Table 1. Experimental and calculated rotational diffusion coefficients for 16 monomeric proteins in H_2O at 20°C

Protein	M_P	PDB	D_R^{SE}	D_R^{calc}	D_R^{expt}	A^{calc}	Ref.
Bovine pancreatic trypsin inhibitor	6.50	6pti	85.4	38.2	42.5	1.32	1
Calbindin D_{9k}, holo form	8.48	1ig5	65.5	33.7	32.9	1.11	2
Human ubiquitin	8.55	1ubq	65.0	28.7	34.6	1.40	3
Ferricytochrome c_{551}	8.68	351c	64.0	33.5	31.6	0.94	4
Plastocyanin, Cu(II) form	10.30	1pcs	53.9	28.8	27.5	1.29	5
Oncogenic protein $p13^{MTCP1}$	12.60	1a1x	44.1	19.3	17.0	1.15	6
Binase	12.94	1gou	42.9	22.0	21.5	1.27	7
Ribonuclease A	13.67	1aqp	40.6	19.3	22.1	1.32	8
Azurin, Cu(I) form	13.93	1e5y	39.9	19.8	21.6	1.29	9
Response regulator Spo0F	14.21	4nat	39.1	21.6	20.2	0.89	10
Hen egg-white lysozyme	14.30	1bwi	38.8	20.1	20.2	1.42	11
Epidermal fatty acid-binding protein	15.15	1b56	36.7	18.8	17.3	1.14	12
Dihydrofolate reductase, folate complex	18.00	1dyi	30.9	15.5	16.7	1.18	13
Bovine β-lactoglobulin, monomer	18.26	1b8e	30.4	15.2	15.2	0.93	14
Adenylate kinase, apo form	23.57	4ake	23.6	9.15	8.62	1.40	15
Savinase	26.68	1svn	20.8	12.7	13.5	1.07	16

M_P is the molar mass in kg mol^{-1}. All rotational diffusion coefficient (D_R) values are given in units of μs^{-1}. D_R^{SE} (SE, Stokes–Einstein) was calculated from Eq. **1** with the partial protein volume obtained from M_P and a specific volume of 0.73 cm^3 g^{-1}, D_R^{calc} was calculated by HYDROPRO with $\sigma_H = 0.30$ nm and atomic coordinates from the quoted Protein Data Bank (PDB) crystal structure, and D_R^{expt} was derived from ^{15}N relaxation data as reported in the quoted references. A^{calc} is the calculated rotational anisotropy, as defined in the text.

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