.1352

OT	HR1	-0.09201	2.677
OT	HR2	-0.09201	2.477
OT	HR3	-0.037888	3.245
OT	HS	-0.135662	2.227
OT	HA1	-0.091005	3.117
OT	HA2	-0.079104	3.117
OT	HA3	-0.06646	3.117
OT	N	-0.191855	3.627
OT	NC2	-0.191855	3.627
OT	NH1	-0.191855	3.627
OT	NH2	-0.191855	3.627
OT	NH3	-0.191855	3.627
OT	NP	-0.191855	3.627
OT	NR1	-0.191855	3.627
OT	NR2	-0.191855	3.627
OT	NR3	-0.191855	3.627
OT	NY	-0.191855	3.627
OT	O	-0.14861	3.477
OT	OB	-0.14861	3.477
OT	OC	-0.14861	3.477
OT	OH1	-0.16731	3.547
OT	OS	-0.16731	3.547
OT	S	-0.287782	3.777
OT	SM	-0.264453	3.752
OT	SS	-0.294108	3.97
OT	CH1	-0.064607	4.5938
OT	CH2	-0.134374	4.0612
OT	CH3	-0.19531	3.8805
OT	CL	-0.113503	3.777
OT	CTL1	-0.06067	4.052
OT	CTL2	-0.10152	3.787
OT	HAL1	-0.063631	3.097
OT	HAL2	-0.071785	3.117
OT	O2L	-0.14861	3.477
OT	OBL	-0.14861	3.477
OT	OSL	-0.135662	3.427
OT	SL	-0.294108	3.877

References

[1] R. B. Best, W. Zheng and J. Mittal, *J. Chem. Theory Comput.*, 2014, **10**, 5113–5124.